

1312	septation ring formation regulator EzrA
1320	hydrolase, haloacid dehalogenase-like family (gph)
1340	sensor histidine kinase (vncS)
1348	transmembrane protein Vexp3 (vex3)
1352	ABC transporter, ATP-binding protein (vex2)
1358	transmembrane protein Vexp1 (vex1)
1366	transposase
1374	integrase, phage family
1390	holin 2
1398	minor structural protein
1400	host specificity protein
1404	minor structural protein
1406	Pbla
1486	homeobox protein drg11
1488	reverse transcriptase
1496	p22 erf-like protein
1498	gp157
1500	tropomyosin 2
1512	gp49 homologous
1526	transcriptional regulator-related protein
1566	chorismate mutase
1572	PTS system component
1576	PTS system, IIB component
1580	PTS system IIA component
1584	lactose phosphotransferase system repressor (lacR)
1594	adhesion lipoprotein (lmb)
1602	GTP pyrophosphokinase (relA)
1606	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)
1616	iron ABC transporter, iron-binding protein
1620	DNA-binding response regulator
1630	PTS system component
1634	PTS system component (manM)
1638	PTS system component (manL)
1642	PTS system component
1658	response regulator BlpR (blpR)
1676	phosphate transport system regulatory protein PhoU
1680	phosphate ABC transporter, ATP-binding protein (pstB)
1684	phosphate ABC transporter, permease protein (pstA)
1690	phosphate ABC transporter, permease protein (pstC)
1694	probable hemolysin precursor
1704	ribosomal protein L11 methyltransferase (prmA)
1710	transcriptional regulator, MerR family (skgA)
1714	acetyltransferase, GNAT family
1716	MutT/nudix family protein
1722	spermidine N1-acetyltransferase
1726	ATPase, AAA family
1736	ABC transporter domain protein
1738	Helix-turn-helix domain protein
1748	integrase, phage family
1756	Helix-turn-helix domain protein
1762	bacteriophage L54a, integrase
1768	LPXTG-motif cell wall anchor domain protein
1776	membrane protein
1778	conjugal transfer protein
1780	IS1381, transposase OrfA/OrfB, truncation
1802	transcriptional regulator (rstR-1)
1806	transcriptional regulator
1808	FtsK/SpoIIIE family protein
1814	aggregation substance

1818	mercuric reductase
1822	transcriptional regulator, MerR family
1824	Mn2+/Fe2+ transporter, NRAMP family
1830	ABC transporter, ATP-binding protein (epiF)
1848	Helix-turn-helix domain protein
1850	type 2 phosphatidic acid phosphatase(PAP2), family
1858	Abortive infection protein family
1868	aminotransferase, class-V
1874	glutathione reductase (gor)
1882	chorismate synthase (aroC)
1886	3-dehydroquinate synthase (aroB)
1900	sulfatase family protein
1914	ABC transporter, ATP-binding protein
1920	smf protein (Smffamily)
1924	transferrin receptor
1928	iron compound ABC transporter, ATP-binding protein
1932	iron compound ABC transporter, permease protein
1942	acetyltransferase, CysE/LacA/LpxA/NodL family
1952	GTP-binding protein
1958	carbon starvation protein A
1960	response regulator (lytR)
1962	GAF domain protein (lytS)
2000	extracellular protein
2004	diarrheal toxin (yukA)
2024	carbamoyl-phosphate synthase, large subunit (carB)
2028	carbamoyl-phosphate synthase, small subunit (carA)
2032	aspartate carbamoyltransferase (pyrB)
2036	dihydroorotate, multifunctional complex type (pyrC)
2040	orotate phosphoribosyltransferase (pyrE)
2048	membrane protein
2062	phosphate ABC transporter, permease protein (pstA-2)
2064	phosphate ABC transporter, ATP-binding protein (pstB)
2070	phosphate transport system regulatory protein PhoU
2072	aminopeptidase N (pepN)
2076	DNA-binding response regulator (arlR)
2080	sensor histidine kinase (arlS)
2088	signal recognition particle protein (ffh)
2102	peptide ABC transporter, peptide-binding protein
2104	integrase/recombinase, phage integrase family
2108	sensor histidine kinase
2112	DNA-binding response regulator (vicR)
2118	ABC transporter, ATP-binding protein
2122	nisin-resistance protein
2130	lipoprotein
2136	gid protein (gid)
2140	transcriptional regulator, GntR family
2142	GMP synthase (guaA)
2152	branched-chain amino acid ABC transporter, permease protein (livM)
2154	branched-chain amino acid ABC transporter, ATP-binding protein (livG)
2156	branched-chain amino acid ABC transporter, ATP-binding protein (livF)
2160	acetoin utilization protein AcuB
2174	DNA polymerase III, delta prime subunit (holB)
2186	copper homeostasis protein (cutC)
2190	phosphoserine aminotransferase (serC)
2202	methylated-DNA-protein-cysteine S-methyltransferase (ogt)
2208	exodeoxyribonuclease III (xth)
2214	PTS system, IIC component
2224	tellurite resistance protein TehB (tehB)
2246	icaA protein

2250	acetyltransferase, GNAT family
2258	oxidoreductase, short chain dehydrogenase/reductase family (fabG)
2266	oxidoreductase, Gfo/Idh/MocA family family
2268	glyoxalase family protein
2272	UDP-N-acetylglucosamine pyrophosphorylase (glmU)
2276	MutT/nudix family protein
2284	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase (mtf)
2296	phosphatidate cytidylyltransferase (cdsA)
2300	membrane-associated zinc metalloprotease
2308	autolysin (flgJ)
2312	DNA polymerase III, alpha subunit, Gram-positive type
2320	nitroreductase family protein superfamily
2326	4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldo
2328	carbohydrate kinase, PfkB family
2336	oxidoreductase, short chain dehydrogenase/reductase family (fabG)
2338	PTS system, IIA component (manL)
2342	glucuronyl hydrolase
2346	PTS system, IIB component (manL)
2350	PTS system, IIC component (manM)
2364	sugar binding transcriptional regulator RegR (regR)
2368	polypeptide deformylase (def)
2380	oxidoreductase, Gfo/Idh/MocA family
2382	endopeptidase O (pepO)
2394	Na+/H+ antiporter
2404	transcriptional regulator
2410	replication initiation protein RepRC
2412	bacteriophage L54a, antirepressor
2416	e11
2422	replicative DNA helicase (dnaB)
2432	GTP-binding protein
2440	arpR protein
2444	gene 17 protein
2458	integrase/recombinase, phage integrase family
2468	bacteriophage L54a, phage D3 terminase
2472	protease
2500	PblB
2504	sensor histidine kinase
2514	N-acetylmuramoy-L-alanine amidase
2518	KH domain protein
2522	ribosomal protein S16 (rpsP)
2526	permease
2528	ABC transporter, ATP-binding protein
2538	carbamoyl-phosphate synthase, large subunit
2540	carbamoyl-phosphate synthase, small subunit (carA)
2550	transcriptional regulator, LysR family
2554	ribosomal protein L27 (rpmA)
2562	ribosomal protein L21 (rplU)
2572	glycerophosphoryl diester phosphodiesterase
2582	nitroreductase family protein
2586	dipeptidase (pepV)
2614	GTP-binding protein HflX (hflX)
2618	galactose-1-phosphate uridylyltransferase (galT)
2626	oxidoreductase, short chain dehydrogenase/reductase family
2630	single-stranded-DNA-specific exonuclease RecJ (recJ)
2638	adenine phosphoribosyltransferase (apt)
2646	Bcl-2 family protein
2654	oxidoreductase, DadA family protein
2658	glucose-1-phosphate thymidyltransferase (rfbA)
2664	dTDP-4-dehydrorhamnose 3,5-epimerase (rfbC)

2682	hyaluronidase
2686	mutator MutT protein (mutX)
2690	MutT/nudix family protein
2694	membrane protein
2702	acetolactate synthase (ilvK)
2706	adherence and virulence protein A (pavA)
2714	ABC transporter, permease protein (rbsC)
2722	metallo-beta-lactamase superfamily protein
2734	ribose 5-phosphate isomerase (rpiA)
2738	phosphopentomutase (deoB)
2742	purine nucleoside phosphorylase, family 2 (deoD)
2750	purine nucleoside phosphorylase (deoD)
2762	capsular polysaccharide biosynthesis protein Cps4A (cps4A)
2768	cpsb protein
2770	cpsc protein
2772	CpsE
2774	CpsF
2776	CpsVG
2778	CpsVH
2780	CpsVM
2782	CpsVN
2784	glycosyl transferase domain protein
2786	glycosyl transferase, family 2/glycosyl transferase family 8
2790	CpsVK
2794	CpsL
2796	neuB protein
2798	UDP-N-acetylglucosamine 2-epimerase
2800	hexapeptide transferase family protein
2802	NeuA
2808	uracil-DNA glycosylase (ung)
2818	DNA topoisomerase IV, B subunit (parE)
2822	DNA topoisomerase IV, A subunit (parC)
2826	branched-chain amino acid aminotransferase (ilvE)
2842	glycerol kinase (glpK)
2848	aerobic glycerol-3-phosphate dehydrogenase (glpD)
2874	ABC transporter, ATP-binding protein
2882	PTS system component (bglP)
2886	glutamate 5-kinase (proB)
2890	gamma-glutamyl phosphate reductase (proA)
2898	cell division protein FtsL (ftsL)
2904	penicillin-binding protein 2X (pbpX)
2910	phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)
2914	ATP-dependent RNA helicase, DEAD/DEAH box family (deaD)
2918	ABC transporter, substrate-binding protein
2924	amino acid ABC transporter, permease protein
2928	amino acid ABC transporter, ATP-binding protein
2932	thioredoxin reductase (trxR)
2940	NAD+ synthetase (nadE)
2944	aminopeptidase C (pepC)
2952	recombination protein U (recU)
2966	Uncharacterized protein family UPF0020 family
2974	autoinducer-2 production protein LuxS (luxS)
2978	KH domain protein
2986	ABC transporter, ATP-binding protein
2994	DNA-binding response regulator (vraR)
3000	guanylate kinase (gmk)
3004	DNA-directed RNA polymerase, omega subunit
3008	primosomal protein N (priA)
3012	methionyl-tRNA formyltransferase (frm)

3016	Sun protein (sun)
3020	protein phosphatase 2C
3032	sensor histidine kinase
3034	DNA-binding response regulator (vraR)
3036	cof family protein/peptidyl-prolyl cis-trans isomerase, cyclophilin typ
3040	S1 RNA binding domain protein (rpsA)
3044	pyruvate formate-lyase-activating enzyme
3062	PTS system, IIB component (celA)
3066	PTS system, cellobiose-specific IIC component (celB)
3068	formate acetyltransferase (pfl)
3072	transaldolase
3080	cysteine synthase A (cysK)
3088	comF operon protein 1 (comFA)
3092	competence protein ComF
3096	ribosomal subunit interface protein (yfiA)
3104	tryptophanyl-tRNA synthetase (trpS)
3108	carbamate kinase (arcC)
3116	ornithine carbamoyltransferase (argF)
3124	arginine deiminase (arcA)
3134	transcriptional regulator, Crp/Fnr family
3138	inosine-5'-monophosphate dehydrogenase (guaB)
3140	MutR
3142	transporter
3146	recF protein (recF)
3158	peptidase, M16 family
3166	ABC transporter, ATP-binding protein
3170	ABC transporter, ATP-binding protein
3178	LysM domain protein (lytN)
3180	immunodominant antigen A (isaA)
3184	L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA)
3188	L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB)
3202	DHH subfamily 1 protein
3206	ribosomal protein L9 (rplI)
3210	replicative DNA helicase (dnaB)
3216	ribosomal protein S4 (rpsD)
3224	transcriptional regulator, TetR family
3236	membrane protein
3238	choline transporter (proWX)
3240	glycine betaine/L-proline transport ATP binding subunit (proV)
3242	DNA-binding response regulator
3244	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family
3246	ornithine carbamoyltransferase (argF)
3248	carbamate kinase (arcC)
3252	membrane protein
3256	sensory box histidine kinase Vick
3258	DNA-binding response regulator
3268	Helix-turn-helix domain protein
3278	integrase
3284	ribosomal protein L33 (rpmG)
3288	ribosomal protein L32 (rpmF)
3300	YitT family protein
3304	YitT family protein
3320	DNA mismatch repair protein MutS (mutS)
3324	cold-shock domain family protein-related protein
3336	drug transporter
3340	Holliday junction DNA helicase RuvA (rvuA)
3352	recA protein (recA)
3386	oxidoreductase, Gfo/Idh/MocA family
3390	acetyltransferase, GNAT family

3394	anaerobic ribonucleoside-triphosphate reductase activating protein (nrd)
3412	ABC transporter, permease protein (rbsC)
3414	ABC transporter, ATP-binding protein (nrtC)
3416	PTS system, mannose-specific IIAB components (manL)
3420	Cof family protein
3432	xanthine/uracil permease family protein
3440	acetyltransferase, GNAT family
3442	transcriptional regulator (cps4A)
3448	HIT family protein (hit)
3460	ABC transporter, permease protein
3472	Uncharacterized BCR, YhbC family COG0779 superfamily
3484	ribosomal protein L7A family
3496	esterase
3500	transcriptional repressor, CopY (copY)
3504	cation-transporting ATPase, E1-E2 family
3508	cation-binding protein-related protein
3520	DNA polymerase I (polA)
3534	DNA-binding response regulator (saeR)
3536	sensor histidine kinase (saeS)
3562	drug resistance transporter, EmrB/QacA subfamily
3566	peptidase M24 family protein
3570	peptidase M24 family protein (pepQ)
3572	cytidine/deoxycytidylate deaminase family protein
3584	translation elongation factor P (efp)
3592	N utilization substance protein B (nusB)
3596	sugar-binding transcriptional regulator, LacI family (scrR)
3600	sucrose-6-phosphate dehydrogenase (scrB)
3606	PTS system IIABC components (scrA)
3610	fructokinase (scrK)
3614	mannose-6-phosphate isomerase, class I (manA)
3622	phospho-2-dehydro-3-deoxyheptonate aldolase (aroH)
3626	holo-(acyl-carrier-protein) synthase (acpS)
3630	alanine racemase (alr)
3634	autolysin (usp45)
3636	ATP-dependent DNA helicase RecG (recG)
3642	shikimate 5-dehydrogenase (aroE)
3652	Cof family protein
3668	ferredoxin-related protein
3676	peptidase t (pepT)
3684	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (mur
3692	iron compound ABC transporter, substrate-binding protein
3698	FecCD transport family protein (sirB)
3704	iron compound ABC transporter, permease protein (sirB)
3710	inorganic pyrophosphatase, manganese-dependent (ppaC)
3714	pyruvate formate-lyase-activating enzyme (pfLA)
3718	CBS domain protein
3730	acid phosphatase
3736	LPXTG-motif cell wall anchor domain protein
3738	LPXTG-site transpeptidase family protein
3742	LPXTG-site transpeptidase family protein
3744	cell wall surface anchor family protein
3746	cell wall surface anchor family protein
3752	glycosyl transferase, group 1 family protein domain protein
3754	EpsQ protein
3756	polysaccharide extrusion protein
3768	dTDP-glucose 4-6-dehydratase
3782	glycosyl transferase domain protein
3788	dTDP-4-dehydrorhamnose reductase (rfbD)
3796	RNA polymerase sigma-70 factor (rpoD)

3802	DNA primase (dnaG)
3816	ABC transporter, ATP-binding protein Vexp2 (vex2)
3818	permease
3820	transmembrane protein Vexp3
3822	transmembrane protein Vexp3
3832	endopeptidase O (pepO)
3834	endopeptidase O (pepO)
3840	serine protease, subtilase family
3842	exotoxin 2
3844	CylK
3854	glycine cleavage system T protein
3856	CylE
3858	ABC transporter homolog CylB
3862	acyl carrier protein homolog AcpC (acpP)
3864	3-oxoacyl-(acyl-carrier-protein) reductase (fabG)
3868	CylD
3876	membrane protein
3912	LPXTG-site transpeptidase family protein
3916	LPXTG-site transpeptidase family protein
3918	LPXTG-site transpeptidase family protein
3920	LPXTG-motif cell wall anchor domain protein
3928	chaperonin, 33 kDa (hsIO)
3932	Tn5252, Orf 10 protein
3934	transposase OrfAB, subunit B
3948	psr protein
3952	shikimate kinase (aroK)
3964	enolase (eno)
3972	MutT/nudix family protein
3976	glycosyl transferase, group 1
3978	preprotein translocase, SecA subunit (secA)
3986	preprotein translocase SecY family protein
3990	glycosyl transferase, family 8
3992	glycosyl transferase, family 2
3998	glycosyl transferase, family 8
4000	glycosyl transferase, family 2/glycosyl transferase family 8
4002	glycosyl transferase, family 8
4012	LPXTG-motif cell wall anchor domain protein (clfB)
4016	transcriptional regulator
4018	excinuclease ABC, B subunit (uvrB)
4022	Abortive infection protein family
4024	amino acid ABC transporter, amino acid-binding protein/permease protein
4026	amino acid ABC transporter, ATP-binding protein
4034	GTP-binding protein, GTP1/Obg family (obg)
4042	aminopeptidase PepS (pepS)
4050	ribosomal small subunit pseudouridine synthase A (rsuA)
4060	lactoylglutathione lyase (gloA)
4064	glycosyl transferase family protein
4072	alkylphosphonate utilization operon protein PhnA (phnA)
4078	glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (glmS)
4090	Phosphofructokinase
4094	DNA polymerase III, alpha subunit (dnaE)
4098	transcriptional regulator, GntR family
4102	ABC transporter, ATP-binding protein
4106	ABC transporter, ATP-binding protein
4116	FtsK/SpoIIIE family protein
4122	Helix-turn-helix domain protein
4152	Helix-turn-helix domain protein
4158	excisionase
4160	transposase

4166	chloramphenicol acetyltransferase (cat)
4174	PilB-related protein
4178	acetyltransferase
4182	Leucine Rich Repeat domain protein
4190	nucleoside diphosphate kinase (ndk)
4206	Protein of unknown function superfamily
4218	hydrolase, haloacid dehalogenase-like family (pho2)
4226	oxygen-independent coproporphyrinogen III oxidase
4236	phosphoglucomutase/phosphomannomutase family protein (femD)
4240	Gram-positive signal peptide, YSIRK family domain protein
4256	cobyrinic acid synthase (cobQ)
4260	lipoate-protein ligase A (lplA)
4264	branched-chain alpha-keto acid dehydrogenase E3 component, lipoamide de
4266	pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltr
4270	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase be
4286	magnesium transporter, CorA family
4294	exonuclease RexB (rexB)
4302	phenylalanyl-tRNA synthetase, beta subunit (pheT)
4324	ATP synthase F1, epsilon subunit (atpC)
4328	ATP synthase F1, beta subunit (atpD)
4332	ATP synthase F1, gamma subunit (atpG)
4338	ATP synthase F1, alpha subunit (atpA)
4342	ATP synthase F1, delta subunit (atpH)
4346	ATP synthase F0, B subunit (atpF)
4350	ATP synthase, F0 subunit A (atpB)
4354	proton-translocating ATPase, c subunit-related protein
4360	glycogen synthase (glgA)
4362	glycogen biosynthesis protein GlgD (glgD)
4366	1,4-alpha-glucan branching enzyme (glgB)
4368	pullulanase
4382	ribonuclease BN
4396	acetyltransferase, GNAT family
4398	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
4402	thiamine-phosphate pyrophosphorylase (thiE)
4406	phosphomethylpyrimidine kinase (thiD)
4410	transcriptional regulator, Deg family (tenA)
4414	ABC transporter, ATP-binding protein
4426	S-adenosylmethionine synthetase (metK)
4440	DNA polymerase III, gamma and tau subunits (dnaX)
4444	GAF domain protein
4448	uridine kinase (udk)
4452	ATP-dependent RNA helicase, DEAD/DEAH box family
4458	peptidoglycan GlcNAc deacetylase (pgdA)
4462	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN)
4466	phosphoenolpyruvate-protein phosphotransferase (ptsI)
4470	phosphocarrier protein hpr
4474	NrdH-redoxin-related protein
4478	ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
4498	glycosyl transferase, family 8
4504	alanyl-tRNA synthetase (alaS)
4512	alkyl hydroperoxide reductase, subunit F (ahpF)
4516	alkyl hydroperoxide reductase, subunit C (ahpC)
4520	ribosomal protein S2 (rpsB)
4524	translation elongation factor Ts (tsf)
4532	transcriptional regulator CtsR (ctsR)
4536	ATP-dependent Clp protease, ATP-binding subunit (clpC)
4540	deoxyribonucleoside kinase
4544	NifR3/Smm1 family protein
4548	chaperonin, 33 kDa (hsIO)

4558	glutamate-cysteine ligase (gshA)
4562	Helix-turn-helix domain, fis-type protein
4566	perfringolysin O regulator protein (pfoR)
4570	adenylosuccinate synthetase (purA)
4578	SgaT protein (sgaT)
4582	PTS system, IIB component (sgaT)
4586	PTS system, IIA component (mtlA)
4590	hexulose-6-phosphate synthase
4594	hexulose-6-phosphate isomerase
4598	L-ribulose-5-phosphate 4-epimerase (araD)
4606	sugar binding transcriptional regulator RegR
4610	D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA)
4622	transcriptional regulator, BglG family
4632	glycine betaine/L-proline transport ATP binding subunit (proV)
4636	amino acid ABC transporter, permease protein
4644	Na ⁺ /H ⁺ exchanger family protein (kefB)
4648	glyoxylase family protein
4652	LPXTG-site transpeptidase family protein
4656	DNA gyrase, A subunit (gyrA)
4660	L-lactate dehydrogenase (ldh)
4664	NADH oxidase (nox)
4680	lipoprotein (bmpD)
4690	pantothenate kinase (coaA)
4694	ribosomal protein S20 (rpsT)
4698	amino acid ABC transporter, amino acid-binding protein (aatB)
4702	amino acid ABC transporter, ATP-binding protein
4726	ribosomal large subunit pseudouridine synthase B (rluB)
4734	Uncharacterized ACR, COG1354
4738	integrase/recombinase, phage integrase family (xerD)
4742	CBS domain protein
4746	phosphoesterase
4750	HAM1 protein
4768	transcriptional regulator, biotin repressor family
4792	amino acid ABC transporter, permease protein
4796	amino acid ABC transporter, substrate-binding protein
4798	6-aminohexanoate-cyclic-dimer hydrolase
4800	transcription elongation factor GreA (greA)
4804	Uncharacterized BCR, YceG family COG1559
4812	UDP-N-acetylmuramate-alanine ligase (murC)
4822	Snf2 family protein
4828	GTP-binding protein (b2511)
4832	primosomal protein Dnal (dnal)
4844	sensor histidine kinase (arlS)
4846	DNA-binding response regulator (arlR)
4852	heat shock protein HtpX (htpX)
4870	potassium uptake protein, Trk family
4874	ABC transporter, ATP-binding protein
4888	phosphoglycerate kinase (pgk)
4896	transcriptional regulator, MerR family
4900	glutamine synthetase, type I (glnA)
4904	secreted 45 kd protein (usp45)
4908	metallo-beta-lactamase superfamily protein
4916	glycoprotease family protein
4926	glycoprotease family protein (gcp)
4938	ribosomal protein S14p/S29e (rpsN)
4952	exonuclease (dnaQ)
4956	transcriptional regulator, merR family
4958	cyclopropane-fatty-acyl-phospholipid synthase (cfa)
4970	1,4-dihydroxy-2-naphthoate octaprenyltransferase (menA)

4972	pyridine nucleotide-disulphide oxidoreductase (ndh)
4974	cytochrome d oxidase, subunit I (cydA)
4976	cytochrome d ubiquinol oxidase, subunit II (cydB)
4980	transport ATP-binding protein CydD
4988	polyisoprenyl synthetase (ispB)
4990	X-pro dipeptidyl-peptidase (pepX)
4998	drug transporter
5002	universal stress protein family
5004	glycerol uptake facilitator protein (glpF)
5012	cppA protein (cppA)
5034	exodeoxyribonuclease V, alpha subunit (recD)
5038	Signal peptidase I
5042	ribonuclease HIII (rmhC)
5062	transcriptional regulator
5068	maltose ABC transporter, permease protein (malD)
5072	maltose ABC transporter, permease protein (malC)
5088	ABC transporter, ATP-binding protein
5092	ABC transporter, permease protein
5106	spspoJ protein (spo0J)
5114	DNA polymerase III, beta subunit (dnan)
5118	Diacylglycerol kinase catalytic domain (presumed) protein
5138	transcription-repair coupling factor (mfd)
5142	S4 domain protein
5156	MesJ/Ycf62 family protein
5160	hypoxanthine phosphoribosyltransferase (hpt)
5164	cell division protein FtsH (ftsH)
5172	hydrolase, haloacid dehalogenase-like family (b2690)
5178	transcriptional regulator, MarR family
5182	3-oxoacyl-(acyl-carrier-protein) synthase III (fabH)
5190	enoyl-(acyl-carrier-protein) reductase (fabK)
5194	malonyl CoA-acyl carrier protein transacylase (fabD)
5198	3-oxoacyl-[acyl-carrier protein] reductase (fabG)
5200	3-oxoacyl-(acyl-carrier-protein) synthase II (fabF)
5202	acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB)
5206	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
5210	acetyl-CoA carboxylase, biotin carboxylase (accC)
5214	acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD)
5218	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA)
5224	seryl-tRNA synthetase (serS)
5234	PTS system, mannose-specific IID component
5246	ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD)
5254	GTP pyrophosphokinase (relA)
5266	ribose-phosphate pyrophosphokinase (prsA)
5270	aminotransferase, class-V
5274	DNA-binding protein
5282	Domain of unknown function
5290	platelet activating factor
5296	transcriptional regulator, AraC family
5302	voltage-gated chloride channel family protein
5318	spermidine/putrescine ABC transporter, ATP-binding protein (potA)
5320	UDP-N-acetylenolpyruvylglucosamine reductase (murB)
5324	bifunctional folate synthesis protein (folK)
5328	dihydronopterin aldolase (folB)
5332	dihydropteroate synthase (folP)
5336	GTP cyclohydrolase I (folE)
5344	rarD protein (rarD)
5348	homoserine kinase (thrB)
5354	Polysaccharide deacetylase family (icaB)
5362	osmoprotectant transporter, BCCT family (opuD)

5384	thiol peroxidase (psaD)
5388	hydrolase
5390	transcriptional regulator, GntR family
5402	gls24 protein
5424	uncharacterized domain 1
5440	cation efflux family protein
5454	dihydroorotate dehydrogenase A (pyrDa)
5458	beta-lactam resistance factor (fibB)
5462	beta-lactam resistance factor (fibA)
5474	HD domain protein
5482	cation-transporting ATPase, E1-E2 family
5486	fructose-1,6-bisphosphatase (fbp)
5488	iron-sulfur cluster-binding protein
5492	peptide chain release factor 2 (prfB)
5496	cell division ABC transporter, ATP-binding protein FtsE (ftsE)
5504	carboxymethylenebutenolidase-related protein
5506	metallo-beta-lactamase superfamily protein
5514	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
5520	asparaginyl-tRNA synthetase (asnS)
5526	inosine-uridine preferring nucleoside hydrolase (iunH)
5528	general stress protein 170
5534	Uncharacterised protein family superfamily
5538	Uncharacterized BCR, COG1481
5546	zinc ABC transporter, zinc-binding adhesion liprotein (adcA)
5560	isochorismatase family protein (entB)
5566	3-hydroxybutyryl-CoA dehydrogenase
5572	pyruvate phosphate dikinase (ppdK)
5574	glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC)
5580	glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA)
5594	GTP-binding protein
5612	iojap-related protein
5626	transcriptional regulator SkgA (skgA)
5630	glycerol uptake facilitator protein (glpF)
5634	dihydroxyacetone kinase family protein
5638	dihydroxyacetone kinase family protein
5640	transcriptional regulator, tetR family
5646	dihydroxyacetone kinase family protein
5654	glutamine amidotransferase, class I
5666	peptidase, M20/M25/M40 family
5668	ABC transporter, ATP-binding protein
5686	pur operon repressor (purR)
5690	cmp-binding-factor 1 (cbf1)
5694	competence-induced protein Ccs50 (ccs50)
5702	ribulose-phosphate 3-epimerase (rpe)
5710	rRNA (guanine-N1-)methyltransferase (rrmA)
5712	dimethyladenosine transferase (ksgA)
5718	primase-related protein
5726	endosome-associated protein
5728	CG17785 gene product
5734	dltD protein (dltD)
5738	D-alanyl carrier protein-related protein
5742	dltB protein (dltB)
5754	DNA-binding response regulator (arlR)
5756	ribosomal protein L34 (rpmH)
5766	penicillin-binding protein 4 (pbp4)
5770	intein-containing protein
5774	NifU family protein
5778	aminotransferase, class-V
5782	Uncharacterized protein family (UPF0051) family

5786	ABC transporter, ATP-binding protein
5790	glycosyl transferase domain protein (llm)
5794	transcriptional regulator MecA (meca)
5798	undecaprenol kinase
5806	amino acid ABC transporter, amino acid-binding protein/permease protein
5808	amino acid ABC transporter, ATP-binding protein
5834	riboflavin biosynthesis protein RibF (ribF)
5850	type I restriction-modification system, S subunit
5860	lipoprotein
5862	aggregation substance
5866	ID479
5896	type II DNA modification methyltransferase Spn5252IP (spn5252IMP)
5916	ribosomal protein L10 (rplJ)
5922	ATP-dependent Clp protease, ATP-binding subunit ClpC (clpC)
5926	homocysteine S-methyltransferase (mmuM)
5932	transcriptional regulator, TetR family
5938	GTP-binding protein (cgpA)
5952	thymidylate synthase (thyA)
5956	condensing enzyme, FabH-related
5960	hydroxymethylglutaryl-CoA reductase, degradative
5974	gene_idK21C13.21~pir T04769~strong similarity to unknown protein, put
5976	FMN-dependent dehydrogenase family protein
5980	phosphomevalonate kinase
5986	diphosphomevalonate decarboxylase (mvaD)
5990	mevalonate kinase (mvk)
5994	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family (PhoR1)
6002	GTP pyrophosphokinase (relA)
6006	transposase for insertion sequence element is904
6016	5'-nucleotidase family
6018	polypeptide deformylase (def)
6022	NADP-specific glutamate dehydrogenase (gdhA)
6026	ABC transporter, ATP-binding/permease protein
6028	ABC transporter, ATP-binding/permease protein
6030	acetyltransferase, GNAT family family
6032	ABC transporter, ATP-binding protein
6040	degV family protein (degV)
6056	carbohydrate kinase, PfkB family (fruB)
6064	beta-lactam resistance factor (fibB)
6070	2-dehydropantoate 2-reductase
6076	PTS system component
6078	pyridine nucleotide-disulphide oxidoreductase family protein (trxB)
6082	tRNA (guanine-N1)-methyltransferase (trmD)
6092	c5a peptidase precursor
6100	Para
6102	transposase family protein (orfA)
6116	Tn5252, relaxase
6120	Tn5252, Orf 10 protein
6124	mercuric reductase
6126	transcriptional regulator, MerR family
6132	cation transport ATPase, E1-E2 family
6138	cation-transporting ATPase, E1-E2 family
6140	cation-transporting ATPase, E1-E2 family
6144	cation-transporting ATPase, E1-E2 family
6146	transcriptional repressor, CopY (copY)
6150	cadmium resistance transporter
6158	membrane protein
6162	flavoprotein (dfp)
6170	lipoate-protein ligase A
6174	FMN oxidoreductase (nemA)

6178	Bacterial luciferase superfamily
6182	glycine cleavage system H protein (gcvH)
6186	Domain of unknown function
6194	lipoate-protein ligase A (lplA)
6198	formate-tetrahydrofolate ligase (fhs)
6202	cardiolipin synthetase (cls)
6220	aminotransferase, class II (aspB)
6222	RNA methyltransferase, TrmH family, group 2
6232	60 kDa chaperonin
6242	purine nucleoside phosphorylase (deoD)
6248	deoxyribose-phosphate aldolase (deoC)
6254	Lyme disease proteins of unknown function
6258	ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD)
6262	penicillin-binding protein 2A (pbp2A)
6266	pathogenicity protein
6268	transcription antitermination protein NusG (nusG)
6272	glycosyl transferase, family 8
6276	glycosyl transferase, family 8
6284	sugar transporter family protein
6292	sensory box histidine kinase
6306	homocysteine S-methyltransferase (metH)
6310	glycerol dehydrogenase
6312	DNA topology modulation protein FlaR
6316	translation initiation factor IF-1 (infA)
6320	adenylate kinase (adk)
6326	ribosomal protein L15 (rplO)
6330	ribosomal protein L30 (rpmD)
6336	ribosomal protein S5 (rpsE)
6344	ribosomal protein L6 (rplF)
6348	ribosomal protein S8 (rpsH)
6352	ribosomal protein S14 (rpsN)
6356	ribosomal protein L5 (rplE)
6360	ribosomal protein L24 (rplX)
6366	ribosomal protein L14 (rplN)
6368	ribosomal protein S17 (rpsQ)
6372	ribosomal protein L29 (rpmC)
6374	ribosomal protein L16 (rplP)
6378	ribosomal protein S3 (rpsC)
6382	ribosomal protein L22 (rplV)
6386	ribosomal protein S19 (rpsS)
6390	ribosomal protein L2 (rplB)
6394	ribosomal protein L23 (rplW)
6398	ribosomal protein L4/L1 family (rplD)
6402	ribosomal protein L3 (rplC)
6408	ribosomal protein S10 (rpsJ)
6414	MATE efflux family protein
6418	threonine synthase (thrC)
6428	Uncharacterized BCR, COG1636 superfamily
6436	4-alpha-glucanotransferase (malQ)
6440	glycogen phosphorylase family protein (malP)
6444	glycerol-3-phosphate transporter (glpT)
6452	rhodanese family protein
6458	ammonium transporter
6464	DNA repair protein RadA (radA)
6472	oxidoreductase, pyridine nucleotide-disulfide, class I
6478	ribose ABC transporter, periplasmic D-ribose-binding protein (rbsB)
6484	ribose ABC transporter, ATP-binding protein (rbsA)
6486	ribose ABC transporter protein (rbsD)
6488	ribokinase (rbsK)

6498	ABC transporter, ATP-binding protein
6502	DNA-binding response regulator (<i>vicR</i>)
6506	argininosuccinate synthase (<i>argG</i>)
6508	argininosuccinate lyase (<i>argH</i>)
6514	bacteriophage L54a, repressor protein
6528	soluble transducer HtrXIII
6542	probable transposase (insertion sequence IS861)
6544	ABC transporter, ATP-binding/permease protein
6550	ABC transporter, ATP-binding/permease protein
6560	Serine hydroxymethyltransferase
6568	HemK protein (hemK)
6572	peptide chain release factor 1 (<i>prfA</i>)
6576	thymidine kinases
6580	4-oxalocrotonate tautomerase (<i>dmpl</i>)
6588	oxidoreductase
6594	oxidoreductase
6600	formate/nitrite transporter family protein
6608	xanthine permease (<i>pbuX</i>)
6612	xanthine phosphoribosyltransferase (<i>xpt</i>)
6616	guanosine monophosphate reductase (<i>guaC</i>)
6620	drug resistance transporter, EmrB/QacA subfamily
6622	oxidoreductase
6624	Kup system potassium uptake protein (<i>kup</i>)
6636	O-methyltransferase
6642	oligoendopeptidase F (<i>pepF</i>)
6646	competence protein CoiA (<i>coiA</i>)
6650	major facilitator superfamily protein superfamily
6652	ribosomal small subunit pseudouridine synthase A (<i>rsuA</i>)
6658	glucosamine-6-phosphate isomerase (<i>nagB</i>)
6662	nodulin-related protein, truncation
6664	S-adenosylmethioninetRNA ribosyltransferase-isomerase (<i>queA</i>)
6674	permease, GntP family
6684	6-phospho-beta-glucosidase (<i>bglA</i>)
6686	PTS system, beta-glucosides-specific IIABC components
6688	transcription antiterminator Lict (<i>licT</i>)
6704	esterase
6706	sugar-binding transcriptional repressor, LacI family
6708	hydrolase, haloacid dehalogenase-like family
6712	DNA internalization-related competence protein ComEC/Rec2
6716	competence protein CelA (<i>celA</i>)
6720	acyltransferase family protein
6732	ATP-dependent RNA helicase Dead (<i>deaD</i>)
6736	lipoprotein, YaeC family
6738	ABC transporter, permease protein
6752	diacylglycerol kinase (<i>dgkA</i>)
6768	formamidopyrimidine-DNA glycosylase (<i>mutM</i>)
6776	epidermin immunity protein F
6788	glycyl-tRNA synthetase, beta subunit (<i>glyS</i>)
6790	acyl carrier protein phosphodiesterase
6800	SsrA-binding protein (<i>smpB</i>)
6822	D-alanine–D-alanine ligase
6824	recombination protein RecR (<i>recR</i>)
6830	penicillin-binding protein 2b
6832	phosphoglycerate mutase (<i>gpmA</i>)
6836	triosephosphate isomerase (<i>tpiA</i>)
6856	phosphoglycerate mutase family protein
6860	D-alanyl-D-alanine carboxypeptidase family
6864	autolysin
6868	heat-inducible transcription repressor HrcA (<i>hrcA</i>)

6872	heat shock protein GrpE (grpE)
6876	chaperone protein dnak
6880	dnaJ protein (dnaJ)
6884	transcriptional regulator, gntR family domain protein
6888	tRNA pseudouridine synthase A (truA)
6892	phosphomethylpyrimidine kinase (thiD)
6910	galactose-6-phosphate isomerase, LacA subunit (lacA)
6922	tagatose 1,6-diphosphate aldolase (lacD)
6932	sugar ABC transporter, ATP-binding protein (msmK)
6936	glucan 1,6-alpha-glucosidase (dexB)
6940	UDP-glucose 4-epimerase (galE)
6942	response regulator (citB)
6950	citrate carrier protein (citS)
6954	malate oxidoreductase (tme)
6958	bacteriocin transport accessory protein
6976	transposase family protein (orfA)
6980	pXO1-128
6986	adhesion lipoprotein (lmb)
6994	DNA-directed RNA polymerase, alpha subunit (rpoA)
6998	ribosomal protein L17 (rplQ)
7040	probable dna-directed rna polymerase delta subunit
7044	CTP synthase (pyrG)
7058	bacteriocin transport accessory protein
7074	translation initiation factor IF-3 (infC)
7100	adenosine deaminase
8468	preprotein translocase, SecE subunit
8476	antigen, 67 kDa
8486	Lipase/Acylhydrolase
8492	peptide ABC transporter, permease protein (oppB)
8494	competence protein CglB (cglB)
8502	peptide ABC transporter, peptide-binding protein
8504	oxidoreductase
8510	amino acid ABC transporter, permease protein (opuBB)
8522	abc transporter atp-binding protein ybf
8530	glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)
8538	sugar ABC transporter, sugar-binding protein
8544	secreted 45 kd protein (usp45)
8556	phosphoglycerate mutase family protein
8566	glycosyl hydrolase, family 3
8576	N-acetylmuramoyl-L-alanine amidase
8596	sensory box histidine kinase (withHAMPandPASd)
8608	aminoglycoside 6-adenylyltransferase
8622	iron compound ABC transporter, permease protein (sirB)
8636	phosphate ABC transporter, permease protein (pstC-2)
8650	branched-chain amino acid transport system II carrier protein (brnQ)
8658	PTS system, IID component
8662	replisome organiser-related protein
8674	alkaline amylopullulanase
8676	exfoliative toxin A
8690	glycerol uptake facilitator protein (glpF)
8698	ABC transporter, ATP-binding protein
8706	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (pgs)
8708	cobalt transport protein
8730	integral membrane protein
8734	yadS protein
8736	cell wall surface anchor family protein
8748	polysaccharide biosynthesis protein
8752	glycosyl transferase domain protein
8764	endopeptidase O

8770	beta-ketoacyl-acyl carrier protein synthase II
8772	ABC transporter, ATP-binding protein
8776	penicillin-binding protein
8778	cell wall surface anchor family protein
8780	cell wall surface anchor family protein
8786	LPXTG-motif cell wall anchor domain protein
8788	6-aminohexanoate-cyclic-dimer hydrolase
8796	NLP/P60 family protein
8802	DNA/RNA non-specific endonuclease
8806	hydroxyethylthiazole kinase (thiM)
8826	PTS system component
8832	sugar ABC transporter, permease protein
8836	potassium uptake protein, Trk family (trkA)
8850	lemA protein (lemA)
8856	cobalt transport protein
8882	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein
8884	spermidine/putrescine ABC transporter, permease protein (potC)
8906	ABC transporter, substrate-binding protein
8908	lipoprotein
8916	sensor histidine kinase
8930	TrsK-like protein (traK)
8936	R5 protein
8962	chromosome assembly protein homolog
8978	ribose ABC transporter, permease protein (rbsC)
8980	permease
8982	sensor histidine kinase (arlS)
8986	hydrolase, haloacid dehalogenase-like family (gph)
8994	dephospho-CoA kinase
8996	oxalateformate antiporter
9004	sensory box protein
9006	host cell surface-exposed lipoprotein
9012	PAP2 family protein
9034	GtrA family protein
9050	lipoprotein signal peptidase (IspA)
9280	alcohol dehydrogenase, zinc-containing (adh)
9284	trigger factor (tig)
9290	fructose-bisphosphate aldolase (fba)
9292	DAK2 domain protein
9296	oligopeptide ABC transporter, permease protein
9298	N-acetylglucosamine-6-phosphate deacetylase (nagA)
9300	transcriptional regulator, DeoR family (lacR)
9302	PTS system, mannose-specific IIC component (manM)
9306	Phosphoglucose isomerase
9310	aspartate--ammonia ligase (asnA)
9312	amino acid ABC transporter, ATP-binding protein
9314	DNA-binding protein HU (hup)
9316	DHH subfamily 1 protein
9318	chloride channel
9320	integrase (int)
9324	DNA/RNA non-specific endonuclease
9326	PTS system component
9328	cell division protein, FtsW/RodA/SpoVE family (ftsW)
9330	LPXTG-motif cell wall anchor domain protein
9332	peptide chain release factor 3 (prfC)
9334	ABC transporter, ATP-binding protein
9336	superoxide dismutase [mn-fe]
9340	phenylalanyl-tRNA synthetase, alpha subunit (pheS)
9342	amino acid ABC transporter, permease protein
9344	phosphate ABC transporter, phosphate-binding protein (pstS)

9346	NOL1/NOP2/sun family protein (sun)
9348	Abortive infection protein family
9350	permease
9352	N-acetylmuramoyl-L-alanine amidase domain protein (usp45)
9354	ABC transporter, ATP-binding protein
9356	phosphoglucomutase (pgm)
9358	oxidoreductase, short chain dehydrogenase/reductase family
9360	phosphate acetyltransferase
9362	gls24 protein
9364	ribosomal protein S1 (rpsA)
9368	dTDP-glucose 4,6-dehydratase (rfbB)
9370	excinuclease ABC, C subunit (uvrC)
9372	MATE efflux family protein
9378	amino acid permease (rocE)
9380	DNA-binding response regulator TrcR (trcR)
9382	16S rRNA processing protein RimM (rimM)
9384	transcriptional regulator
9388	ribosomal protein L20 (rplT)
9394	sugar-binding transcriptional repressor, LacI family (malR)
9396	proton/peptide symporter family protein
9398	amino acid permease
9400	exoribonuclease, VacB/Rnb family (vacB)
9402	multi-drug resistance efflux pump (pmrA)
9404	adhesion lipoprotein (psaA)
9406	iron-dependent transcriptional regulator (sirR)
9410	branched-chain amino acid ABC transporter, amino acid-binding protein (
9412	amino acid permease
9414	SpoU rRNA Methylase family protein
9416	sodium/dicarboxylate symporter (gltP-2)
9418	branched-chain amino acid transport system II carrier protein (brnQ)
9420	alcohol dehydrogenase, zinc-containing
9422	aminotransferase, class I (aspB)
9424	ribosomal protein S6 (rpsF)
9426	A/G-specific adenine glycosylase (mutY)
9428	acid phosphatase (olpA)
9430	ribosomal protein S12 (rpsL)
9434	microcin immunity protein MccF (mccF-1)
9436	undecaprenyl diphosphate synthase (uppS)
9438	preprotein translocase, YajC subunit (yajC)
9440	chaperonin, 10 kDa (groES)
9444	YitT family protein
9446	serine protease (htrA)
9448	ribose-phosphate pyrophosphokinase (prsA)
9450	aromatic amino acid aminotransferase (araT)
9452	Recombination protein O (recO)
9454	Abortive infection protein family
9456	fatty acid/phospholipid synthesis protein PlsX (plsX)
9458	acyl carrier protein (acpP)
9462	phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)
9464	alcohol dehydrogenase, iron-containing
9466	ribosomal protein L18 (rplR)
9468	preprotein translocase, SecY subunit
9470	transcriptional regulator ComX1 (comX1)
9472	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)
9478	sugar-binding transcriptional regulator, LacI family (rbsR)
9480	SPFH domain/Band 7 family
9488	zinc ABC transporter, permease protein (adcB)
9492	abortive infection protein
9494	hydrolase, haloacid dehalogenase-like family

9496	response regulator (lytT)
9500	transketolase, C-terminal subunit
9502	polyribonucleotide nucleotidyltransferase (ppn)
9504	serine O-acetyltransferase (cysE)
9508	ribosomal protein L13 (rplM)
9510	replication initiation protein
9518	amino acid ABC transporter, amino acid-binding protein
9522	glycyl-tRNA synthetase, alpha subunit (glyQ)
9524	NADH oxidase
9528	transketolase (tkt)
9534	penicillin-binding protein 1A (pbp1A)
9536	cell division protein DivIVA (divlVA)
9538	sensor histidine kinase
9540	serine/threonine protein kinase (pknB)
9542	transcriptional regulator
9544	PTS system, IIA component (lacF)
9546	glycerol dehydrogenase (gldA)
9548	aspartate kinase (thrA)
9550	enoyl-CoA hydratase/isomerase family protein
9552	acyl carrier protein (acpP)
9564	ABC transporter, ATP-binding protein
9566	N utilization substance protein A (nusA)
9568	ribosome-binding factor A (rbfA)
9570	Cof family protein
9572	CoA binding domain protein (b0965)
9574	transcriptional regulator, Fur family
9578	queuine tRNA-ribosyltransferase (tgt)
9580	ribonuclease P protein component (rnpA)
9582	serine protease, subtilase family
9584	glycosyl transferase domain protein
9586	transcriptional activator, AraC family
9588	transcriptional regulator, TetR family
9590	transcriptional regulator, AraC family
9594	surface protein Rib
9596	transposase, mutator family
9600	acetyltransferase, GNAT family
9602	Transposase, Mutator family
9606	UDP-sugar hydrolase
9610	anthranilate synthase component II (trpG)
9612	biotin synthetase (bioB)
9616	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)
9618	yImF protein (yImF)
9620	amino acid ABC transporter, permease protein
9622	phosphoglucomutase (pgm)
9624	YjeF-related protein, C-terminus
9626	FemAB family protein (fibA)
9628	Cof family protein
9630	cell division ABC transporter, permease protein FtsX (ftsX)
9632	oxidoreductase, short-chain dehydrogenase/reductase family (fabG)
9634	aspartate aminotransferase (aspC)
9638	ribosomal protein L31 (rpmE)
9640	nrdI protein (nrdI)
9642	ribosomal protein L19 (rplS)
9644	bacteriophage L54a, repressor protein
9646	bacteriophage L54a, antirepressor
9652	single-strand binding protein (ssb)
9660	pneumococcal surface protein A
9666	DNA-binding response regulator (vncR)
9668	transposase OrfAB, subunit B

9670	cell division protein, FtsW/RodA/SpoVE family (rodA)
9672	DNA gyrase, B subunit (gyrB)
9674	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)
9676	RNA methyltransferase, TrmA family
9680	transcriptional regulator, AraC family
9682	ABC transporter, ATP-binding protein
9690	CylJ
9696	permease
9698	regulatory protein
9700	carbohydrate kinase, pfkB family
9702	beta-glucuronidase
9704	2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldo
9706	3-oxoacyl-(acyl-carrier-protein) reductase
9708	catabolite control protein A (ccpA)
9712	ribonuclease III (rnc)
9714	SMC family, C-terminal domain family
9718	S1 RNA binding domain protein
9722	prolipoprotein diacylglycerol transferase (lgt)
9724	riboflavin synthase, alpha subunit (ribE)
9726	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (ri
9728	lysyl-tRNA synthetase (lysS)
9734	Transposase subfamily
9738	translation elongation factor Tu (tuf)
9740	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-a
9746	Glutathione S-transferases domain protein
9754	Ribonucleotide reductases
9756	biotin--acetyl-CoA-carboxylase ligase
9760	Uncharacterized protein family SNZ family
9762	methionine aminopeptidase, type I (map)
9764	DNA ligase, NAD-dependent (ligA)
9766	glucose-1-phosphate adenyltransferase (glgC)
9768	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
9770	acetyltransferase, GNAT family
9772	exonuclease RexA (rexA)
9774	tRNA modification GTPase TrmE (trmE)
9776	ABC transporter, ATP-binding protein
9778	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase al
9782	Mur ligase family protein
9786	HD domain protein
9788	translation elongation factor G (fusA)
9796	pyruvate kinase (pyk)
9798	Signal peptidase I
9802	cytidine deaminase (cdd)
9804	sugar ABC transporter, ATP-binding protein
9806	sugar ABC transporter, permease protein
9808	acetyltransferase, GNAT family
9810	ABC transporter, permease protein
9812	SatD
9814	Helix-turn-helix domain, fis-type protein
9816	phosphate ABC transporter, ATP-binding protein (pstB-1)
9818	tRNA pseudouridine synthase B (truB)
9820	Acetyltransferase (GNAT) family
9822	DNA topoisomerase I (topA)
9824	ribonuclease HII (mhB)
9830	orotidine 5'-phosphate decarboxylase (pyrF)
9832	aspartate-semialdehyde dehydrogenase (asd)
9836	pantothenate metabolism flavoprotein (dfp)
9840	Sua5/YciO/YrdC/YwlC family protein
9844	thiamine biosynthesis protein ApbE

9846	Domain of unknown function
9848	DNA repair protein RadC (radC)
9850	glycosyl hydrolase, family 1 (bglA)
9852	Cof family protein (b0844)
9854	spermidine/putrescine ABC transporter, permease protein (potH)
9856	folylpolyglutamate synthase (folC)
9858	homoserine dehydrogenase (hom)
9860	succinate-semialdehyde dehydrogenase (gabD-1)
9862	membrane protein
9864	ATP-dependent DNA helicase PcrA (pcrA)
9866	uracil permease (uraA)
9868	sodiumalanine symporter family protein
9878	capsular polysaccharide biosynthesis protein Cps4B (cps4B)
9880	transcriptional regulator, LysR family
9882	CpslaS
9884	chloride channel protein
9886	tributyrin esterase (estA)
9888	ABC transporter, ATP-binding protein (potA)
9890	alpha-acetolactate decarboxylase (budA)
9892	TPR domain protein
9896	metallo-beta-lactamase superfamily protein
9898	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)
9902	glycerophosphoryl diester phosphodiesterase
9904	transposase OrfAB, subunit B
9906	IS3-Spn1, transposase
9908	transposase OrfAB, subunit B (orfB)
9910	reverse transcriptase
9916	transposase OrfAB, subunit B
9918	integrase, phage family (int)
9920	transcription regulator
9922	TnpA
9926	structural gene for ultraviolet resistance (uvra)
9930	Helicases conserved C-terminal domain protein
9932	abortive infection bacteriophage resistance protein (abiEi)
9944	ribosomal protein L7/L12 (rplL)
9948	ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX)
9950	dihydrofolate reductase (folA)
9952	hemolysin
9954	transcriptional regulator, MarR family
9958	polyA polymerase family protein
9960	PTS system, fructose specific IIABC components (fruA-1)
9962	lactose phosphotransferase system repressor (lacR)
9964	choline binding protein D (cbpD)
9968	pyrimidine operon regulatory protein (pyrR)
9970	ribosomal large subunit pseudouridine synthase D (rluD)
9972	thiamine biosynthesis protein Thil (thil)
9974	3-dehydroquinate dehydratase, type I (aroD)
9976	iron compound ABC transporter, ATP-binding protein (fepC)
9980	transcriptional regulator
9982	glycosyl transferase domain protein
9984	Cps9H
9988	4-diphosphocytidyl-2C-methyl-D-erythritol synthase (ispD)
9990	licD1 protein (licD1)
9996	large conductance mechanosensitive channel protein (mscl)
10000	maltose ABC transporter, maltose-binding protein
10004	nucleotide sugar synthetase-like protein
10006	transcriptional regulator
10008	oxidoreductase, aldo/keto reductase family
10010	NAD(P)H-flavin oxidoreductase

10016	transcriptional regulator MutR
10018	GTP-binding protein Era (era)
10022	peptide methionine sulfoxide reductase (msrA)
10026	peptide ABC transporter, ATP-binding protein
10028	peptide ABC transporter, ATP-binding protein (amiE)
10030	peptide ABC transporter, peptide-binding protein
10032	transposase, IS30 family
10034	transcriptional regulator, LysR family
10036	spoE family protein (ftsK)
10044	methionyl-tRNA synthetase (metG)
10046	D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA)
10048	acetyltransferase, GNAT family
10050	phosphoserine aminotransferase (serC)
10054	thymidylate kinase (tmk)
10060	branched-chain amino acid ABC transporter, permease protein (llyH)
10062	ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)
10064	uracil phosphoribosyltransferase (upp)
10066	potassium uptake protein, Trk family (trkH)
10068	glutamate racemase (murl)
10070	membrane protein
10072	HD domain protein
10074	Acylphosphatase
10076	spoilIJ family protein
10078	acetyltransferase, GNAT family
10080	glucose-inhibited division protein B (gidB)
10082	potassium uptake protein, Trk family
10084	ABC transporter, permease protein
10088	isochorismatase family protein
10092	halocid dehalogenase-like hydrolase superfamily
10094	membrane protein
10096	glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)
10098	CBS domain protein protein
10100	transcriptional regulator (codY)
10102	universal stress protein family
10104	L-asparaginase (ansA)
10106	oxidoreductase, aldo/keto reductase 2 family
10108	preprotein translocase, SecA subunit (secA)
10112	excinuclease ABC, A subunit (uvrA)
10114	magnesium transporter, CorA family (corA)
10116	thioredoxin (trx)
10118	MutS2 family protein (mutS2)
10122	DNA-damage inducible protein P (dinP)
10124	formate acetyltransferase (pfl)
10126	transcriptional regulator, Crp family
10128	transport ATP-binding protein CydC
10138	ribosomal-protein-alanine acetyltransferase (rimI)
10140	hydrolase
10144	D-alanine-activating enzyme (dltA)
10148	carbohydrate kinase, FGGY family
10150	transaldolase
10160	Helix-turn-helix domain protein
10164	single-strand binding protein (ssb)
10166	type II DNA modification methyltransferase Spn5252IP (spn5252IMP)
10174	integrase, phage family
10178	Cyclic nucleotide-binding domain protein
10180	transcriptional regulator, MarR family
10182	prolyl-tRNA synthetase (proS)
10184	leucine-rich protein
10186	lacX protein, truncation (lacX)

10188	tagatose-6-phosphate kinase (lacC)
10190	galactose-6-phosphate isomerase, LacB subunit (lacB)
10192	neuraminidase
10198	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase domain protein
10200	ABC transporter, ATP-binding protein
10202	PTS system, IIABC components (ptsG)
10204	phosphate regulon response regulator PhoB (phoB)
10212	Uncharacterized ACR, COG2161 subfamily
10216	abortive phage resistance protein
10222	TnpA
10226	acetyltransferase, GNAT family
10230	ABC transporter domain protein
10234	5-methyltetrahydropteroylglutamate--homocysteine methyltransferase (
10236	branched-chain amino acid transport protein AzlC (azlC)
10240	DNA-binding response regulator (srrA)
10242	leucyl-tRNA synthetase (leuS)
10246	NupC family protein
10248	transcriptional regulator, GntR family
10252	glyoxalase family protein
10254	anaerobic ribonucleoside-triphosphate reductase (nrdD)
10256	competence-induced protein Ccs4
10262	competence/damage-inducible protein CinA (cinA)
10264	DNA-3-methyladenine glycosylase I (tag)
10268	DNA mismatch repair protein HexB (hexB)
10270	arginine repressor (argR)
10272	arginyl-tRNA synthetase (argS)
10274	aspartyl-tRNA synthetase (aspS)
10276	histidyl-tRNA synthetase (hisS)
10280	AGR_pAT_51p
10286	hydrolase, alpha/beta hydrolase fold family
10288	phage infection protein
10290	Glucose inhibited division protein A (gidA)
10292	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU)
10296	arginine/ornithine antiporter (arcD)
10298	chromosomal replication initiator protein DnaA (dnaA)
10302	peptidyl-tRNA hydrolase (pth)
10310	phosphotyrosine protein phosphatase
10316	ribosomal protein L36 (rpmJ)
10318	ribosomal protein S13/S18 (rpsM)
10328	L-lactate dehydrogenase (ldh)
10330	ribosomal protein L28 (rpmB)
10362	RNA polymerase sigma-70 factor, ECF subfamily
10384	BioY family protein
10386	AtsA/ElaC family protein
10388	cytidine/deoxycytidylate deaminase family protein
10394	phosphorylase, Pnp/Udp family
10396	transcriptional regulator, MerR family
10402	methyltransferase (ubiE)
10412	type IV prepilin peptidase
10416	ylmG protein (ylmG)
10444	transposase OrfAB, subunit B
10446	IS150-like transposase
10452	Bacterial regulatory proteins, tetR family domain protein
10454	cell wall surface anchor family protein, authentic frameshift (clfB)
10456	transposase OrfAB, subunit A (orfA)
10460	chaperonin, 33 kDa (hslO)
10472	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
10482	sprT protein
10490	transcriptional regulator, MarR family

10498	transcriptional regulator
10504	glycogen biosynthesis protein GlgD (glgD)
10536	ribonucleoside-diphosphate reductase, alpha subunit, truncation (nrdD)
10538	LPXTG-motif cell wall anchor domain
10550	membrane protein
10554	arsenate reductase (arsC)
10564	transposase, authentic frameshift
10570	transposase OrfAB, subunit A (orfA)
10574	Tn5252, Orf 9 protein
10580	IS3-Spn1, transposase
10584	transcriptional regulator, ArsR family
10628	ribosomal protein L35 (rpml)
10630	cytidylate kinase (cmk)
10636	MutT/nudix family protein
10644	preprotein translocase, SecG subunit
10680	ribosomal protein S18 (rpsR)
10682	single-strand binding protein (ssb)
10692	glyceraldehyde 3-phosphate dehydrogenase (gap)
10694	translation elongation factor G (fusA)
10696	ribosomal protein S7 (rpsG)
10704	phosphinothricin N-acetyltransferase (pat)
10730	nrdI protein (nrdl)
10732	accessory gene regulator protein C (blpH)
10744	rhodanese family protein (pspE)
10746	cAMP factor
10758	competence/damage-inducible protein CinA (cinA)
10770	transcriptional regulator, ArgR family (argR)
10772	FliP family
10794	peptide ABC transporter, peptide-binding protein
10800	ribosomal protein S21 (rpsU)
10802	transposase, IS30 family
10816	mucin 2 precursor, intestinal
10854	SV40-transformed marker protein pG1-related protein
10856	SV40-transformed marker protein pG1-related protein
10858	SV40-transformed marker protein pG1-related protein
10860	SV40-transformed marker protein pG1-related protein
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10864	SV40-transformed marker protein pG1-related protein
10866	SV40-transformed marker protein pG1-related protein
10910	transcriptional regulator
10920	ribosomal protein S11 (rpsK)
10922	elaA protein
10926	5-formyltetrahydrofolate cyclo-ligase family protein
10938	inositol monophosphatase family protein
10940	amino acid ABC transporter, amino acid-binding protein (artI)
10944	Holliday junction DNA helicase RuvB (rvB)
10946	D-alanyl-D-alanine carboxypeptidase (dacA)
10948	lipoprotein (bmpD)
10950	peptidase, U32 family
10952	protease maturation protein
10954	glutamyl-tRNA synthetase (gltX)
10956	GTP-binding protein LepA (lepA)
10960	translation initiation factor if-2
10962	phosphoenolpyruvate carboxylase (ppc)
10964	calcium E1-E2-type ATPase
10966	serine protease, subtilase family

CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134,
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2. A protein having 50% or greater sequence identity to a protein according to claim 1.

- 5 3. A protein comprising a fragment of 7 or more consecutive amino acids from an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 10 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 15 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 20 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 25 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 30 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 35 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 40 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590,

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4. An antibody which binds to a protein according to any one of claims 1 to 3.

5. The antibody of claim 4, wherein said antibody is a monoclonal antibody, a chimeric antibody, a humanised antibody, or a fully human antibody.

10 6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.

7. A nucleic acid molecule according to claim 6, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65,
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8. A nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ IDs 10967, 10968,
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9. A nucleic acid molecule comprising a fragment of 10 or more consecutive nucleotides from a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47,
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10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 6 to 9.

11. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 6 to 10.
12. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 6 to 11 under high stringency conditions.
- 5 13. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
14. A composition according to claim 13, being an immunogenic composition, a vaccine composition or a diagnostic composition.
15. A composition according to claim 13 or claim 14 for use as a pharmaceutical.
16. The use of a composition according to claim 13 in the manufacture of a medicament for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly *S.agalactiae* and *S.pyogenes*.
- 10 17. A method of treating a patient, comprising administering to the patient a therapeutically effective amount of the composition of claim 13.
18. A hybrid protein represented by the formula NH₂-A-[X-L-]_n-B-COOH, wherein X is an amino acid sequence as defined in claim 1, L is an optional linker amino acid sequence, A is an optional N-terminal amino acid sequence, B is an optional C-terminal amino acid sequence, and n is an integer greater than 1.
- 15 19. A kit comprising primers for amplifying a template sequence contained within a *Streptococcus* nucleic acid sequence, the kit comprising a first primer and a second primer, wherein the first primer is substantially complementary to said template sequence and the second primer is substantially complementary to a complement of said template sequence, wherein the parts of said primers which have substantial complementarity define the termini of the template sequence to be amplified.
- 20 20. A kit comprising first and second single-stranded oligonucleotides which allow amplification of a *Streptococcus* template nucleic acid sequence contained in a single- or double-stranded nucleic acid (or mixture thereof), wherein: (a) the first oligonucleotide comprises a primer sequence which is substantially complementary to said template nucleic acid sequence; (b) the second oligonucleotide comprises a primer sequence which is substantially complementary to the complement of said template nucleic acid sequence; (c) the first oligonucleotide and/or the second oligonucleotide comprise(s) sequence which is not complementary to said template nucleic acid; and (d) said primer sequences define the termini of the template sequence to be amplified.
- 25 21. The kit of claim 20, wherein the non-complementary sequence(s) of (c) comprise a restriction site and/or a promoter sequence.
22. A computer-readable medium containing one or more of SEQ IDs 1 to 12024.
- 30 23. A process for detecting *Streptococcus* in a biological sample, comprising the step of contacting nucleic acid according to any of claims 6 to 12 with the biological sample under hybridising conditions.
24. The process of claim 23, wherein the process involves nucleic acid amplification.

25. A process for determining whether a compound binds to a protein according to claim 1, claim 2 or claim 3, comprising the step of contacting a test compound with a protein according to claim 1, claim 2 or claim 3 and determining whether the test compound binds to said protein.

26. A compound identified by the process of claim 25.

5 27. A composition comprising a protein according to claim 1, claim 2 or claim 3 and one or more of the following antigens:

- a protein antigen from *Helicobacter pylori*;
- a protein antigen from *N.meningitidis* serogroup B;
- an outer-membrane vesicle (OMV) preparation from *N.meningitidis* serogroup B;
- a saccharide antigen from *N.meningitidis* serogroup A, C, W135 and/or Y;
- 10 – a saccharide antigen from *Streptococcus pneumoniae*;
- an antigen from hepatitis A virus;
- an antigen from hepatitis B virus;
- an antigen from hepatitis C virus;
- an antigen from *Bordetella pertussis*;
- 15 – a diphtheria antigen;
- a tetanus antigen;
- a saccharide antigen from *Haemophilus influenzae* B.
- an antigen from *N.gonorrhoeae*;
- an antigen from *Chlamydia pneumoniae*;
- 20 – an antigen from *Chlamydia trachomatis*;
- an antigen from *Porphyromonas gingivalis*;
- polio antigen(s);
- rabies antigen(s);
- measles, mumps and/or rubella antigens;
- 25 – influenza antigen(s);
- an antigen from *Moraxella catarrhalis*; and/or
- an antigen from *Staphylococcus aureus*.

28. A composition comprising two or more proteins, wherein each protein is a protein according to claim 1, claim 2 or claim 3.

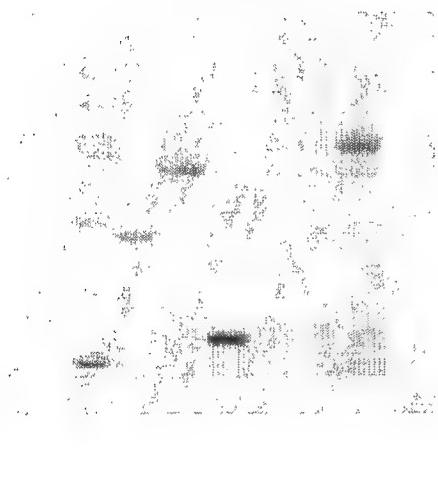
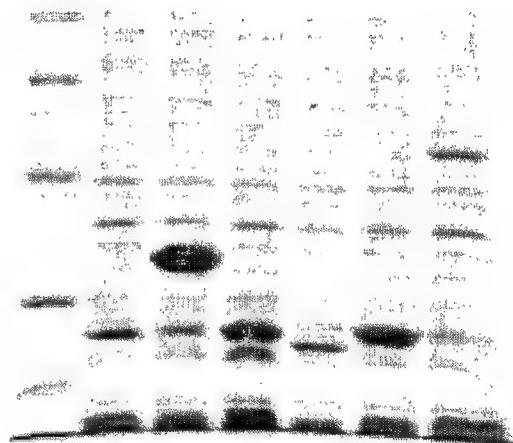
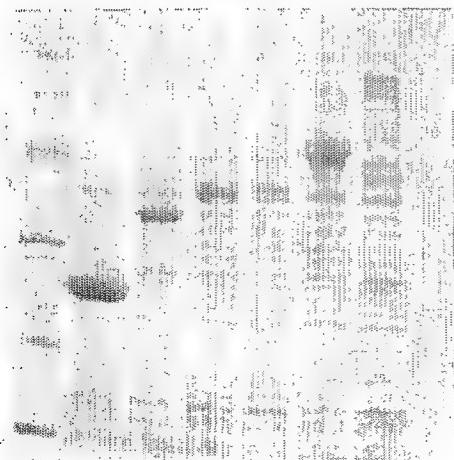
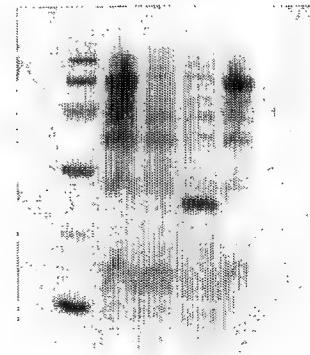
FIGURE 1**FIGURE 2****FIGURE 3****FIGURE 4****FIGURE 5****FIGURE 6**

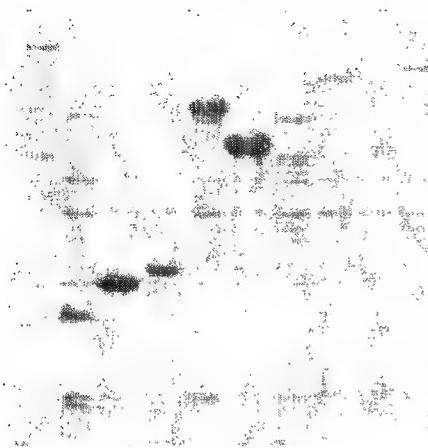
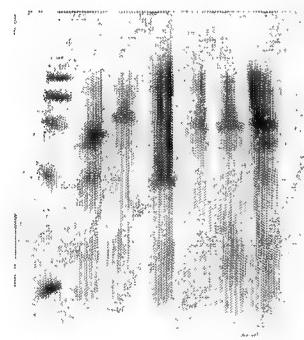
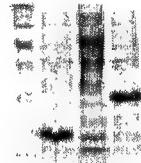
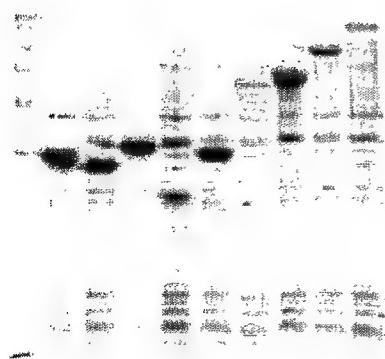
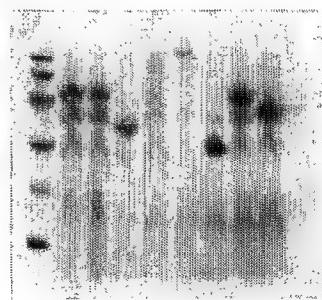
FIGURE 7**FIGURE 8****FIGURE 9****FIGURE 10****FIGURE 11****FIGURE 12**

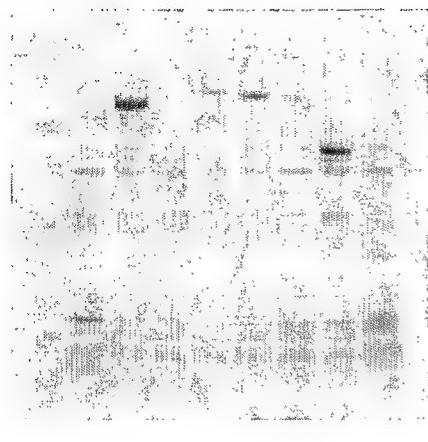
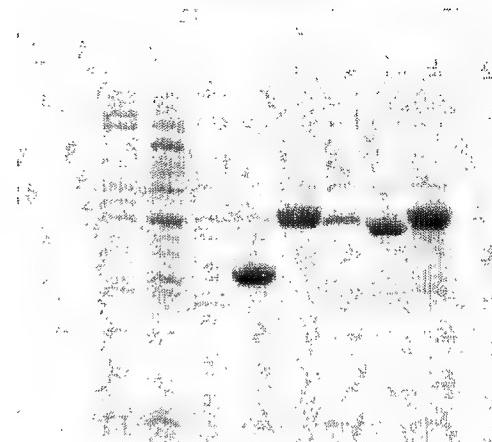
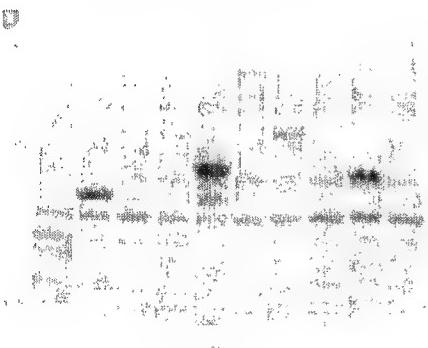
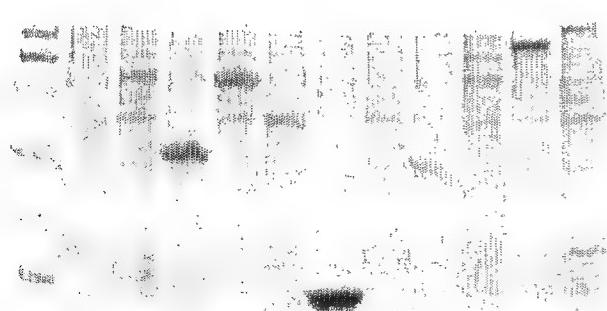
FIGURE 13**FIGURE 14****FIGURE 15****FIGURE 16****FIGURE 17****FIGURE 18**

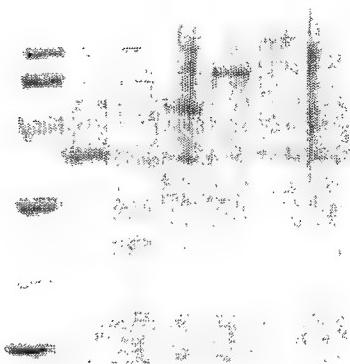
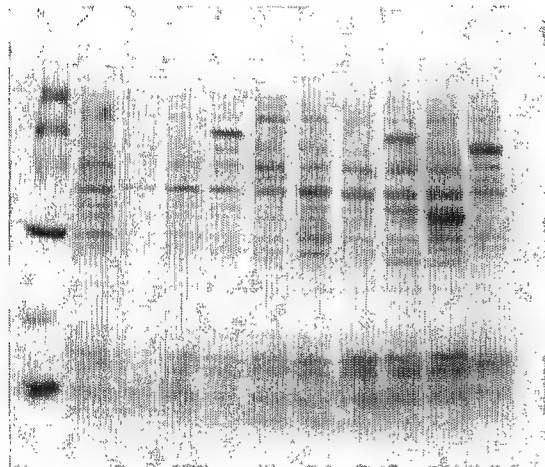
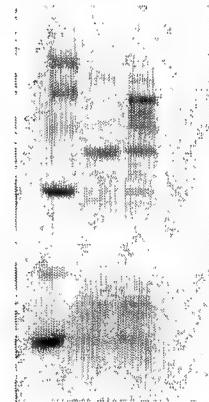
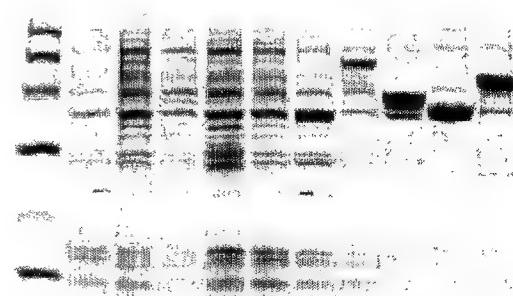
FIGURE 19**FIGURE 20****FIGURE 21****FIGURE 22****FIGURE 23****FIGURE 24**

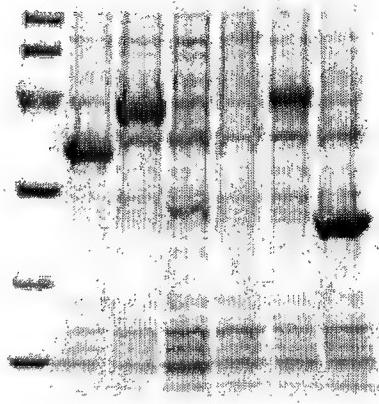
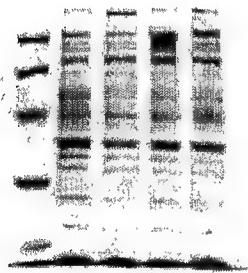
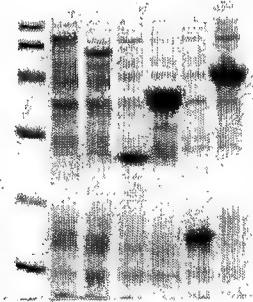
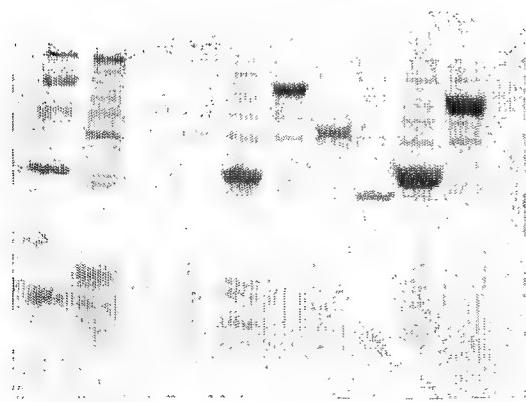
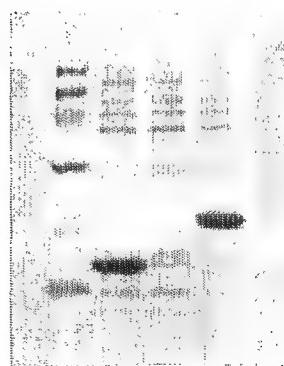
FIGURE 25**FIGURE 26****FIGURE 27****FIGURE 28****FIGURE 29****FIGURE 30**

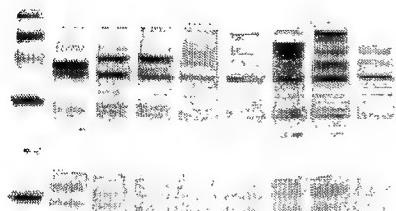
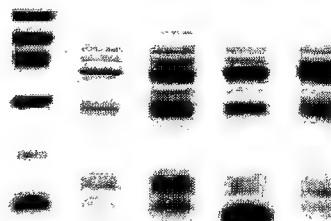
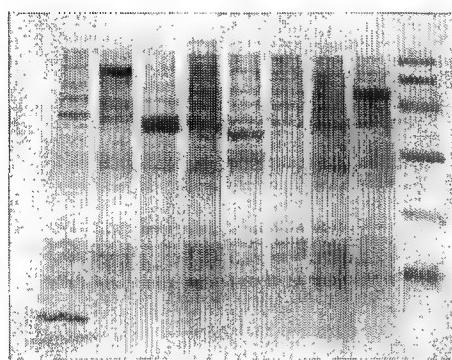
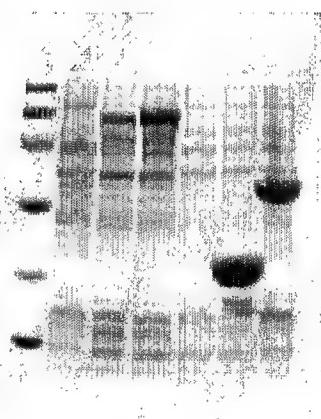
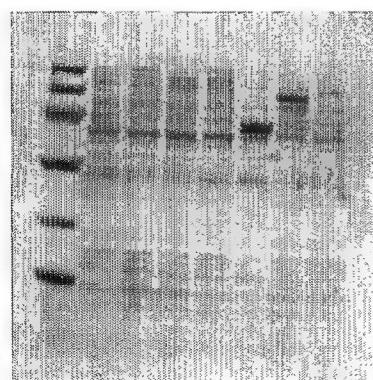
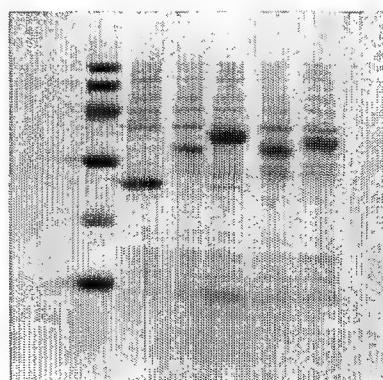
FIGURE 31**FIGURE 32****FIGURE 33****FIGURE 34****FIGURE 35****FIGURE 36**

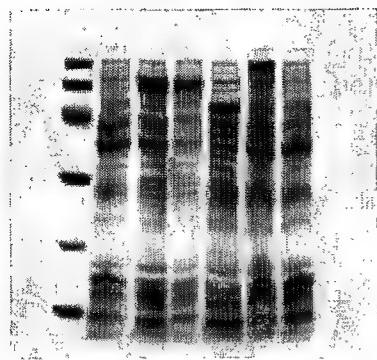
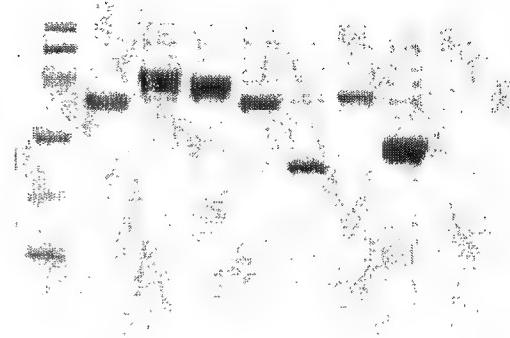
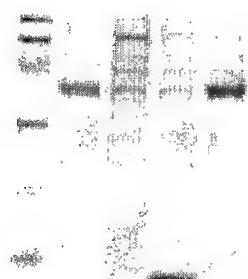
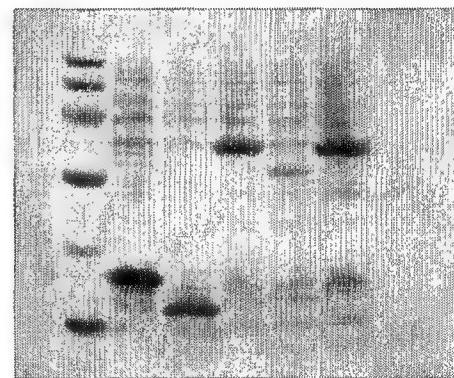
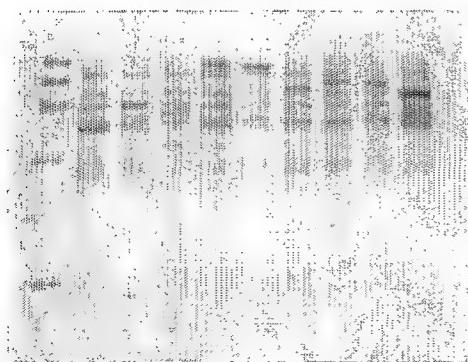
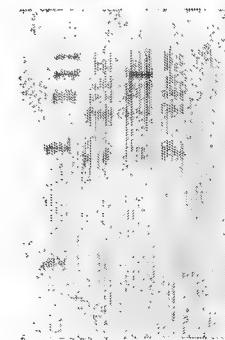
FIGURE 37**FIGURE 38****FIGURE 39****FIGURE 40****FIGURE 41****FIGURE 42**

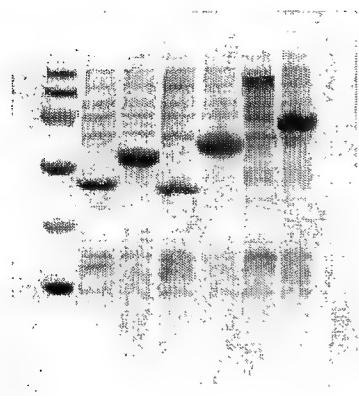
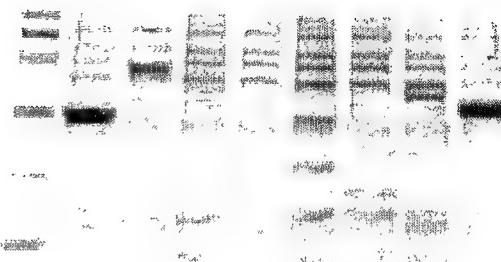
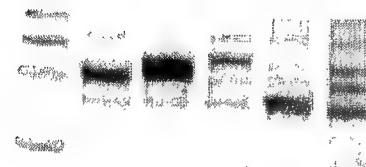
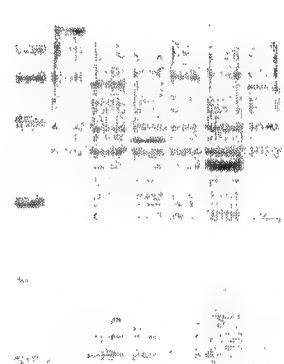
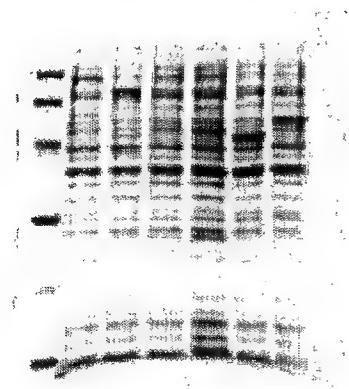
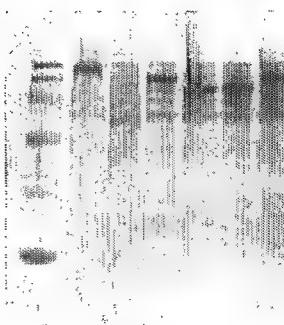
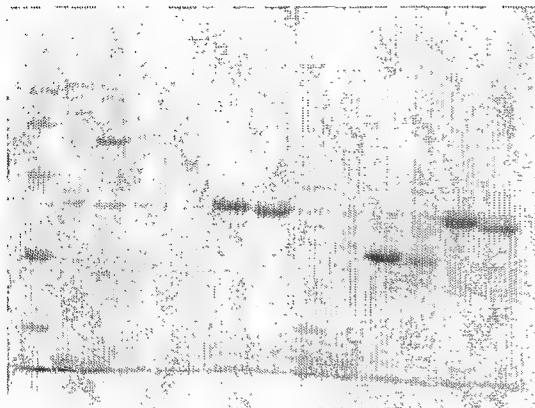
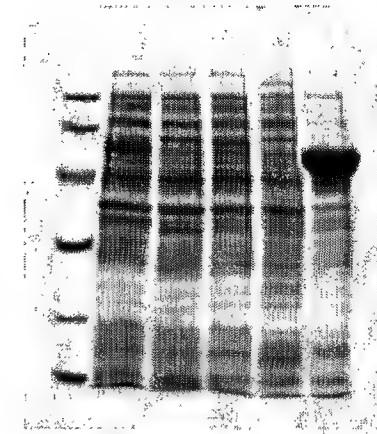
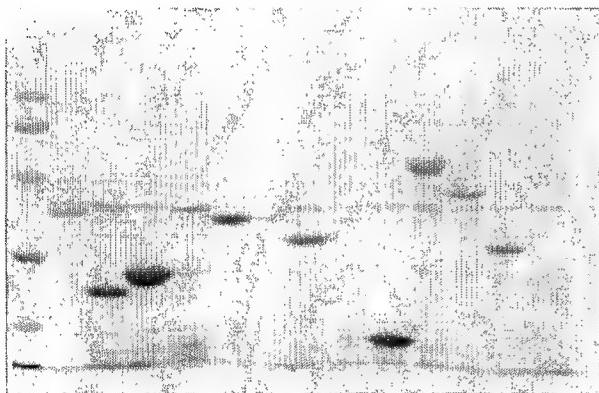
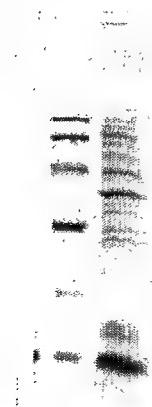
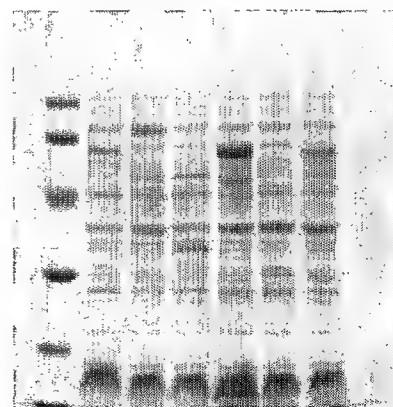
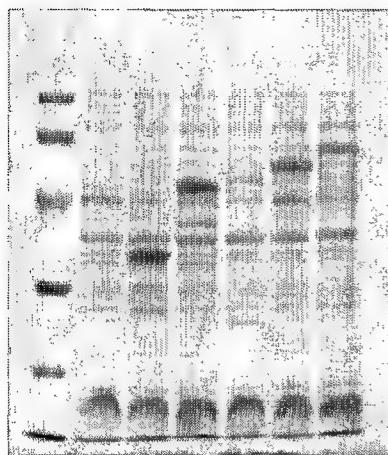
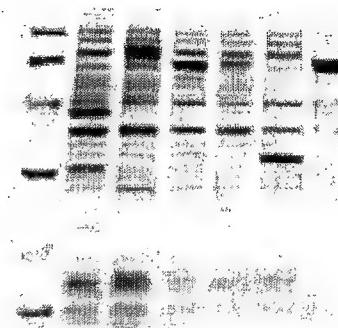
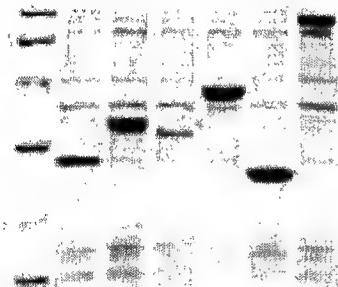
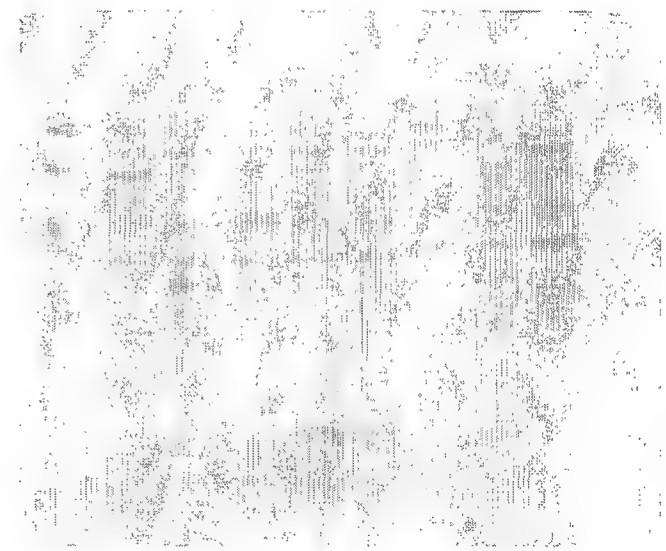
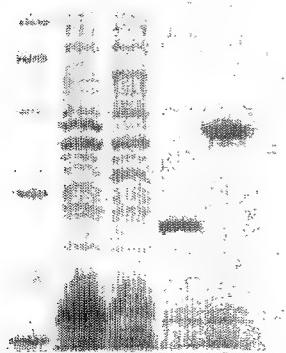
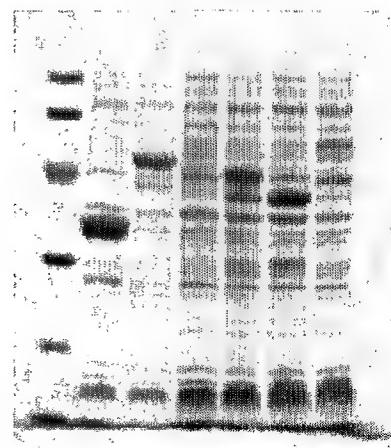
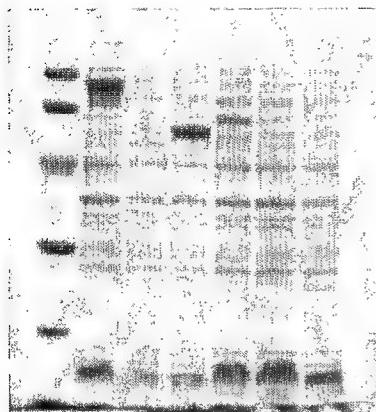
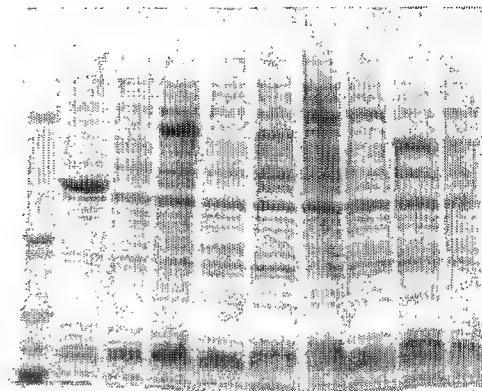
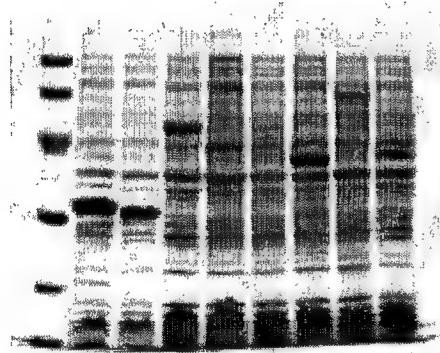
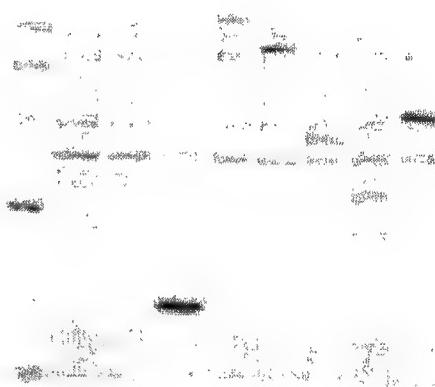
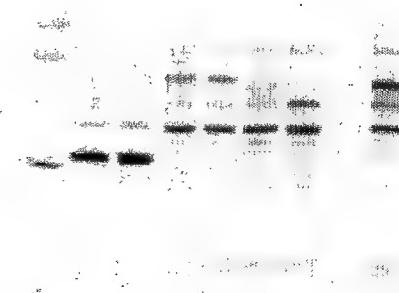
FIGURE 43**FIGURE 44****FIGURE 45****FIGURE 46****FIGURE 47****FIGURE 48**

FIGURE 49**FIGURE 50****FIGURE 51****FIGURE 52****FIGURE 53****FIGURE 54**

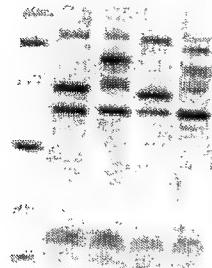
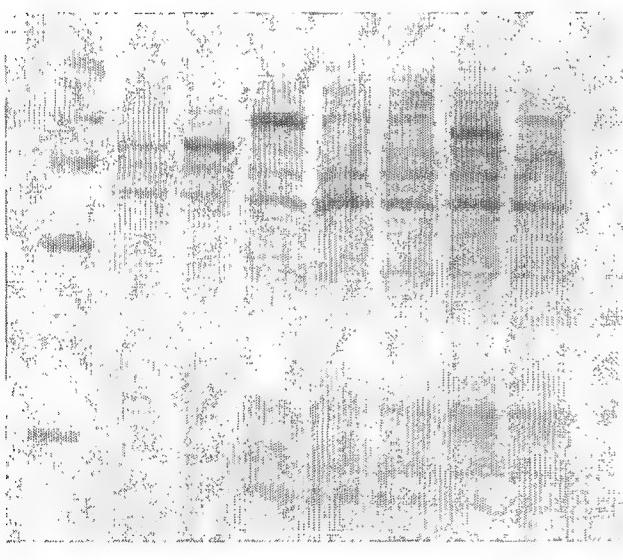
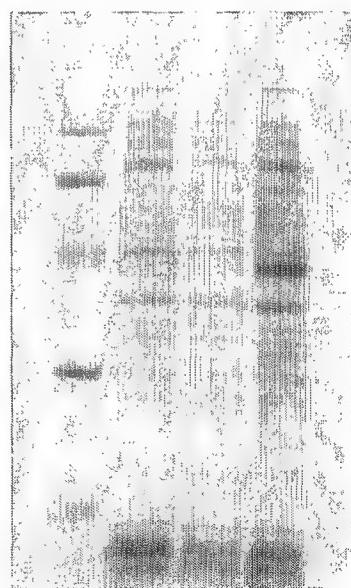
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FIGURE 55**FIGURE 56****FIGURE 57****FIGURE 58****FIGURE 59****FIGURE 60**

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FIGURE 61**FIGURE 62****FIGURE 63****FIGURE 64****FIGURE 65****FIGURE 66**

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FIGURE 67**FIGURE 68****FIGURE 69****FIGURE 70**

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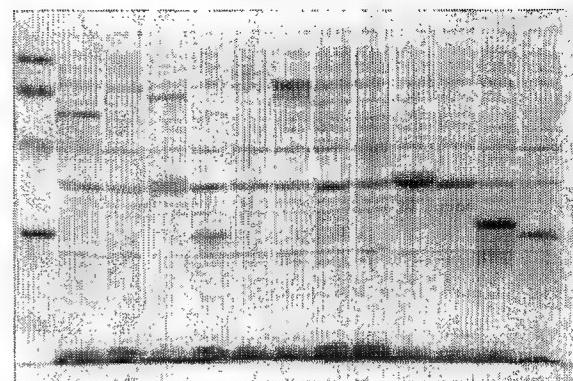
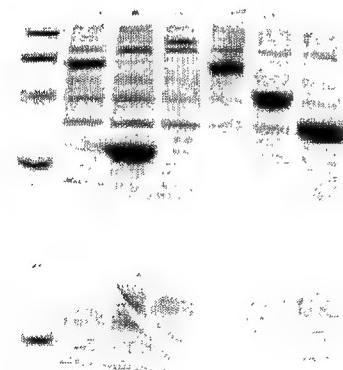
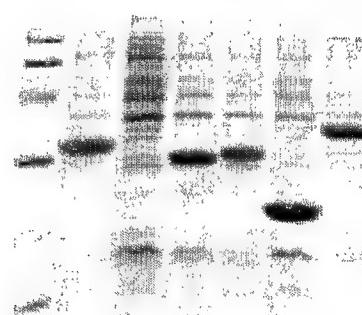
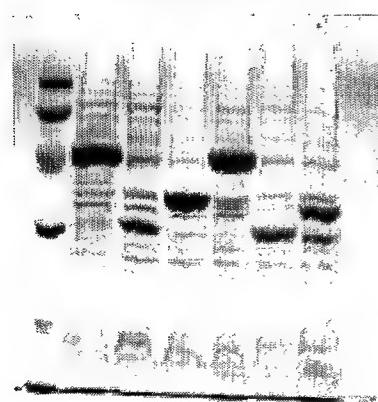
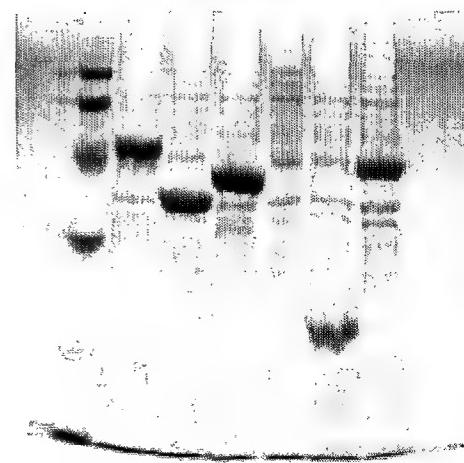
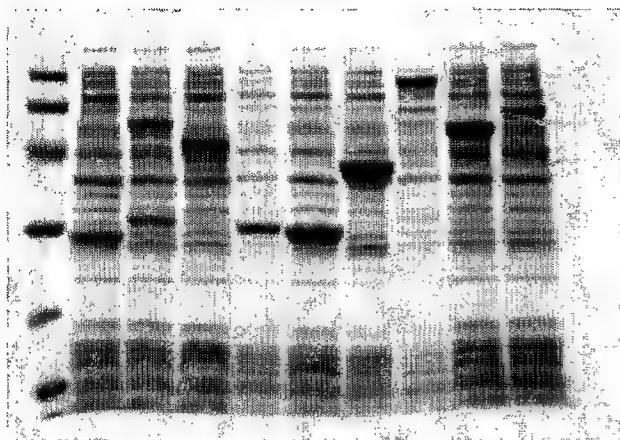
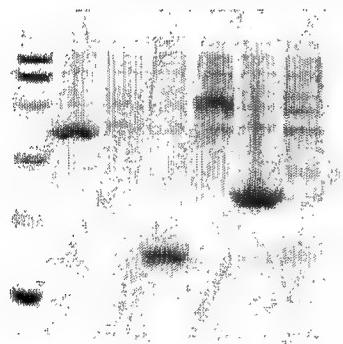
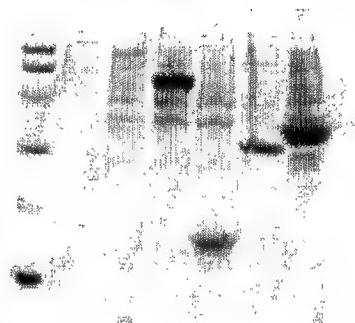
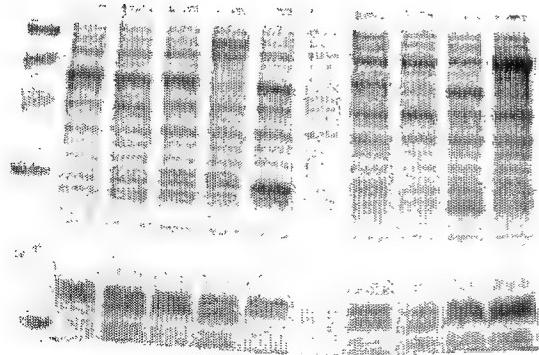
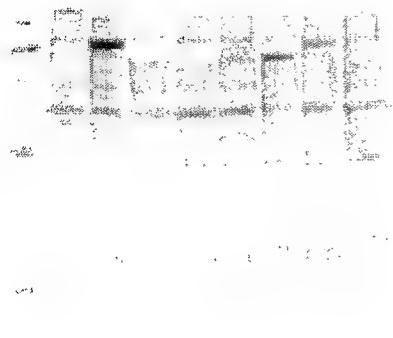
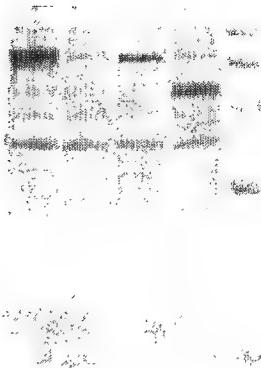
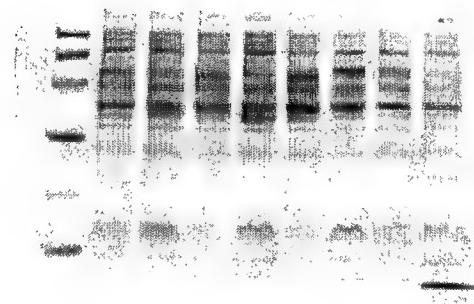
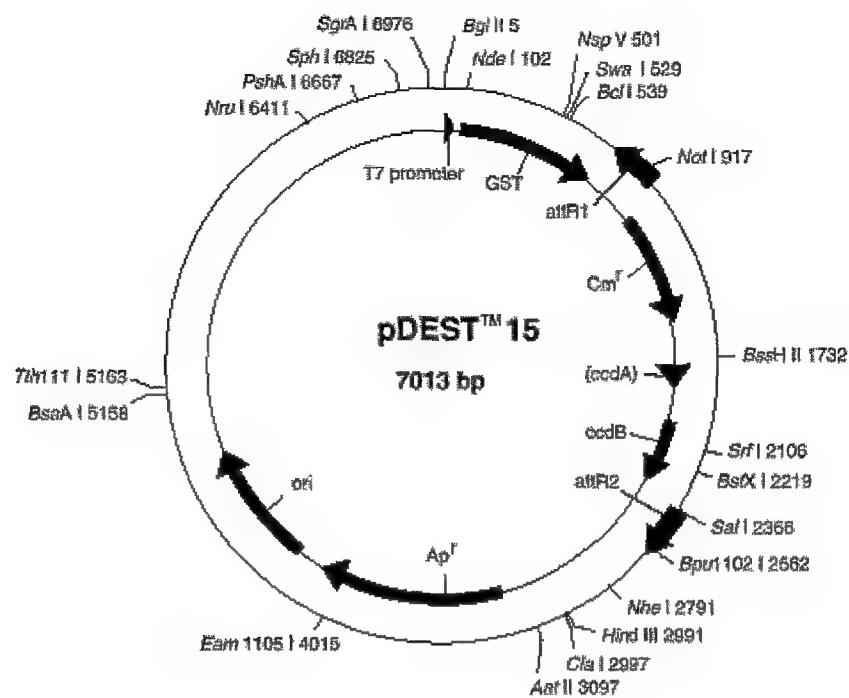
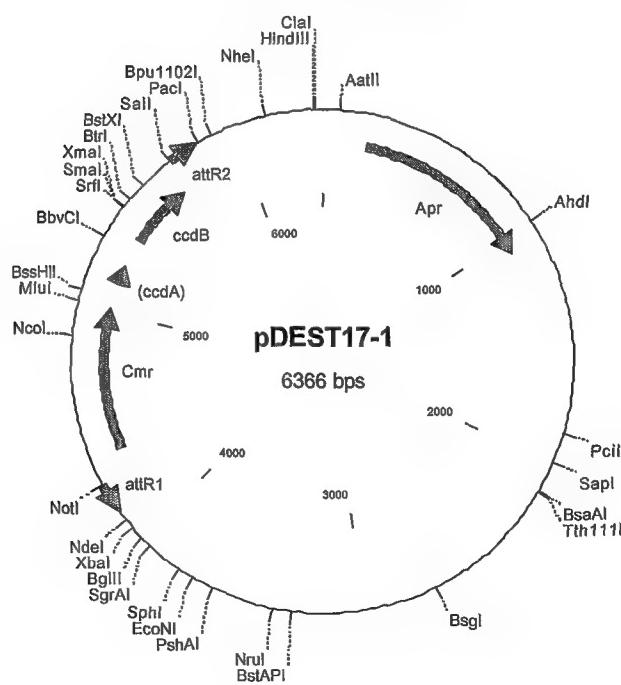
FIGURE 71**FIGURE 72****FIGURE 73****FIGURE 74****FIGURE 75****FIGURE 76**

FIGURE 77**FIGURE 78****FIGURE 79****FIGURE 80****FIGURE 81****FIGURE 82**

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FIGURE 83**FIGURE 84****FIGURE 85**

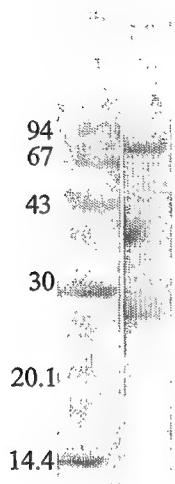
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FIGURE 86A**FIGURE 86B**

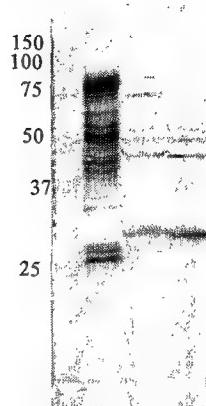
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FIGURE 87**FIGURE 87A**

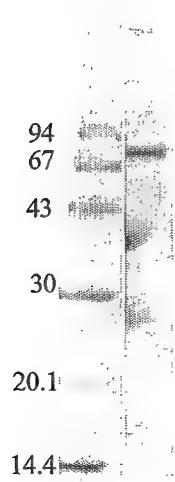
LMW 1

**FIGURE 87B**

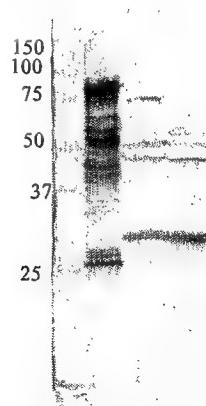
kD MW 1 2 3

**FIGURE 88****FIGURE 88A**

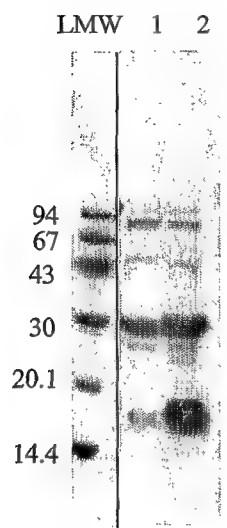
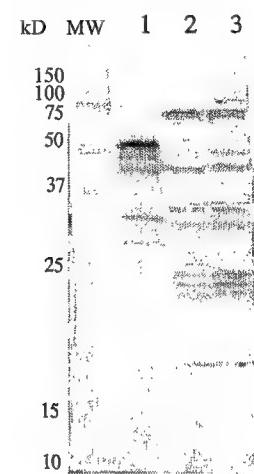
LMW 1

**FIGURE 88B**

kD MW 1 2 3



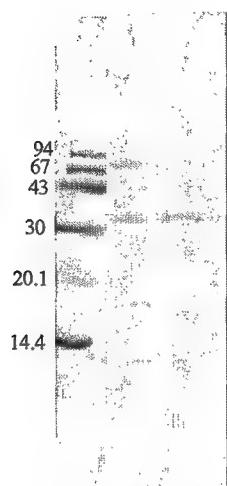
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FIGURE 89**FIGURE 89A****FIGURE 89B**

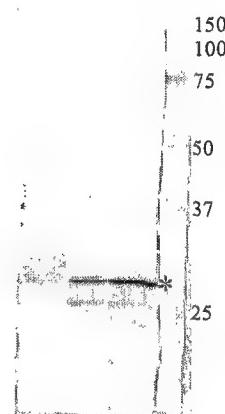
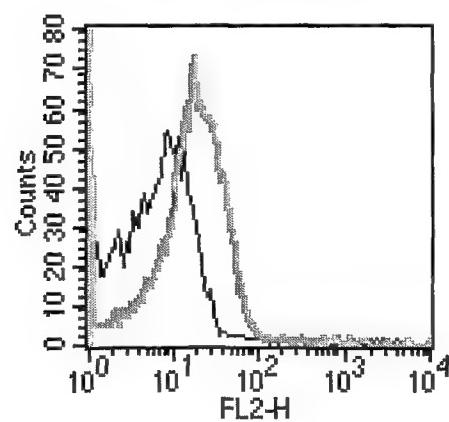
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FIGURE 90**FIGURE 90A**

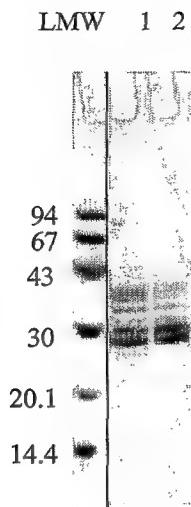
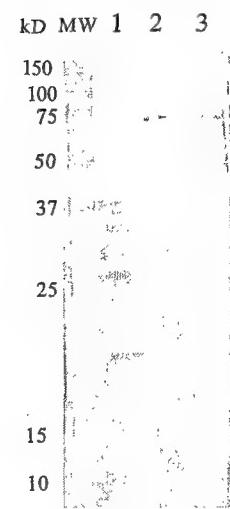
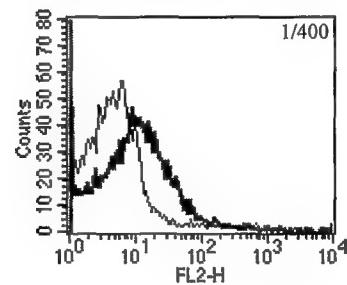
LMW 1 2

**FIGURE 90B**

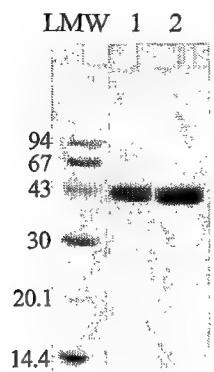
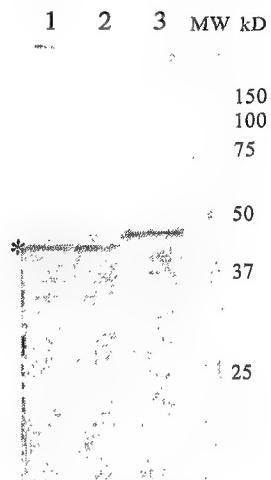
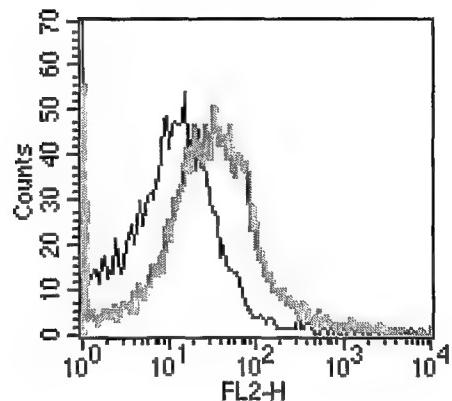
1 2 3 MW kD

**FIGURE 90C**

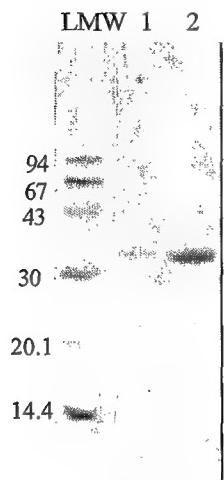
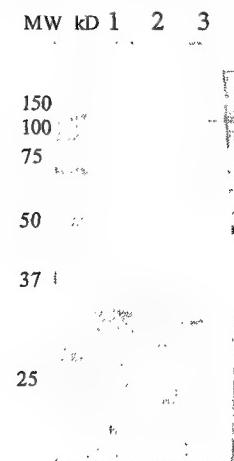
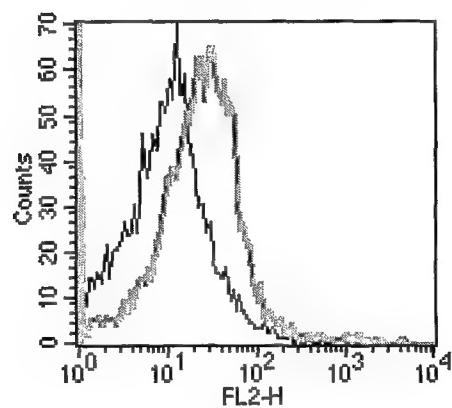
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FIGURE 91**FIGURE 91A****FIGURE 91B****FIGURE 91C**

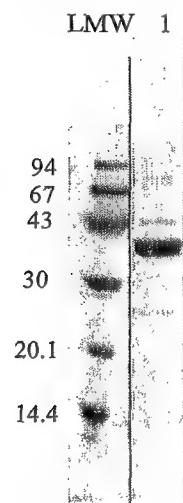
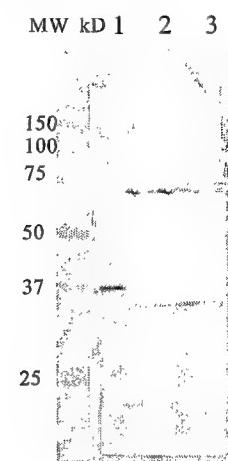
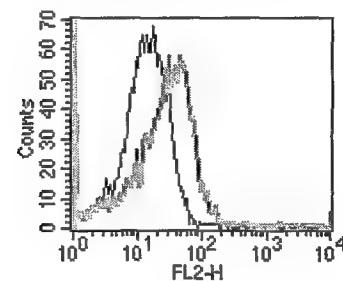
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FIGURE 92**FIGURE 92A****FIGURE 92B****FIGURE 92C**

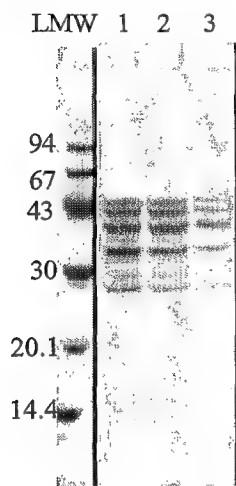
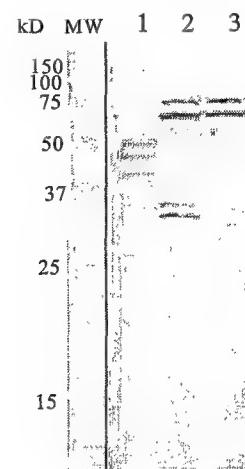
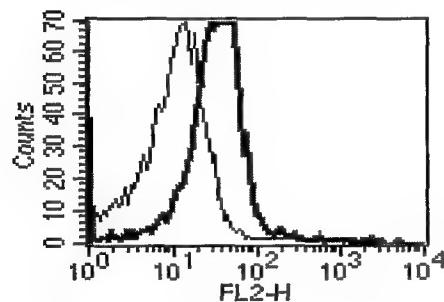
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FIGURE 93**FIGURE 93A****FIGURE 93B****FIGURE 93C**

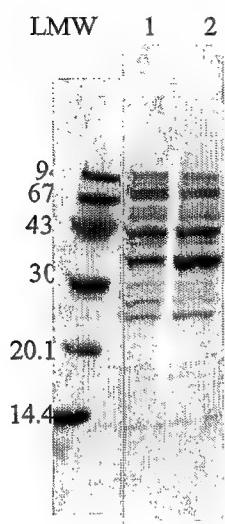
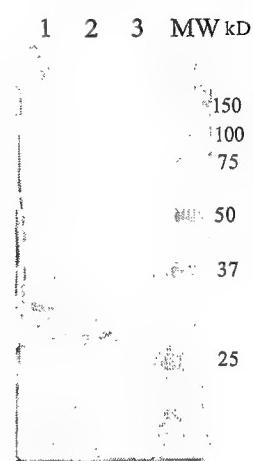
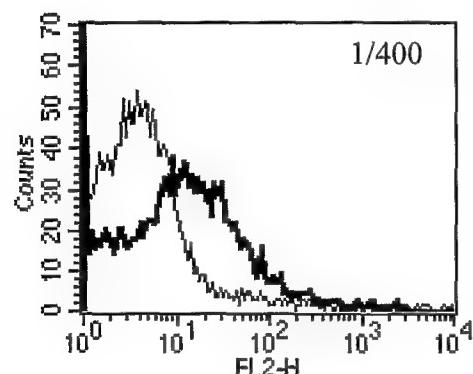
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FIGURE 94**FIGURE 94A****FIGURE 94B****FIGURE 94C**

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FIGURE 95**FIGURE 95A****FIGURE 95B****FIGURE 95C**

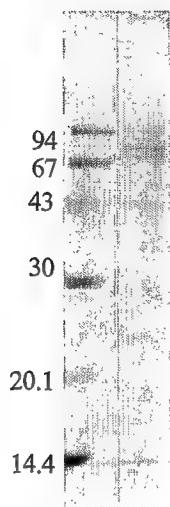
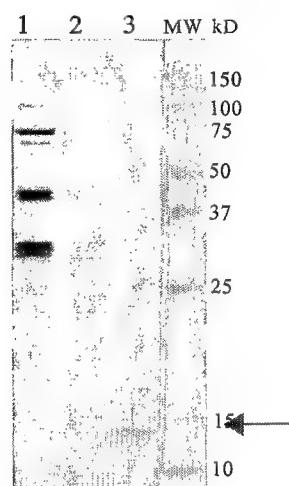
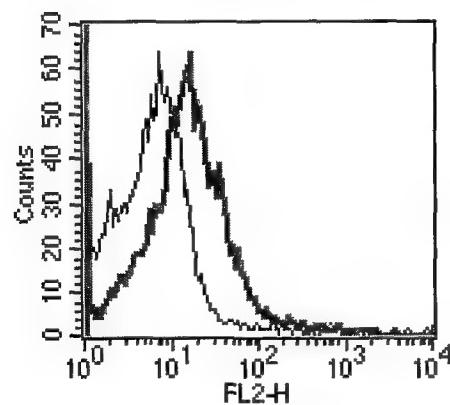
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FIGURE 96**FIGURE 96A****FIGURE 96B****FIGURE 96C**

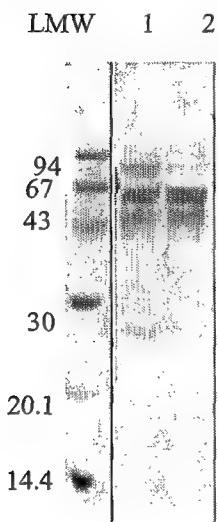
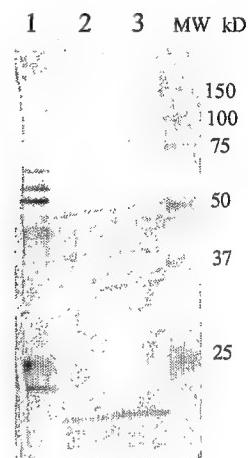
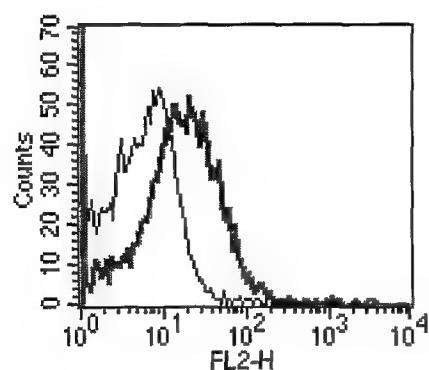
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FIGURE 97**FIGURE 97A**

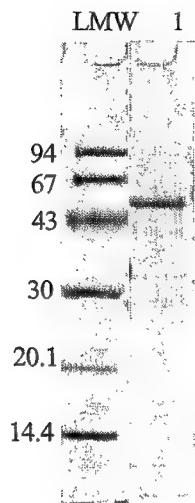
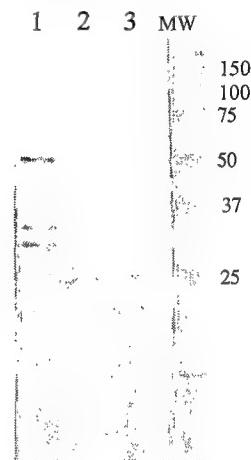
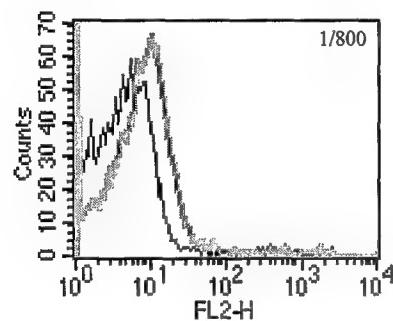
LMW 1

**FIGURE 97B****FIGURE 97C**

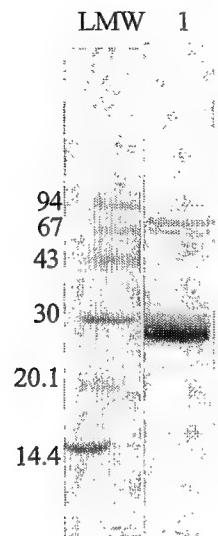
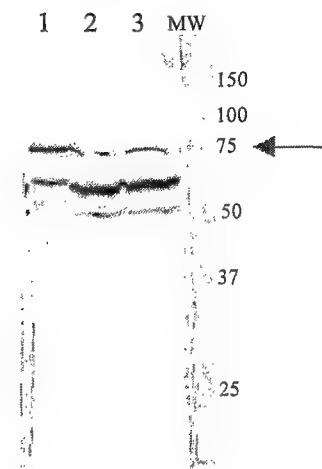
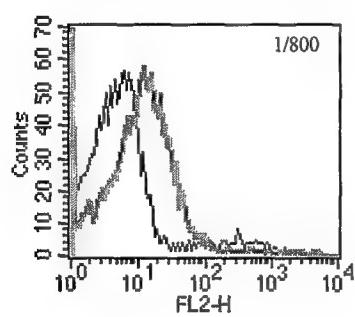
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FIGURE 98**FIGURE 98A****FIGURE 98B****FIGURE 98C**

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FIGURE 99**FIGURE 99A****FIGURE 99B****FIGURE 99C**

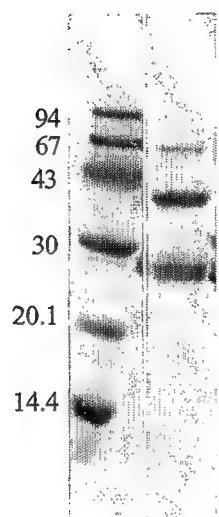
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FIGURE 100**FIGURE 100A****FIGURE 100B****FIGURE 100C**

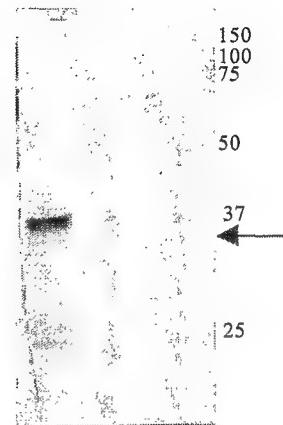
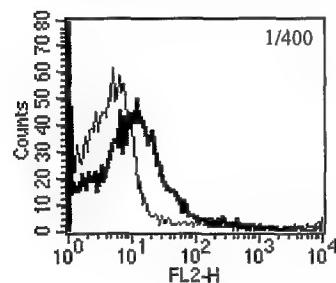
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FIGURE 101**FIGURE 101A**

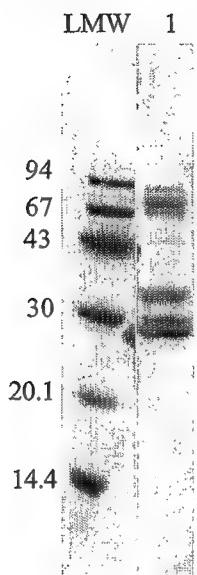
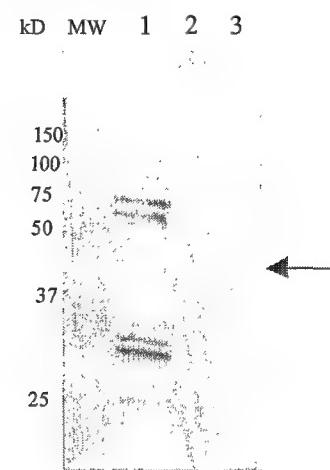
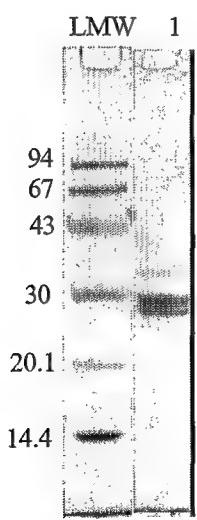
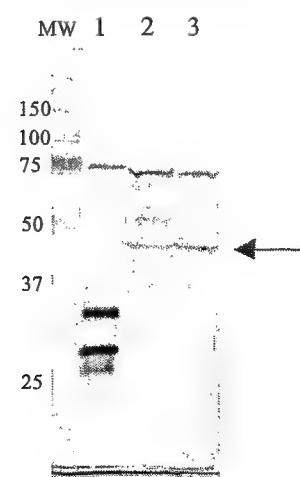
LMW 1

**FIGURE 101B**

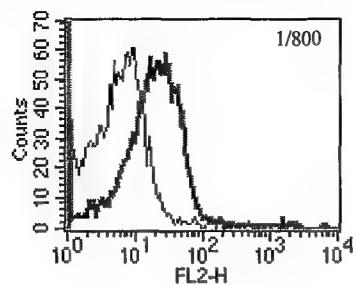
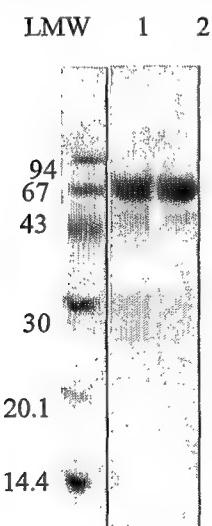
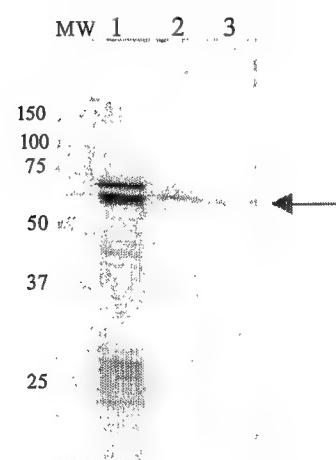
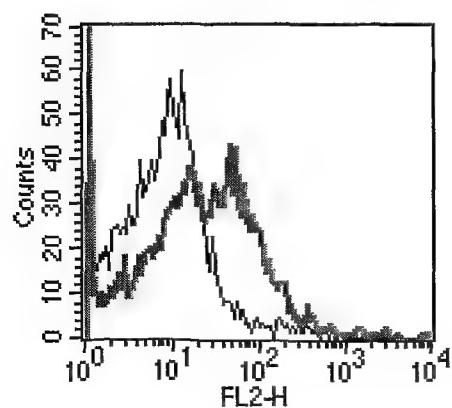
1 2 3 MW

**FIGURE 101C**

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FIGURE 102**FIGURE 102A****FIGURE 102B****FIGURE 103****FIGURE 103A****FIGURE 103B**

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FIGURE 103C**FIGURE 104****FIGURE 104A****FIGURE 104B****FIGURE 104C**

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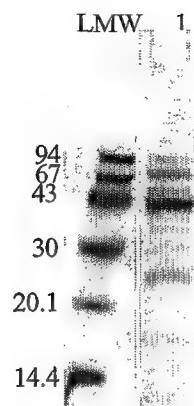
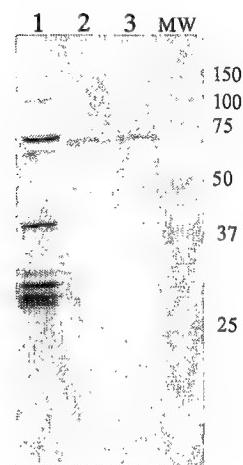
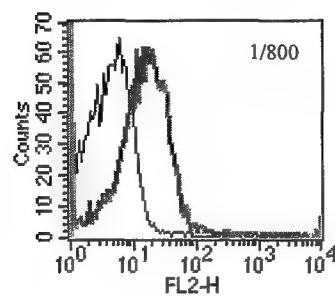
FIGURE 105**FIGURE 105A****FIGURE 105B****FIGURE 105C**

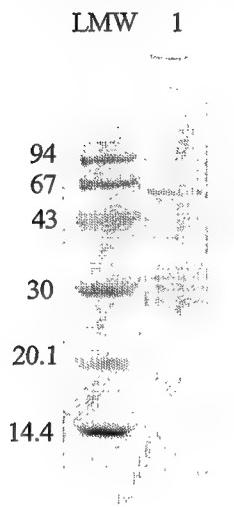
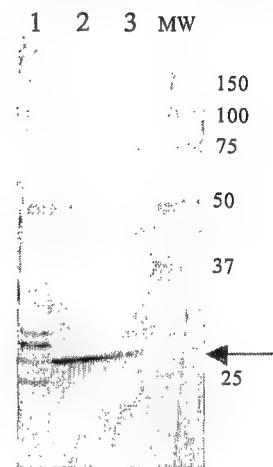
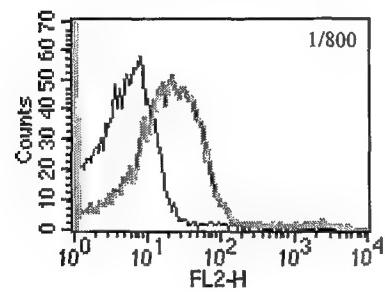
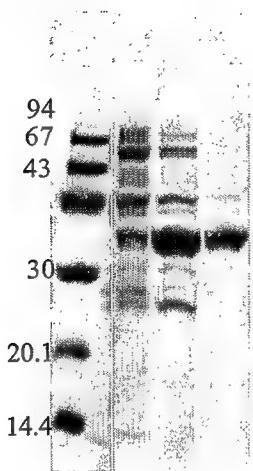
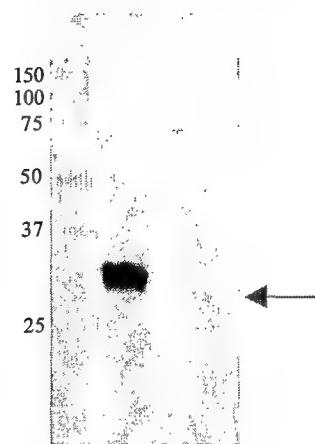
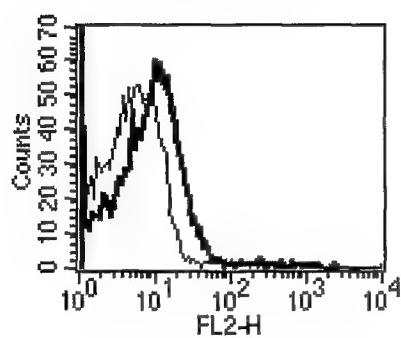
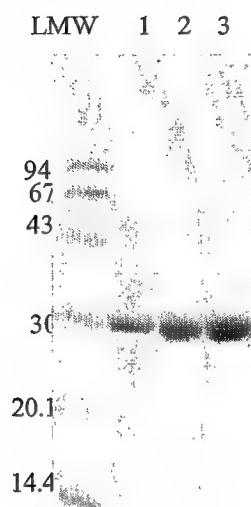
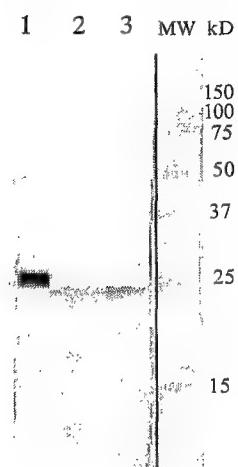
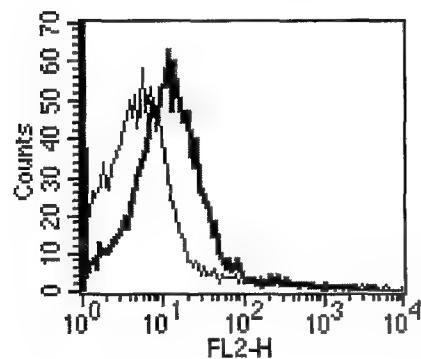
FIGURE 106**FIGURE 106A****FIGURE 106B****FIGURE 106C**

FIGURE 107**FIGURE 107A**

LMW 1 2 3

**FIGURE 107B****FIGURE 107C**

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FIGURE 108**FIGURE 108A****FIGURE 108B****FIGURE 108C**

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FIGURE 109**FIGURE 109A**

LMW 1 2

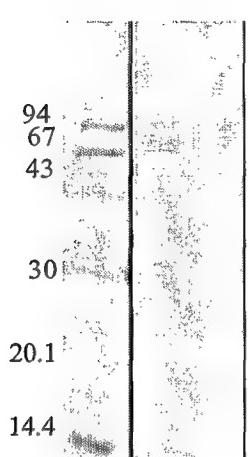
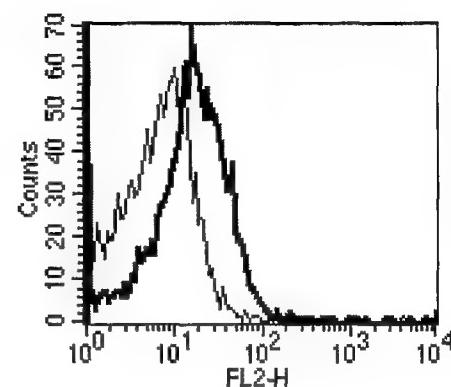
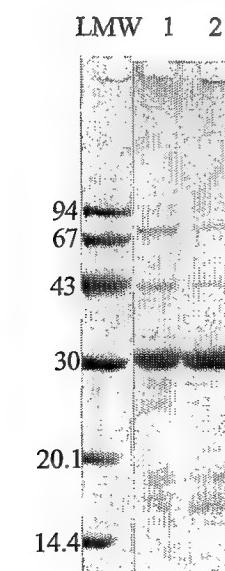
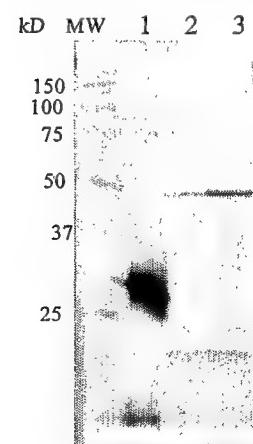
**FIGURE 109B****FIGURE 110****FIGURE 110A****FIGURE 110B**

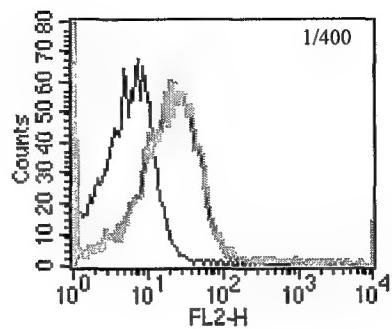
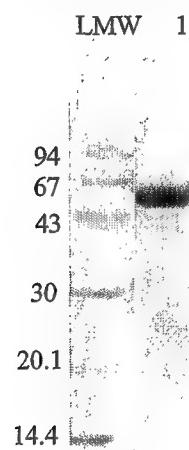
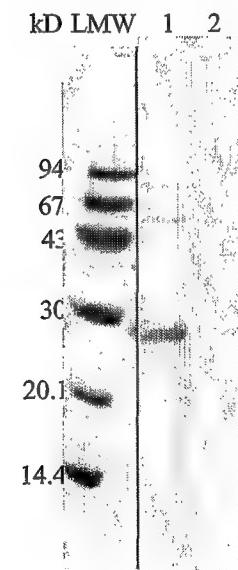
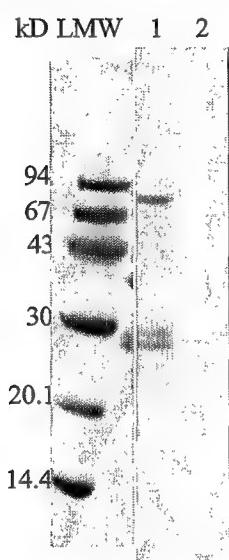
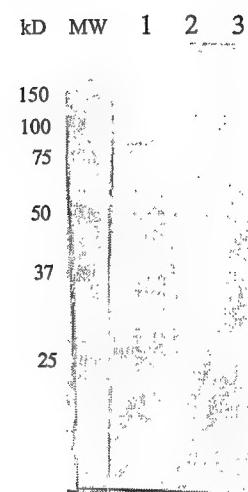
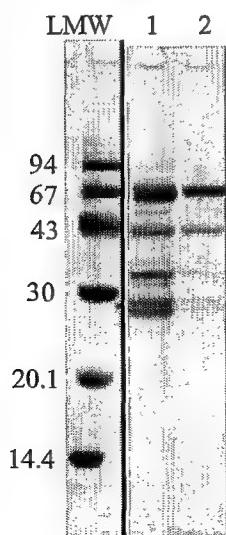
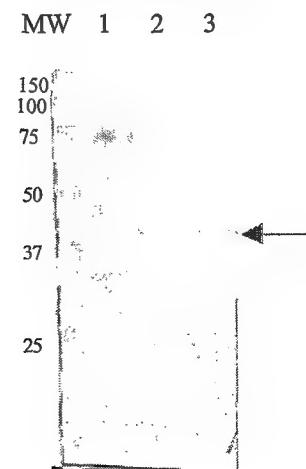
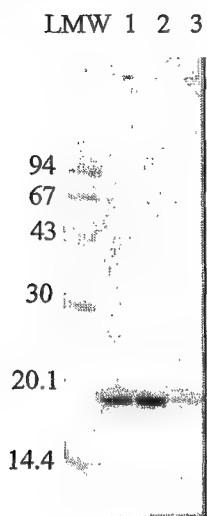
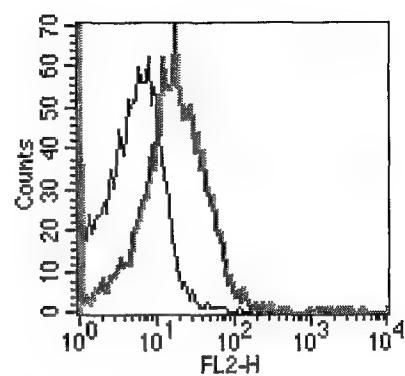
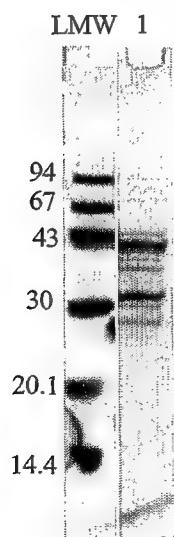
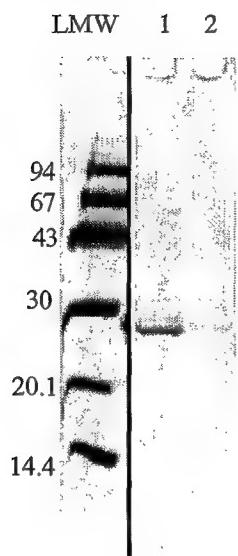
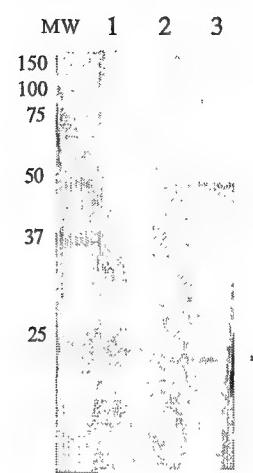
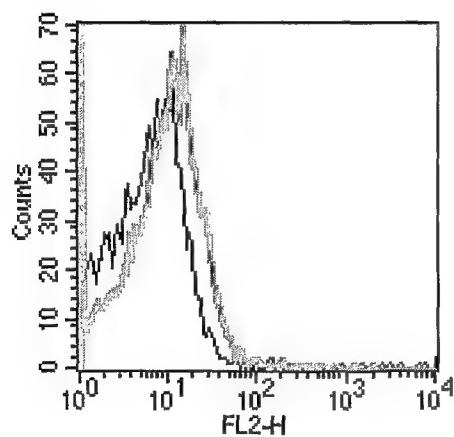
FIGURE 110C**FIGURE 111****FIGURE 113**

FIGURE 112**FIGURE 112A****FIGURE 112B****FIGURE 114****FIGURE 114A****FIGURE 114B**

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FIGURE 115**FIGURE 115A****FIGURE 115B****FIGURE 116****FIGURE 116A**

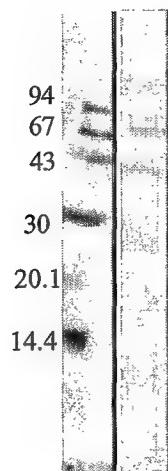
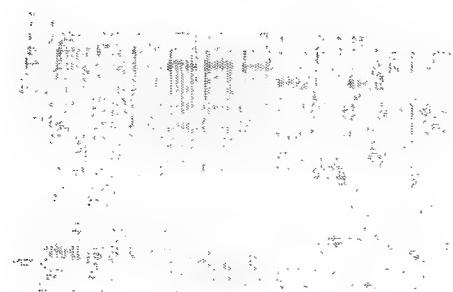
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FIGURE 117**FIGURE 117A****FIGURE 117B****FIGURE 117C**

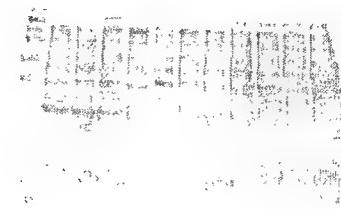
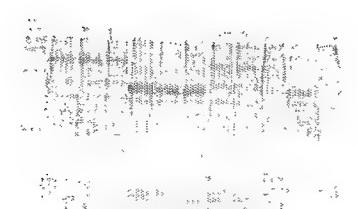
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FIGURE 118

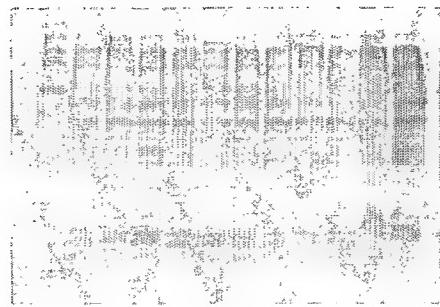
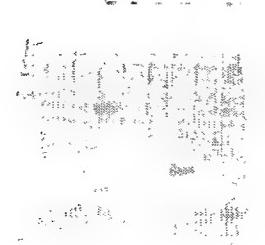
LMW 1

**FIGURE 119****FIGURE 120**

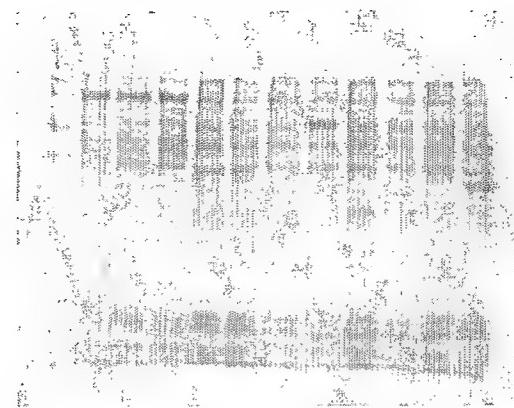
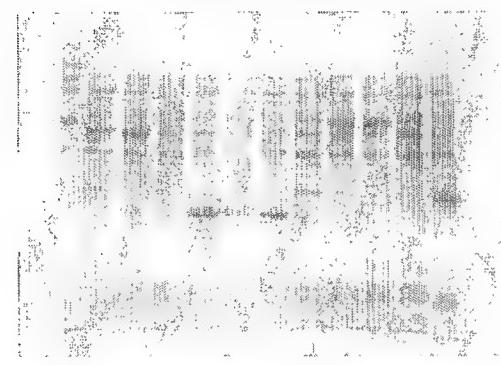
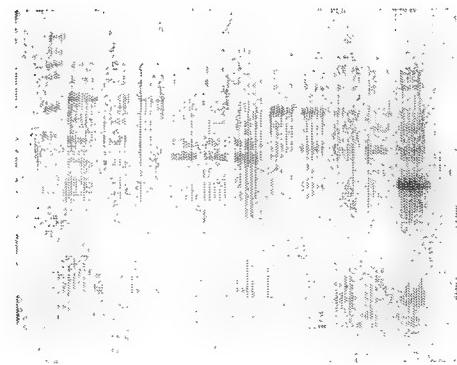
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FIGURE 121**FIGURE 122****FIGURE 123****FIGURE 124**

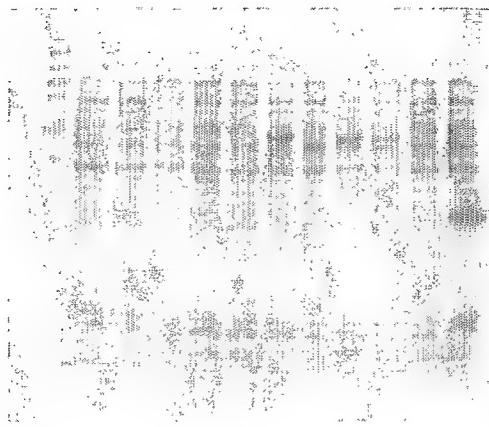
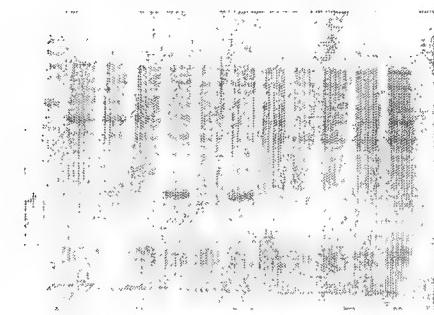
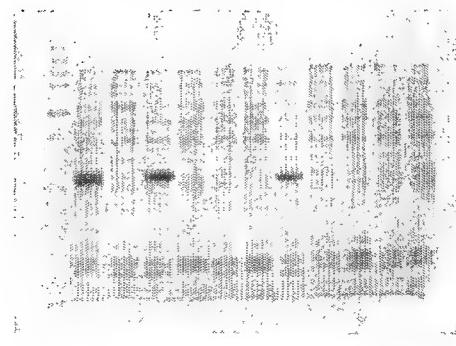
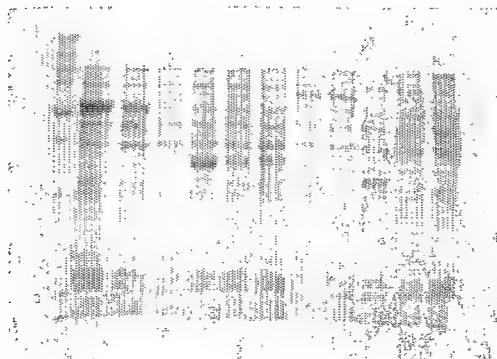
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FIGURE 125**FIGURE 126****FIGURE 127****FIGURE 128**

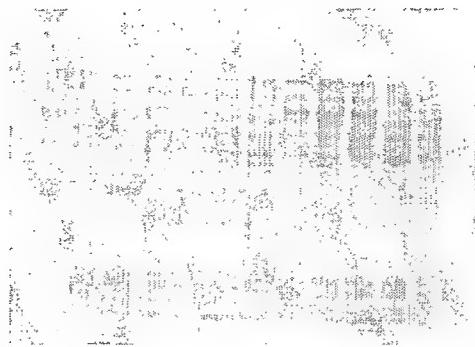
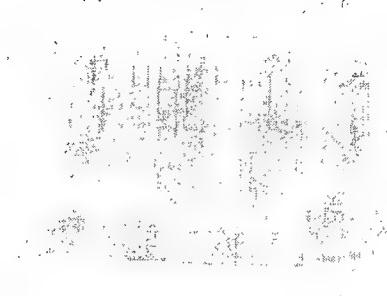
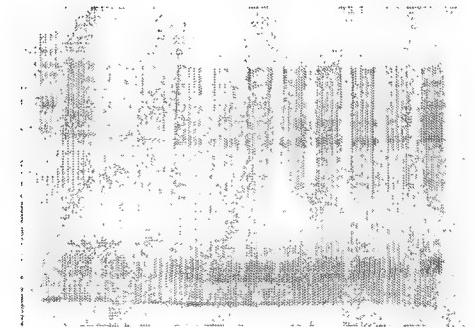
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FIGURE 129**FIGURE 130****FIGURE 131**

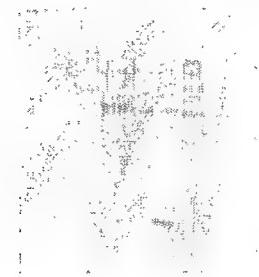
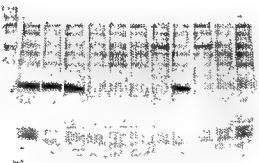
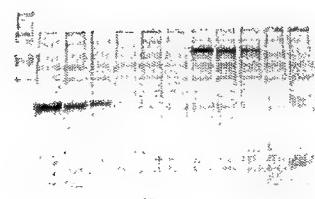
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FIGURE 132**FIGURE 133****FIGURE 134****FIGURE 135**

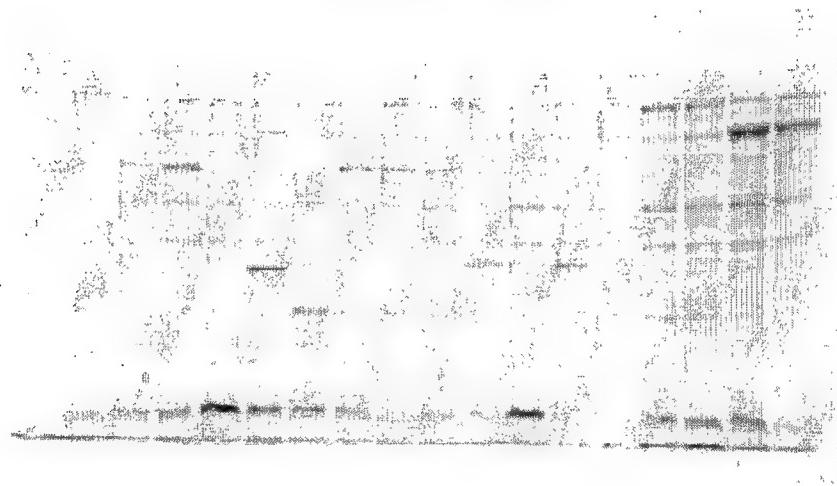
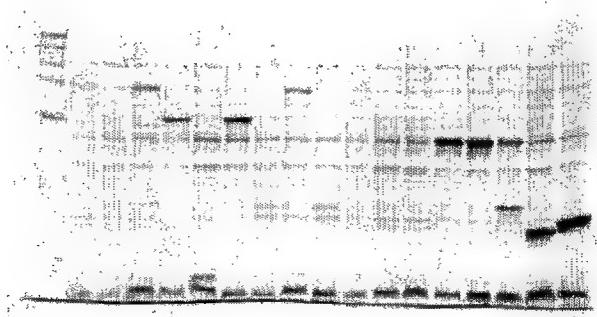
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FIGURE 136**FIGURE 137****FIGURE 138****FIGURE 139**

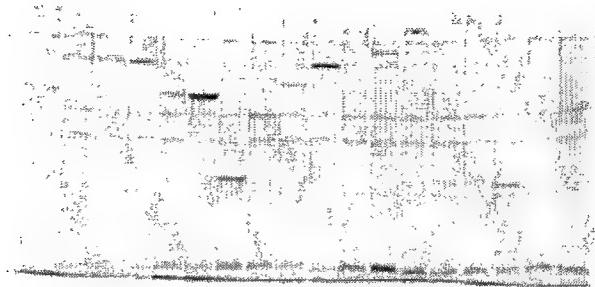
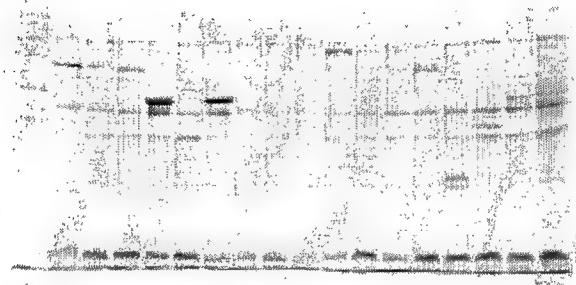
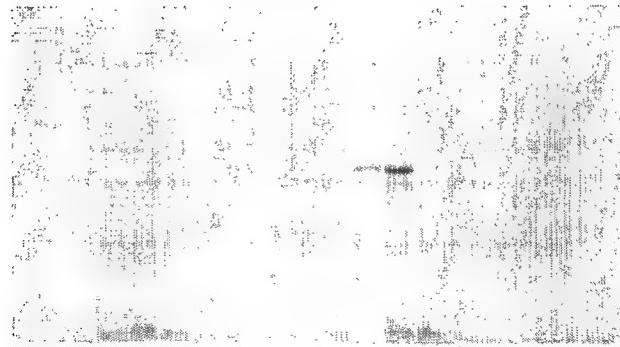
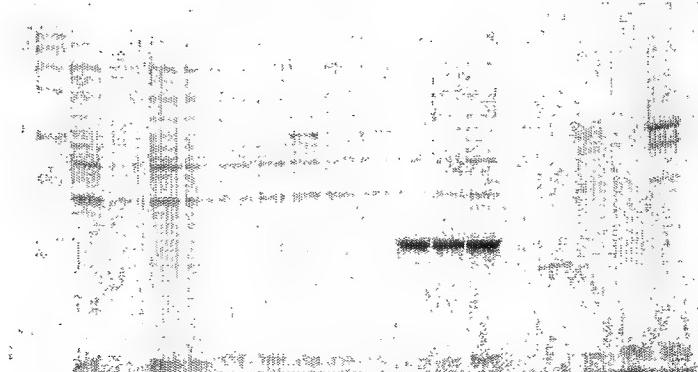
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FIGURE 140**FIGURE 141****FIGURE 142****FIGURE 143**

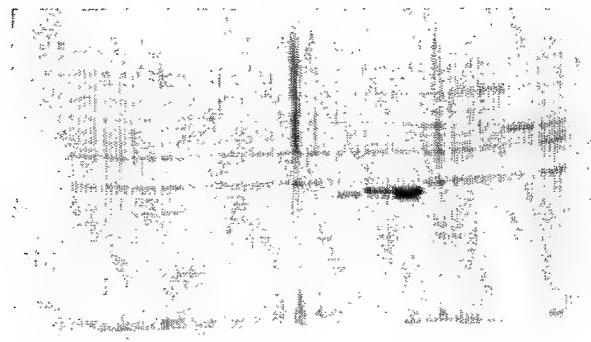
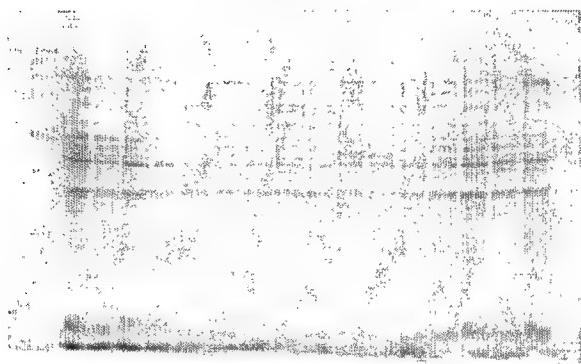
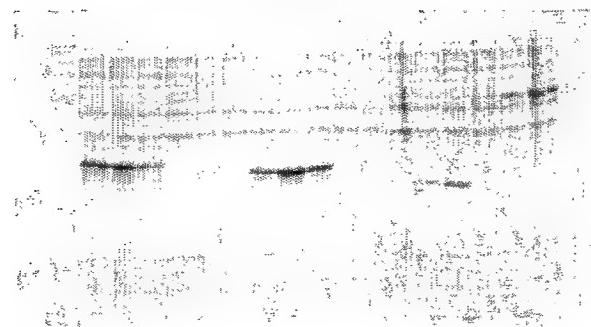
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FIGURE 144**FIGURE 145****FIGURE 146**

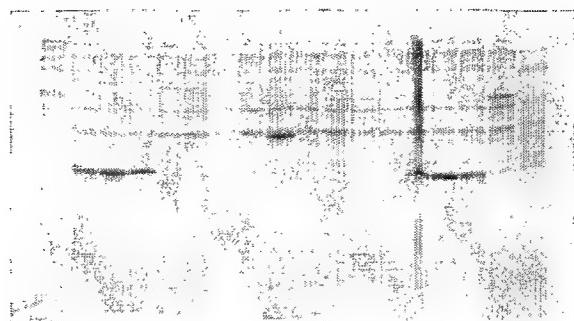
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FIGURE 147**FIGURE 148****FIGURE 149****FIGURE 150**

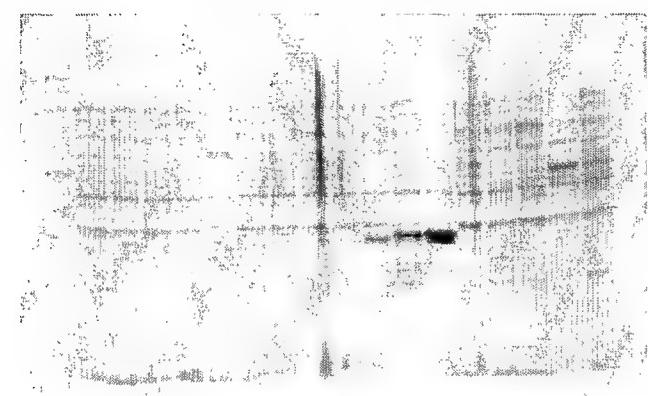
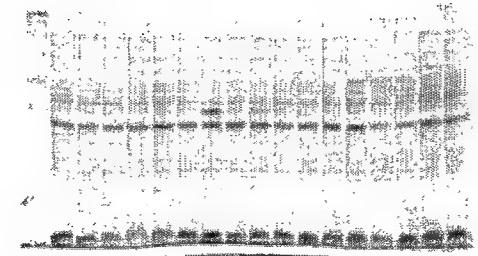
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FIGURE 151**FIGURE 152****FIGURE 153****FIGURE 154**

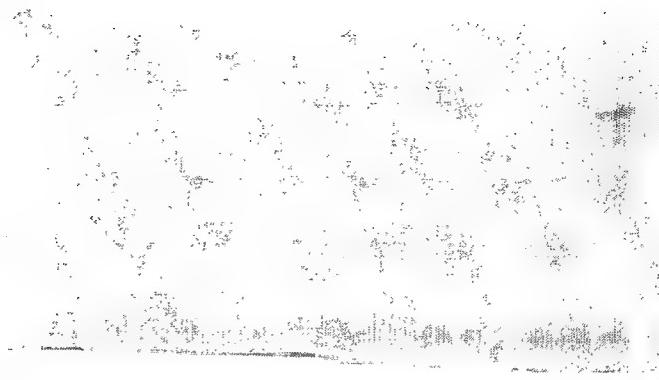
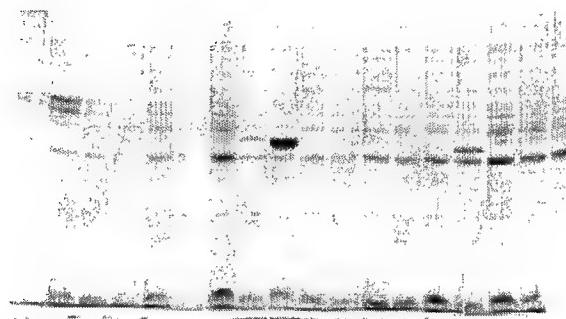
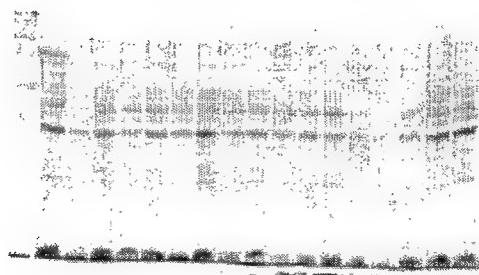
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FIGURE 155**FIGURE 156****FIGURE 157****FIGURE 158**

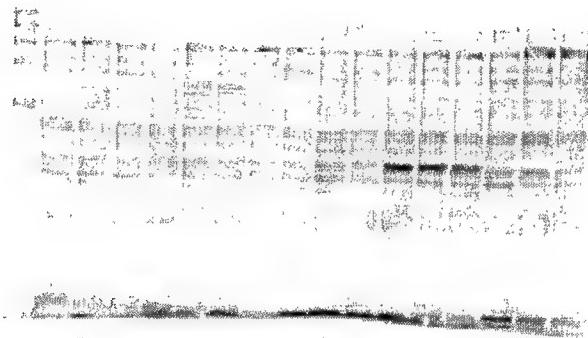
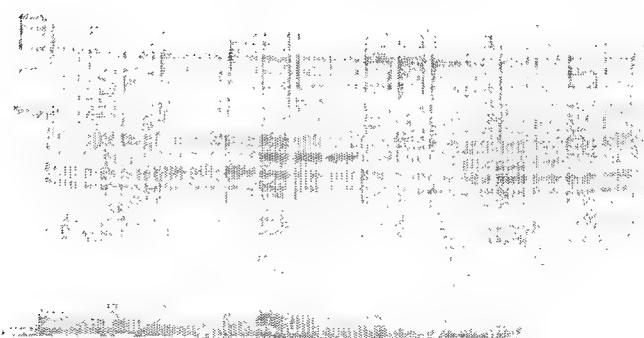
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FIGURE 159**FIGURE 160****FIGURE 161****FIGURE 162**

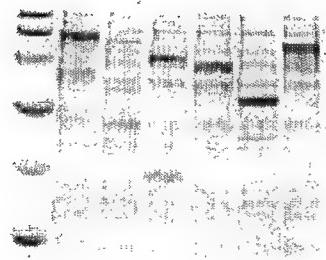
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FIGURE 163**FIGURE 164****FIGURE 165**

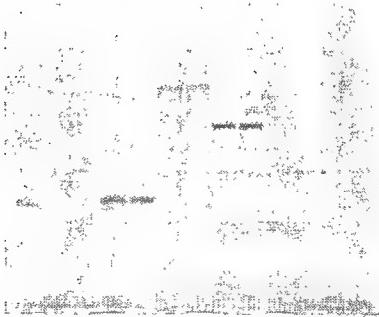
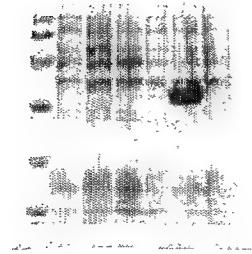
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FIGURE 166**FIGURE 167****FIGURE 168**

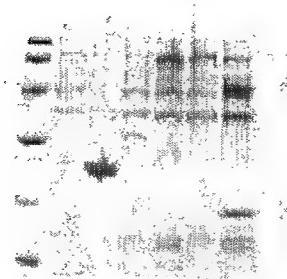
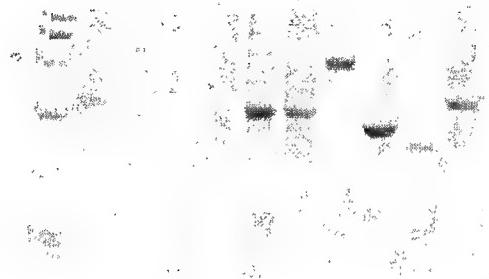
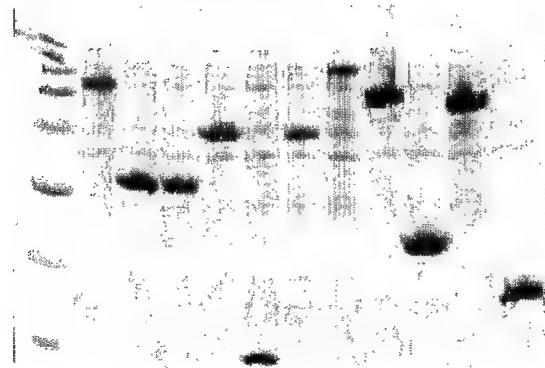
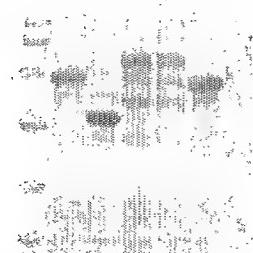
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FIGURE 169**FIGURE 170****FIGURE 171****FIGURE 172**

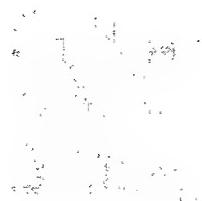
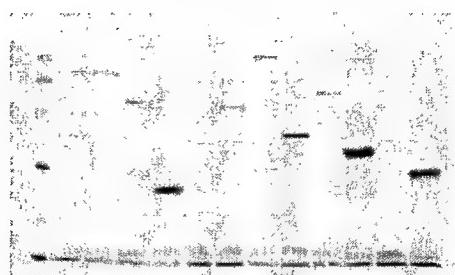
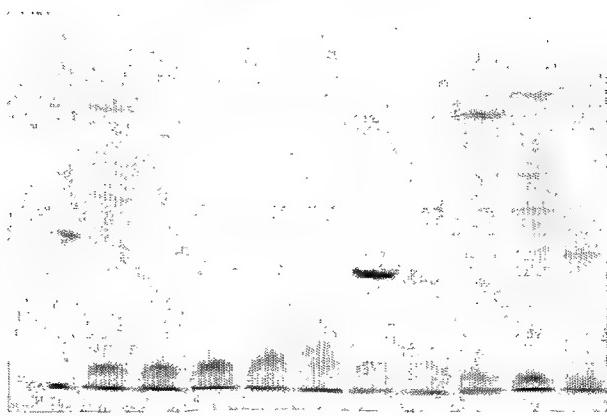
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FIGURE 173**FIGURE 174****FIGURE 175****FIGURE 176**

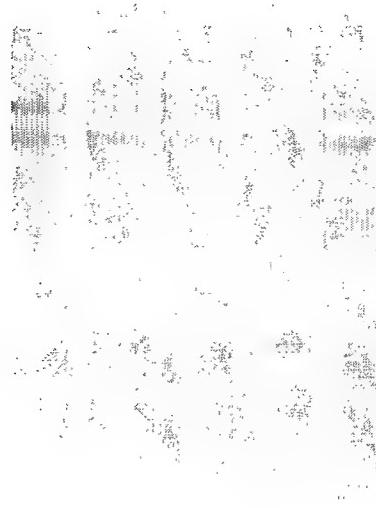
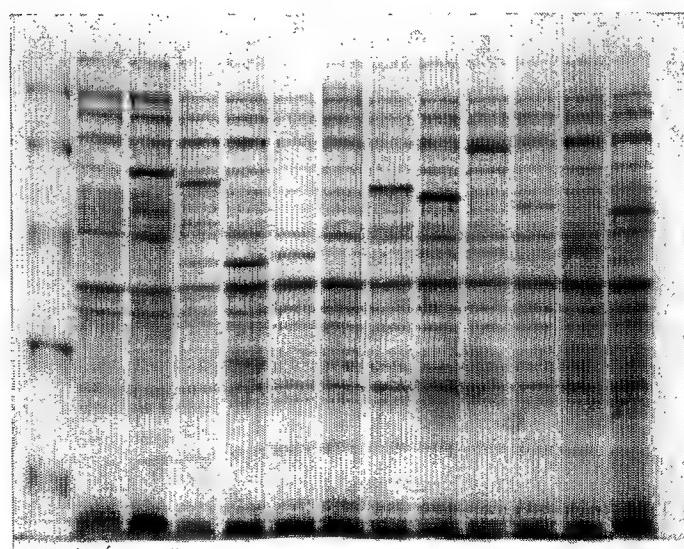
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FIGURE 177**FIGURE 178****FIGURE 179****FIGURE 180**

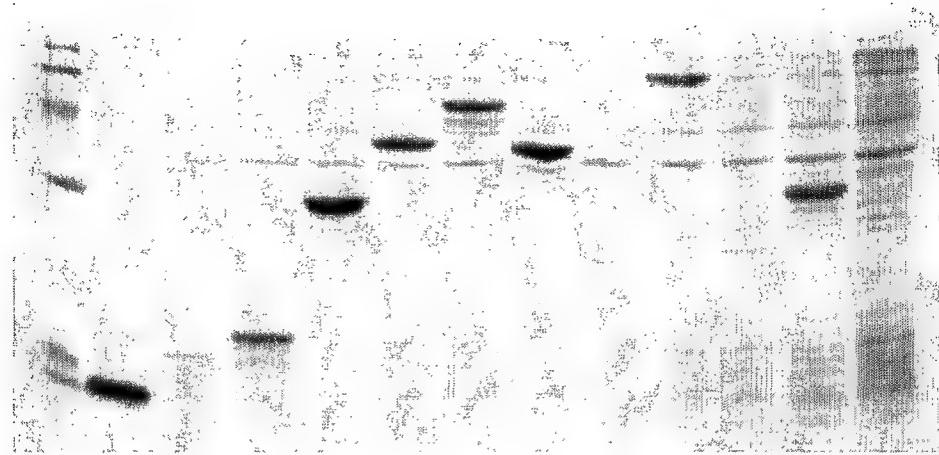
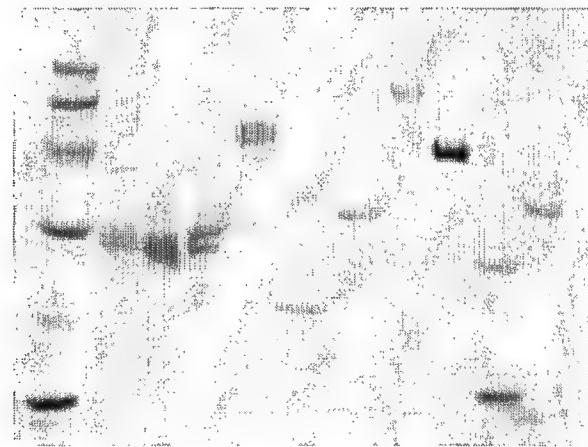
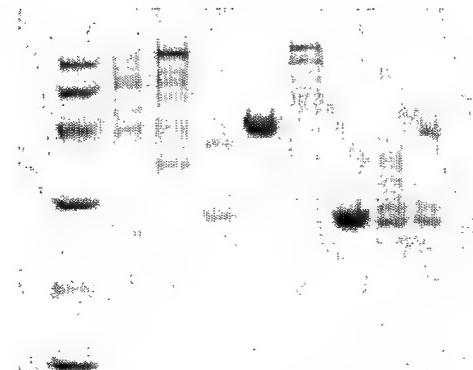
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FIGURE 181**FIGURE 182****FIGURE 183****FIGURE 184**

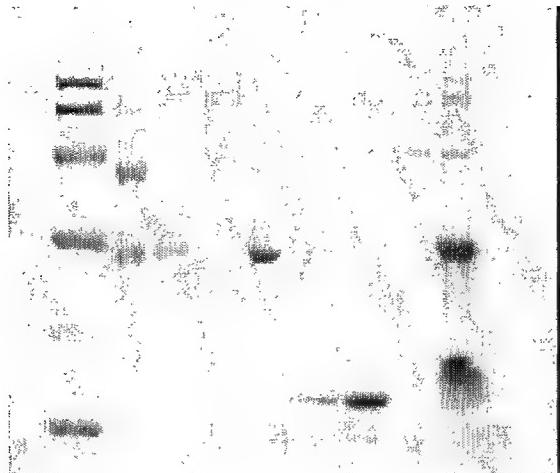
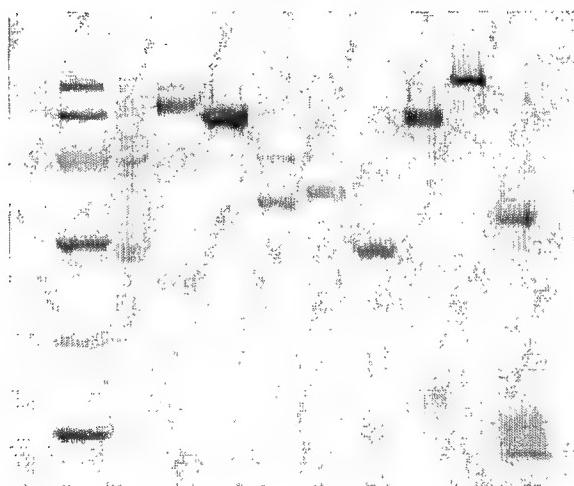
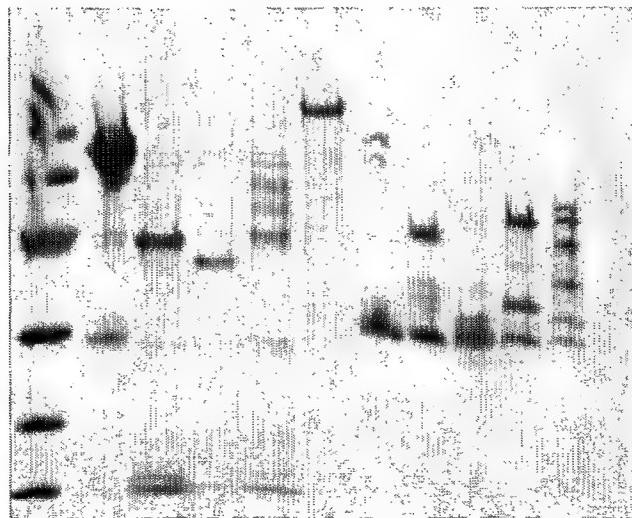
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FIGURE 185**FIGURE 186****FIGURE 187**

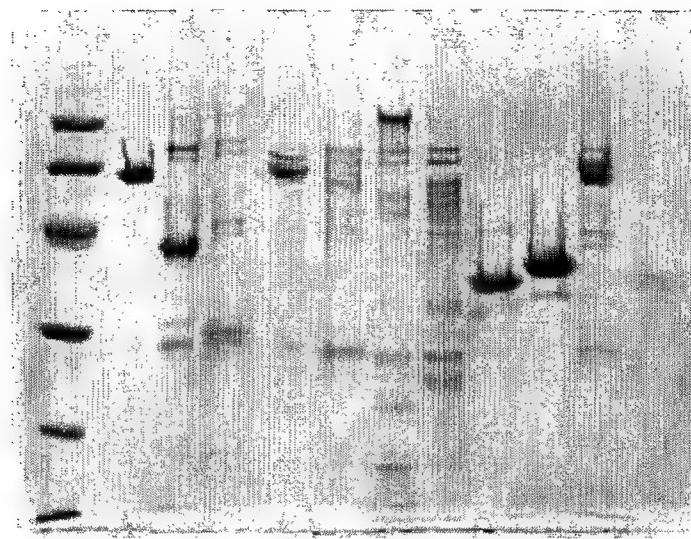
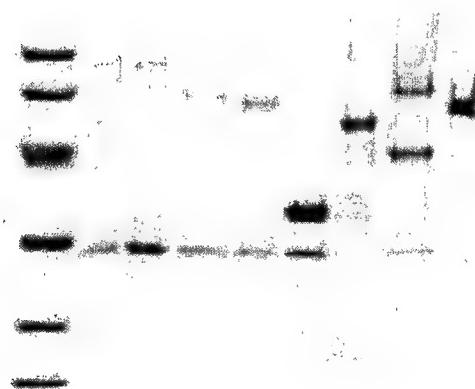
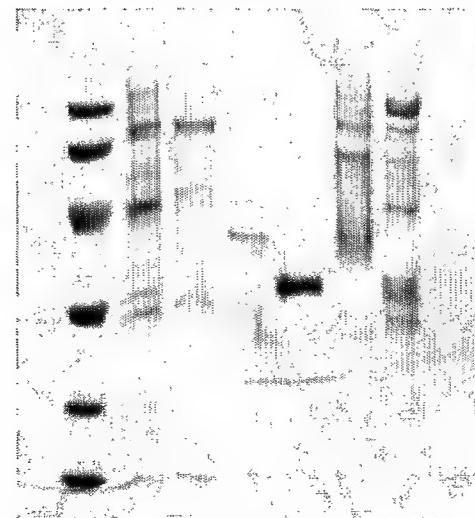
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FIGURE 188**FIGURE 189****FIGURE 190**

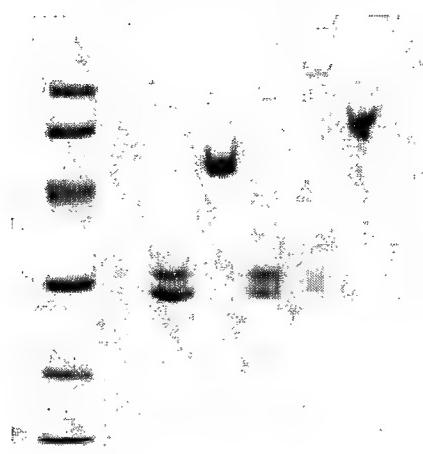
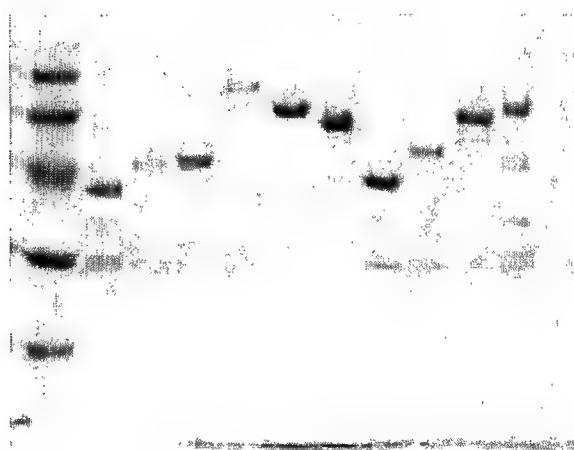
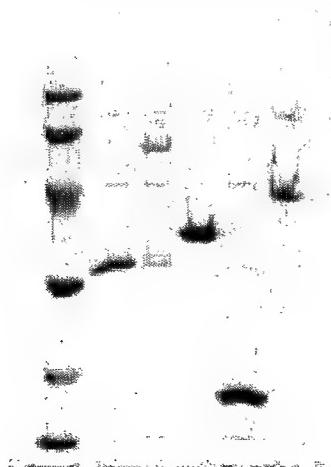
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FIGURE 191**FIGURE 192****FIGURE 193**

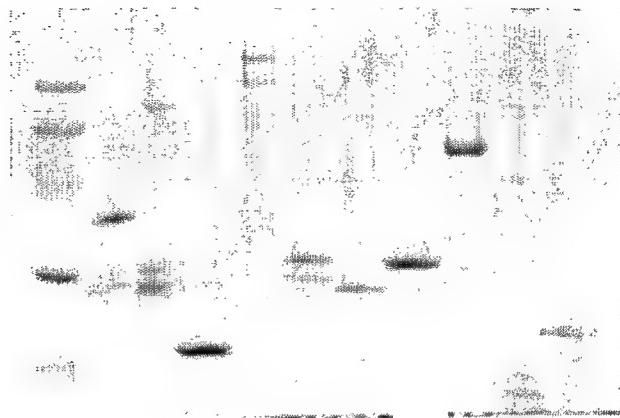
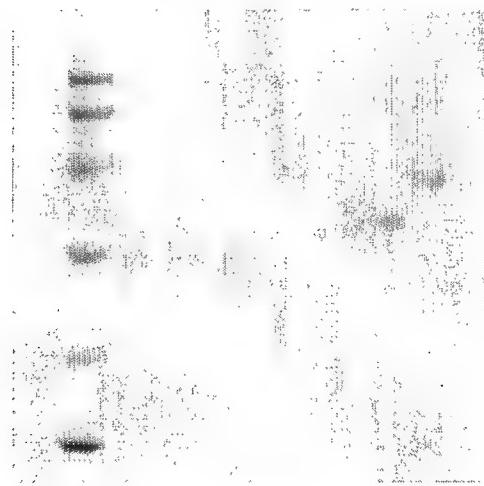
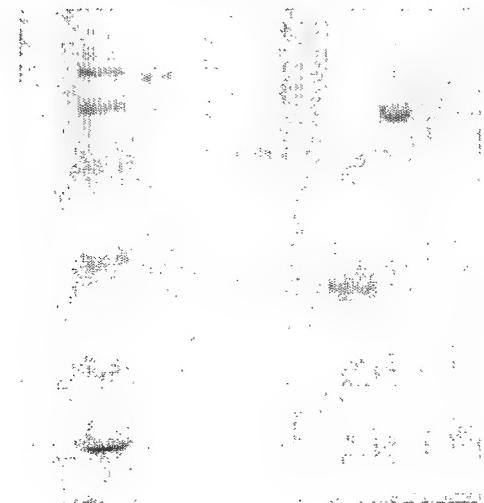
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FIGURE 194**FIGURE 195****FIGURE 196**

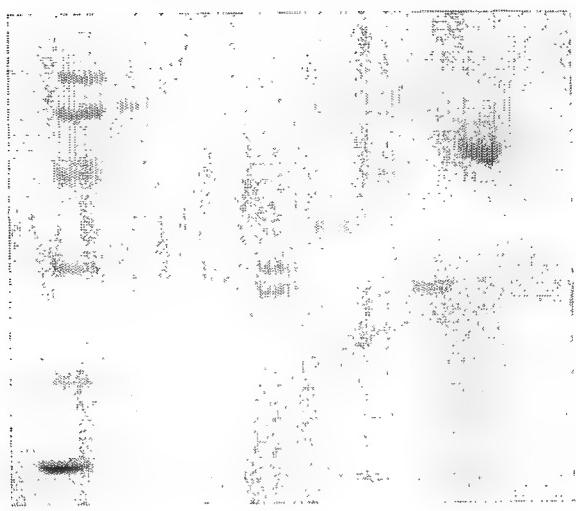
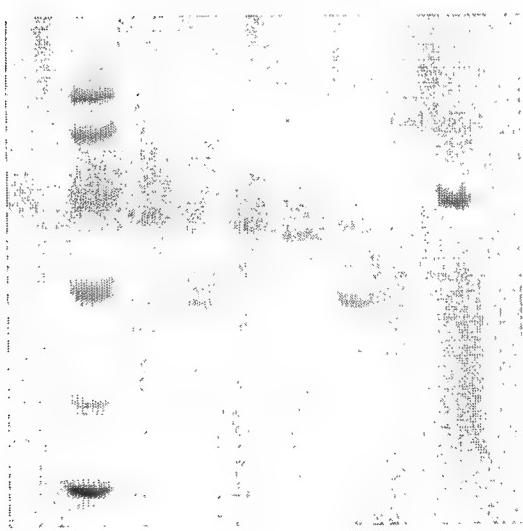
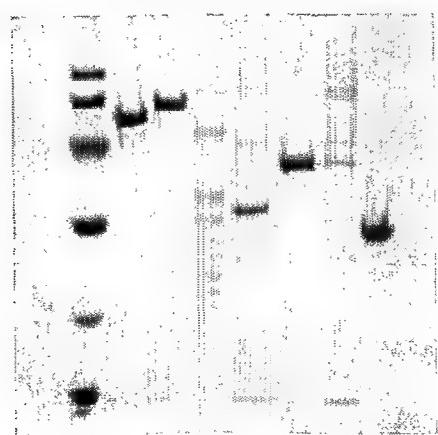
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FIGURE 197**FIGURE 198****FIGURE 199**

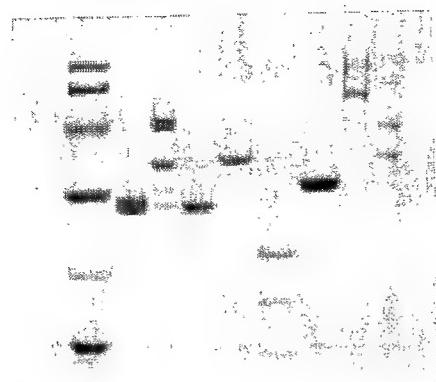
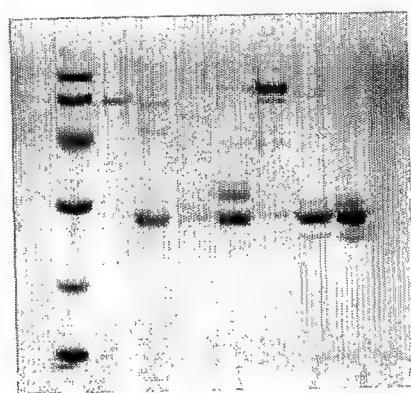
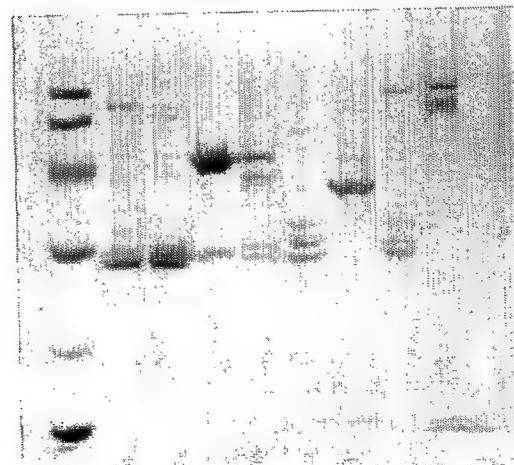
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FIGURE 200**FIGURE 201****FIGURE 202**

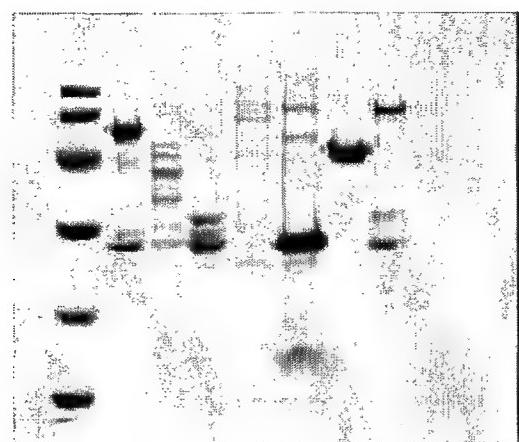
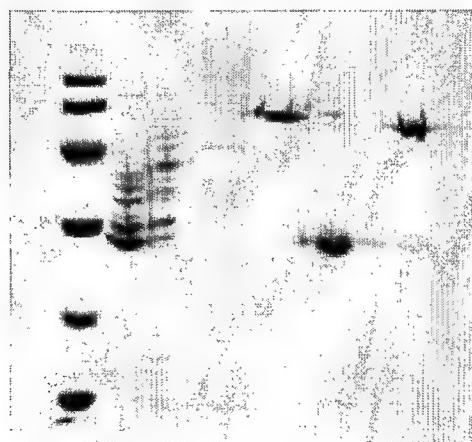
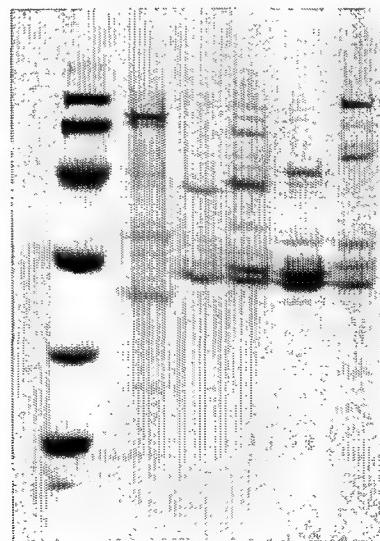
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FIGURE 203**FIGURE 204****FIGURE 205**

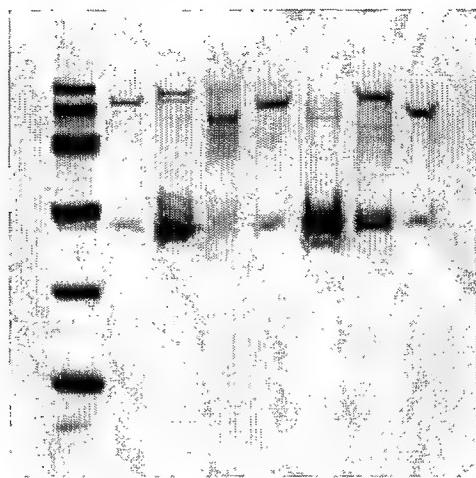
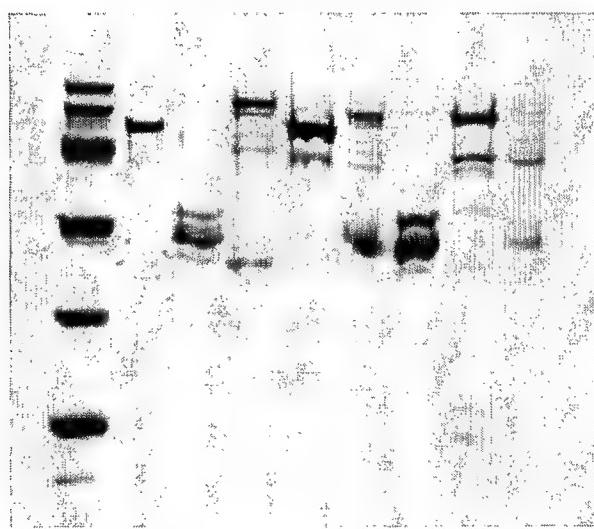
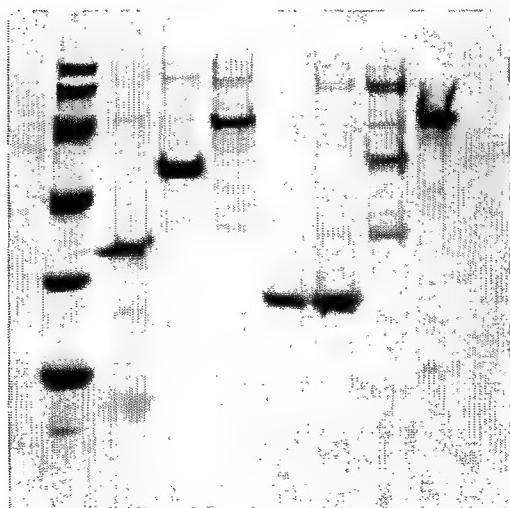
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FIGURE 206**FIGURE 207****FIGURE 208**

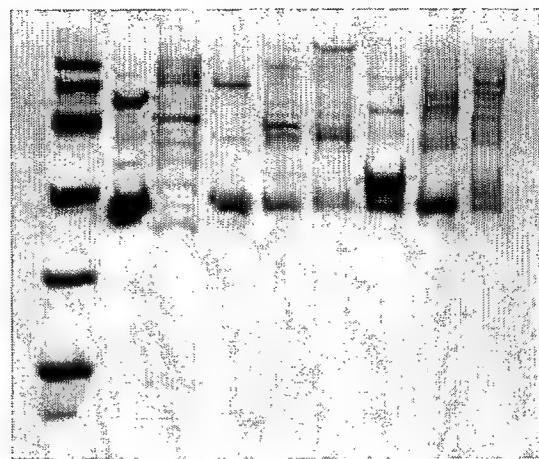
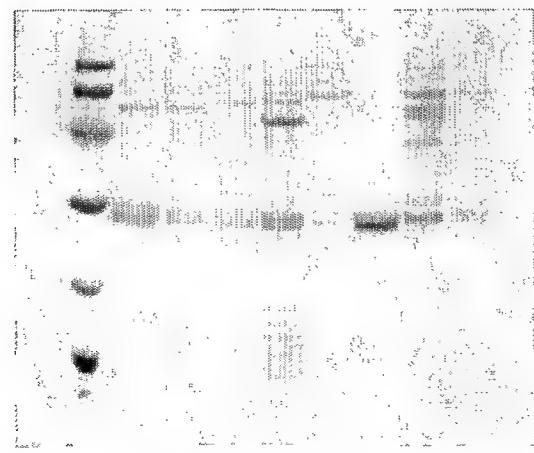
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FIGURE 209**FIGURE 210****FIGURE 211**

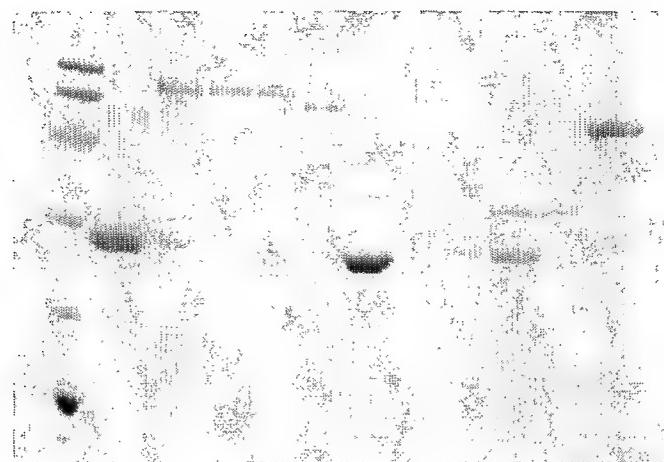
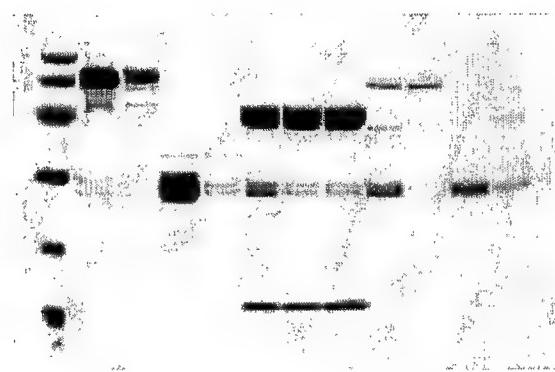
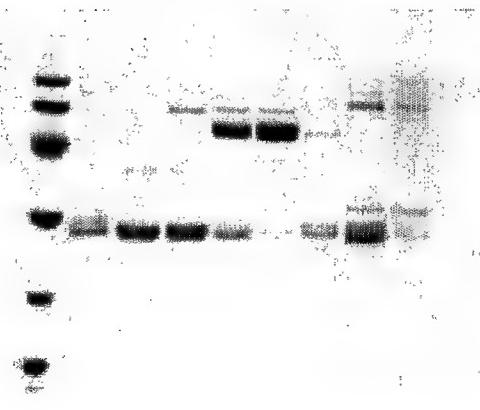
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FIGURE 212**FIGURE 213****FIGURE 214**

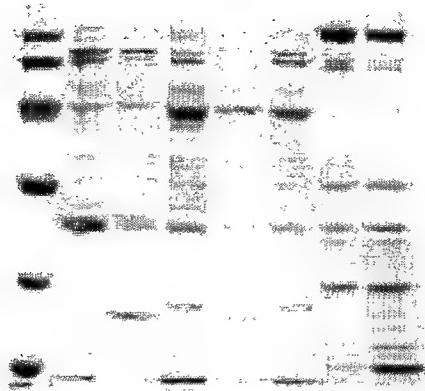
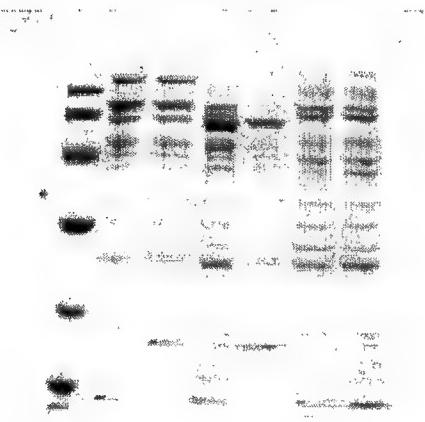
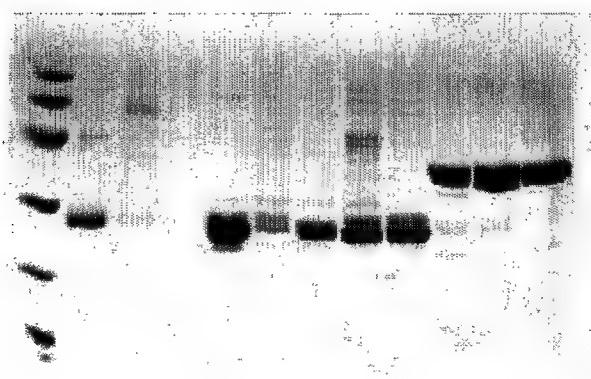
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FIGURE 215**FIGURE 216****FIGURE 217**

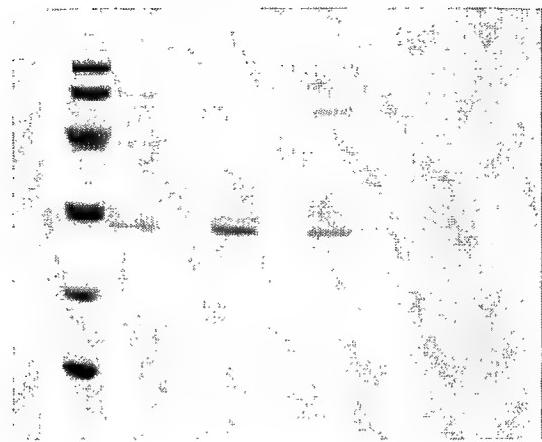
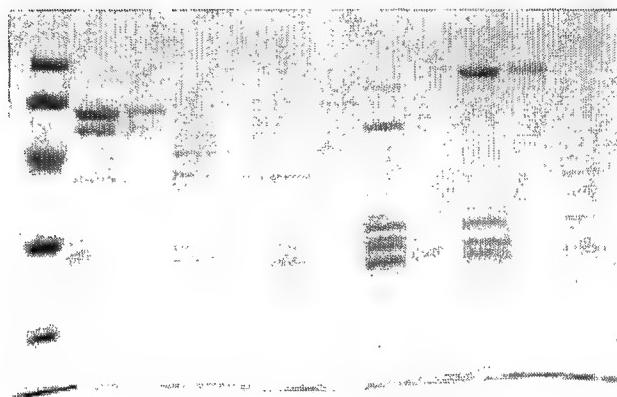
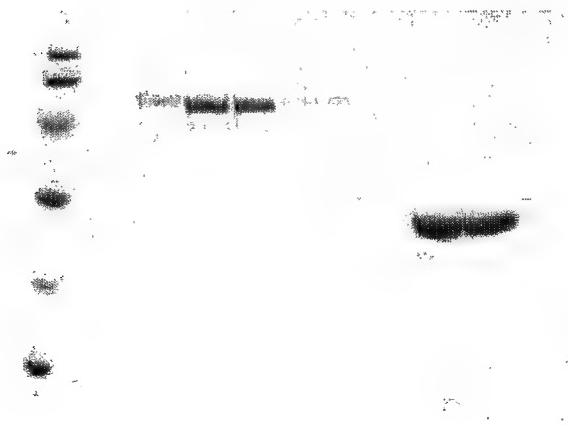
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FIGURE 218**FIGURE 219****FIGURE 220**

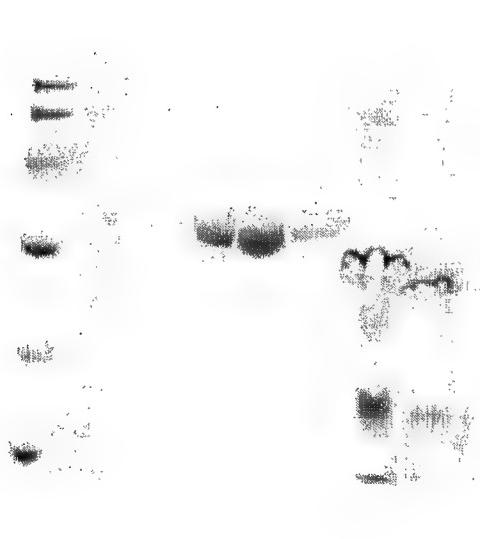
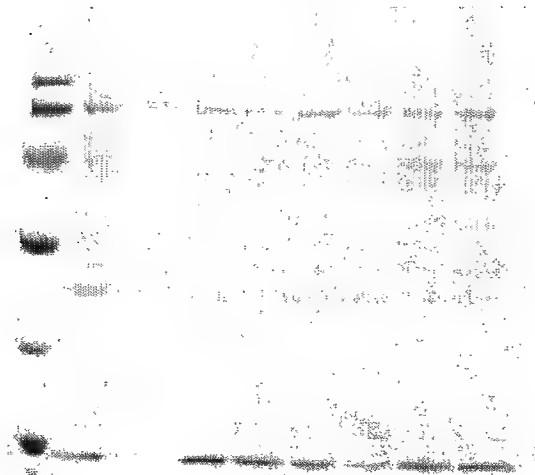
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FIGURE 221**FIGURE 222****FIGURE 223**

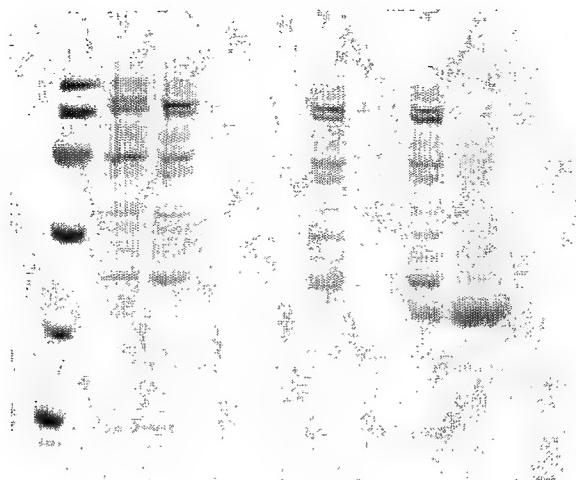
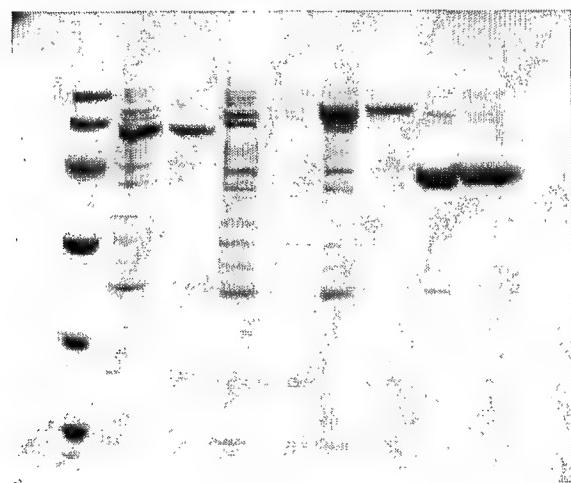
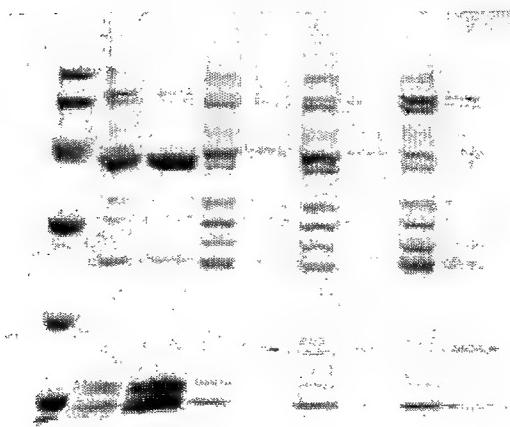
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FIGURE 224**FIGURE 225****FIGURE 226**

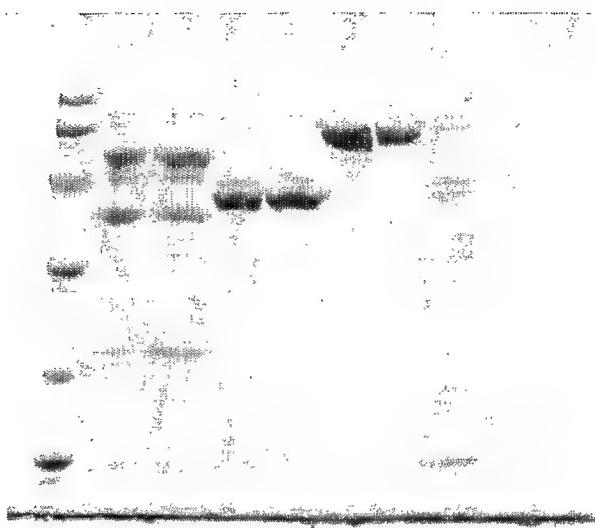
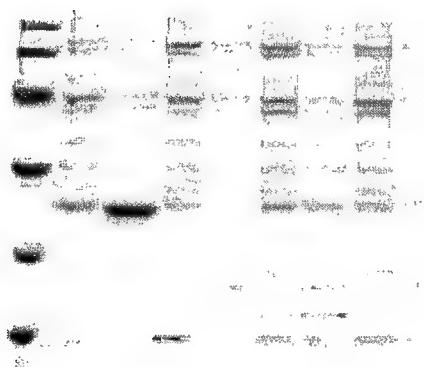
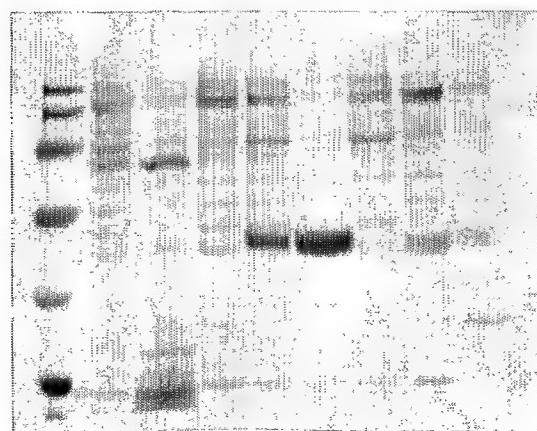
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FIGURE 227**FIGURE 228****FIGURE 229**

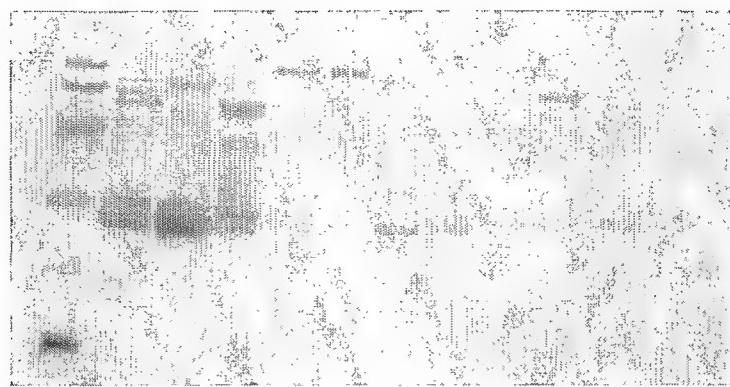
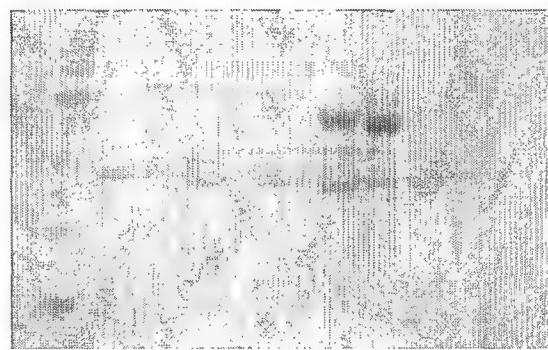
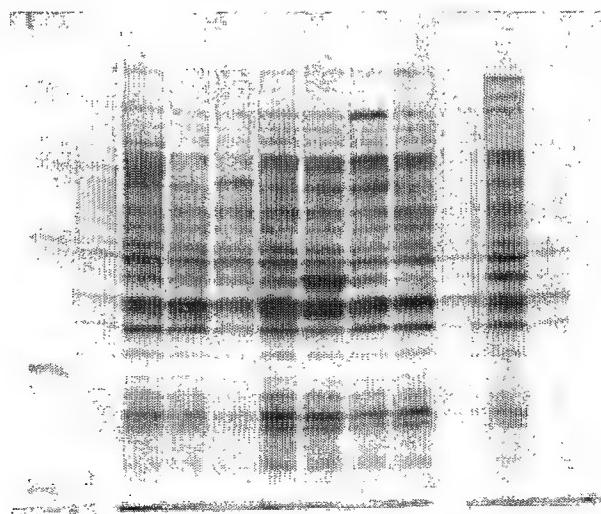
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FIGURE 230**FIGURE 231****FIGURE 232**

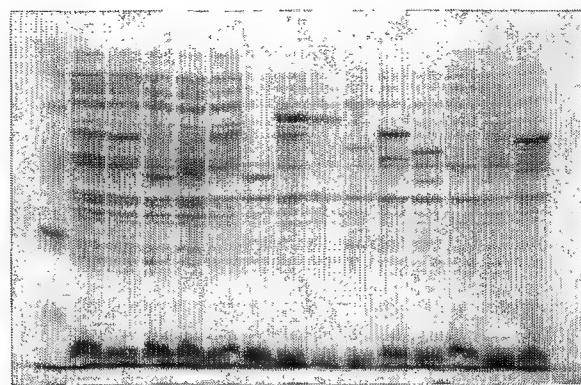
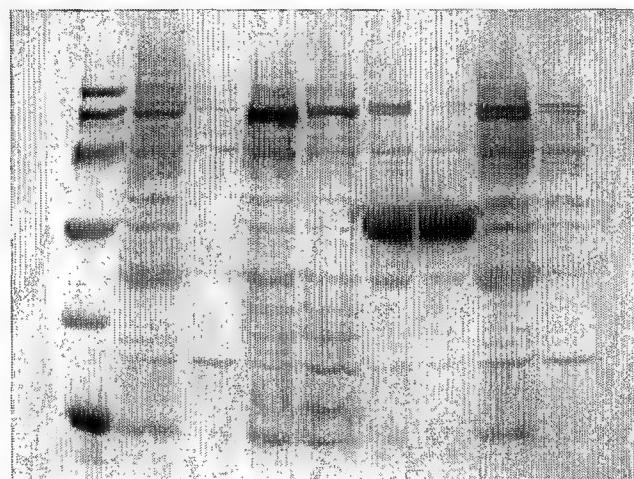
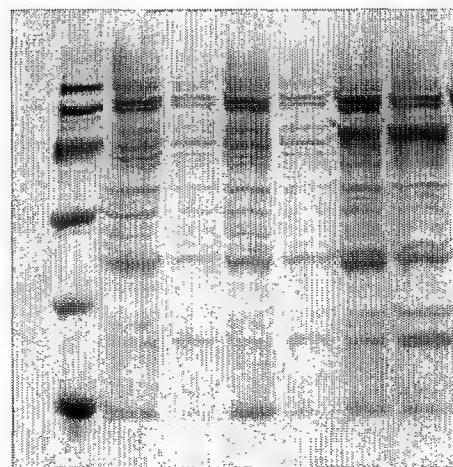
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FIGURE 233**FIGURE 234****FIGURE 235**

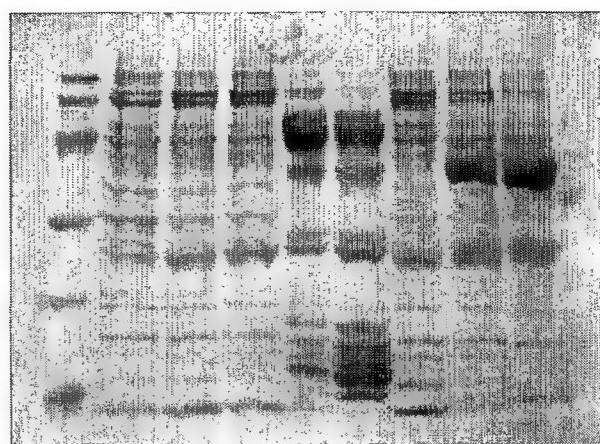
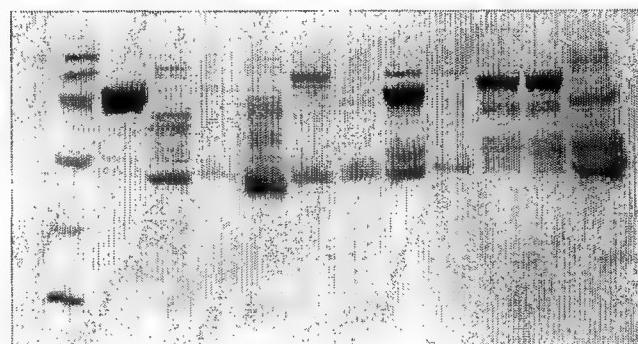
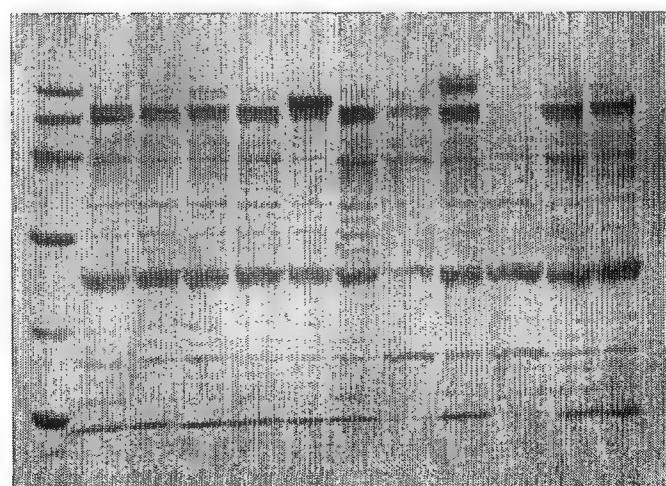
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FIGURE 236**FIGURE 237****FIGURE 238**

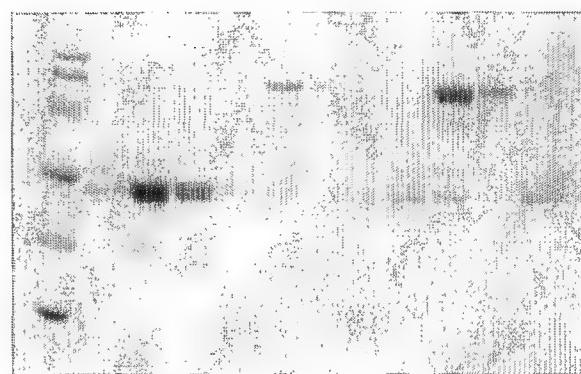
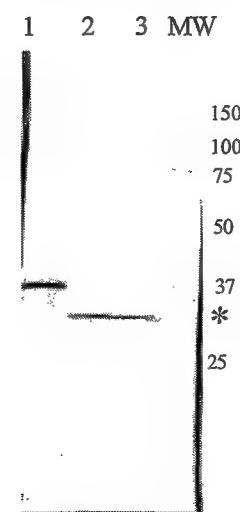
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FIGURE 239**FIGURE 240****FIGURE 241**

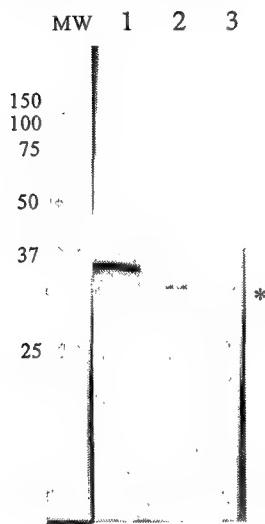
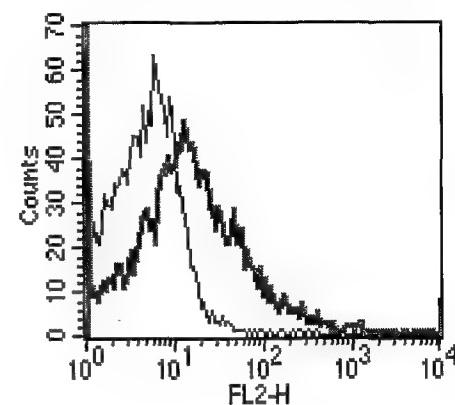
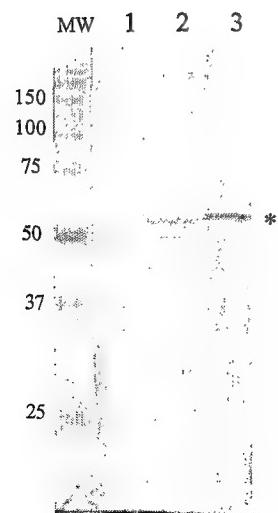
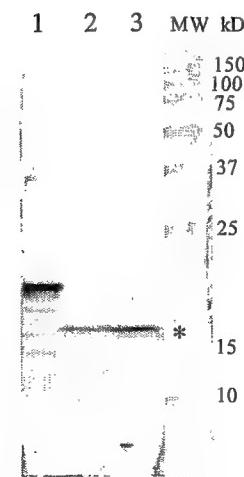
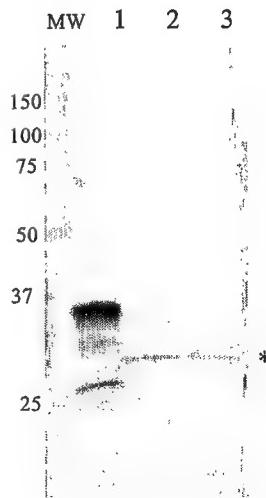
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FIGURE 242**FIGURE 243****FIGURE 244**

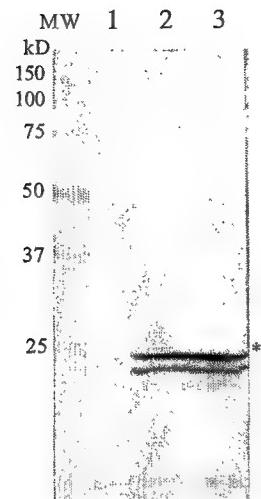
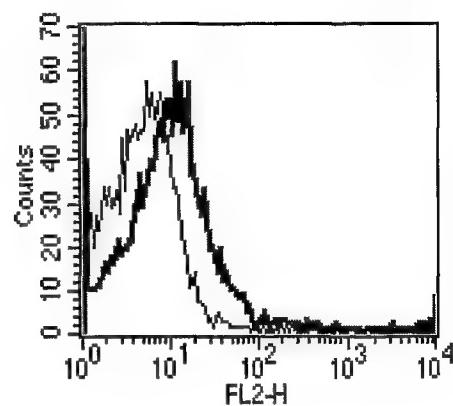
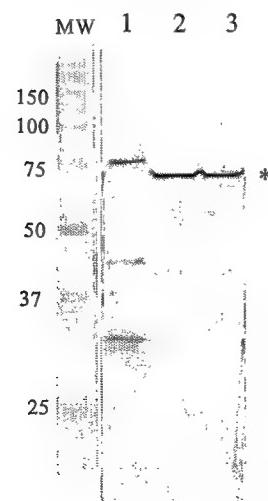
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FIGURE 245**FIGURE 246****FIGURE 247**

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FIGURE 248**FIGURE 248A****FIGURE 248B****FIGURE 249****FIGURE 250****FIGURE 251**

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FIGURE 252**FIGURE 252A****FIGURE 252B****FIGURE 253**

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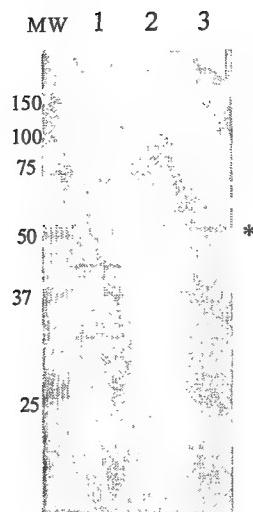
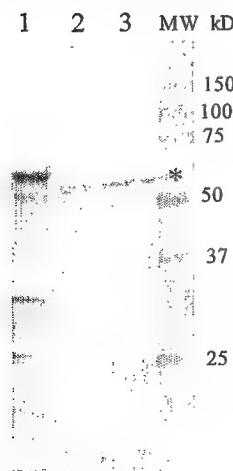
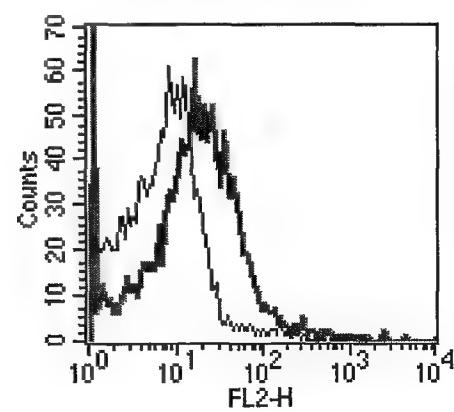
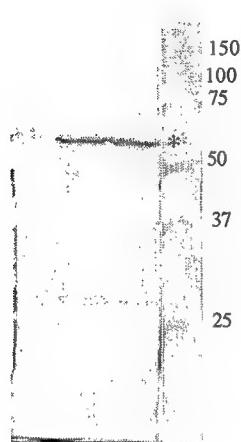
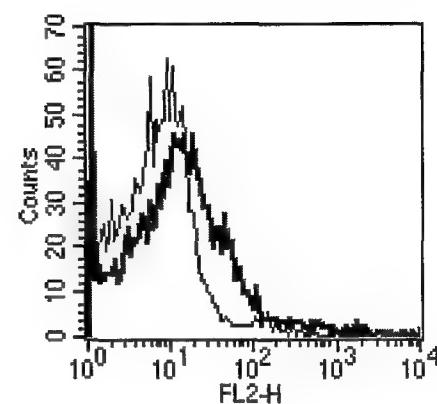
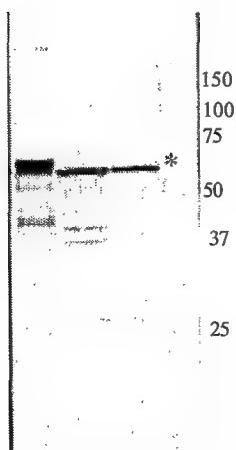
FIGURE 254**FIGURE 255****FIGURE 255A****FIGURE 255B**

FIGURE 256**FIGURE 256A**

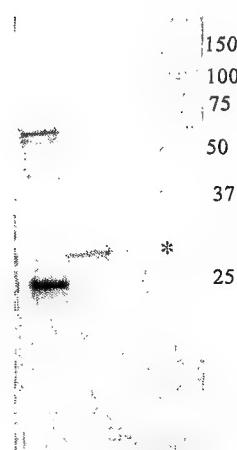
1 2 3 MW kD

**FIGURE 256B****FIGURE 257**

1 2 3 MW kD

**FIGURE 258**

1 2 3 MW kD



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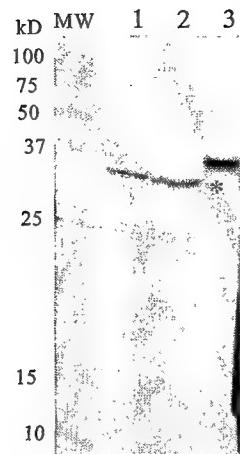
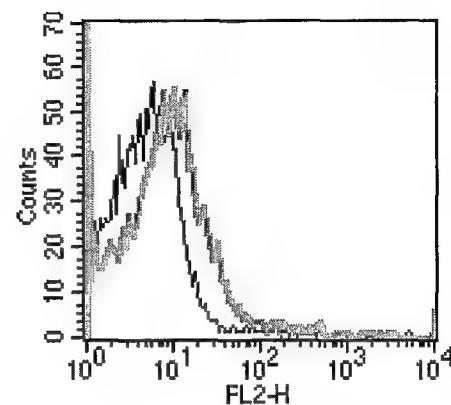
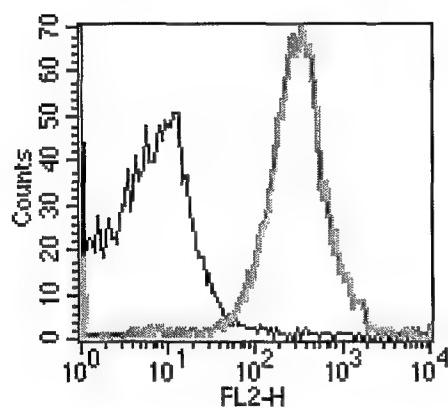
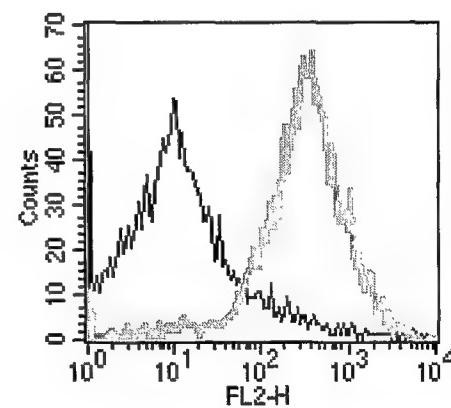
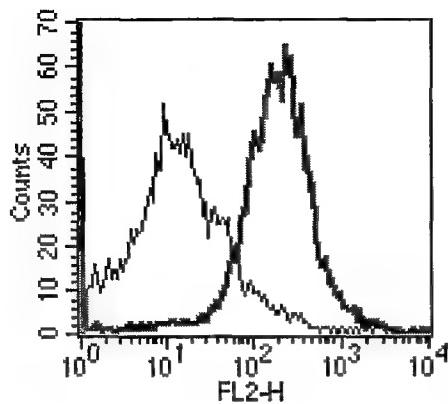
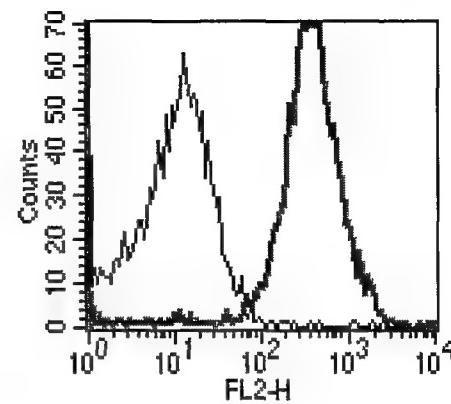
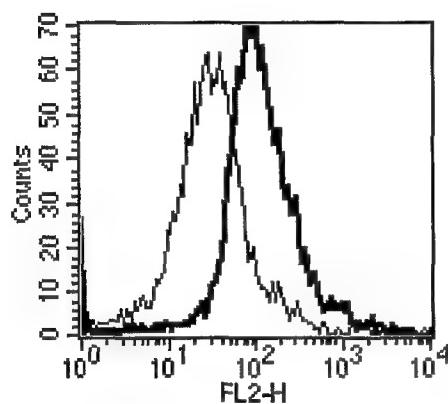
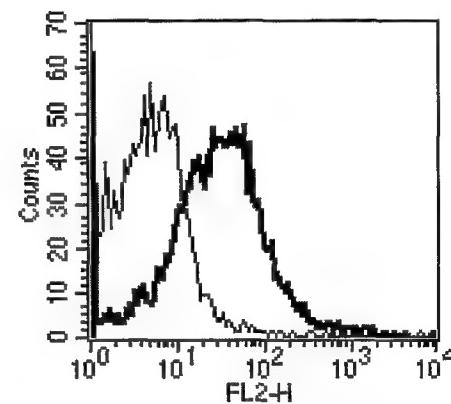
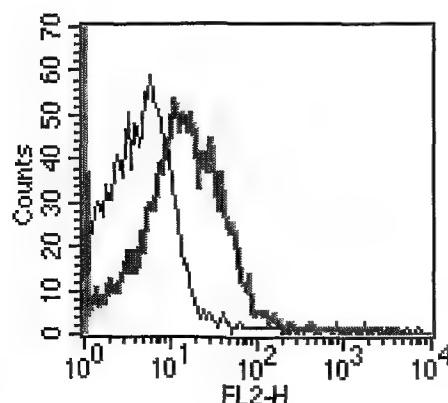
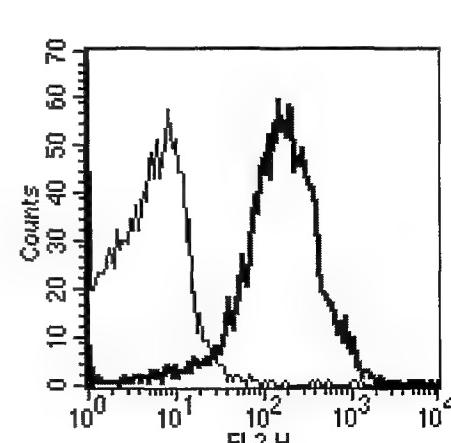
FIGURE 259A**FIGURE 259B****FIGURE 260****FIGURE 261**

FIGURE 262**FIGURE 263****FIGURE 264****FIGURE 265****FIGURE 266****FIGURE 267**

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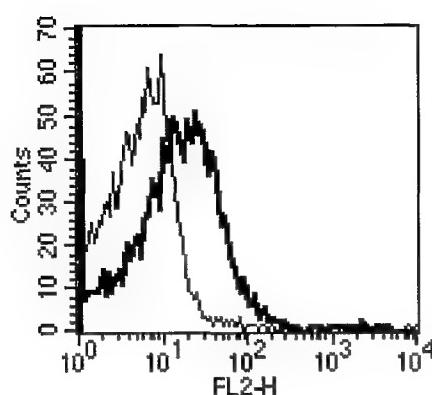
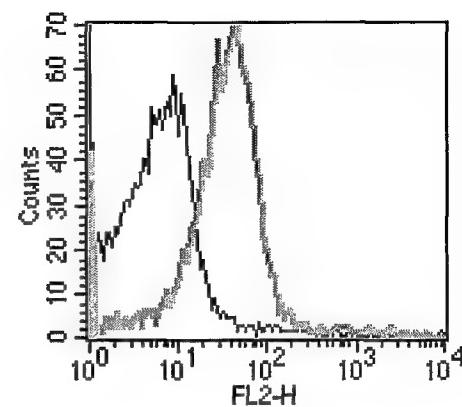
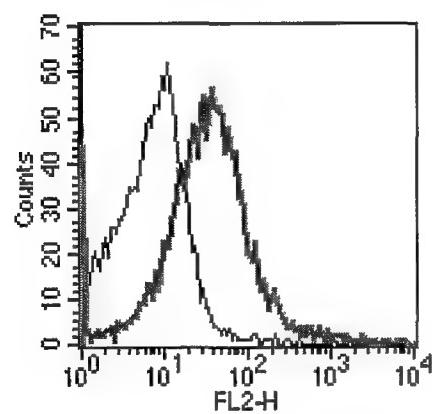
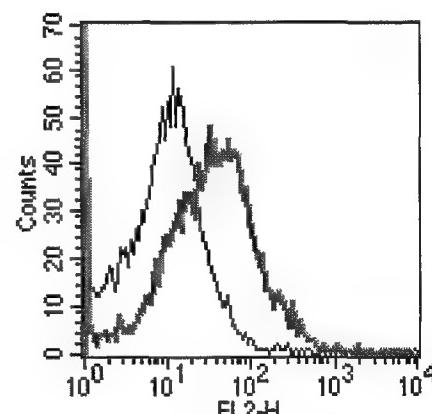
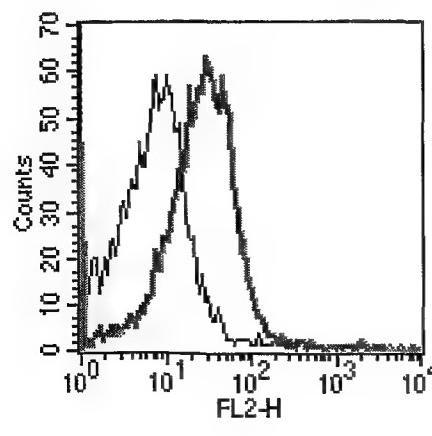
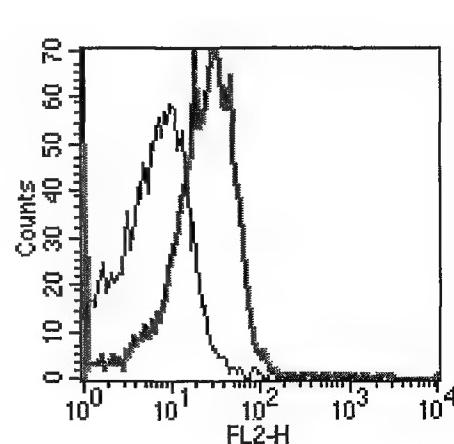
FIGURE 268**FIGURE 269****FIGURE 270****FIGURE 271****FIGURE 272****FIGURE 273**

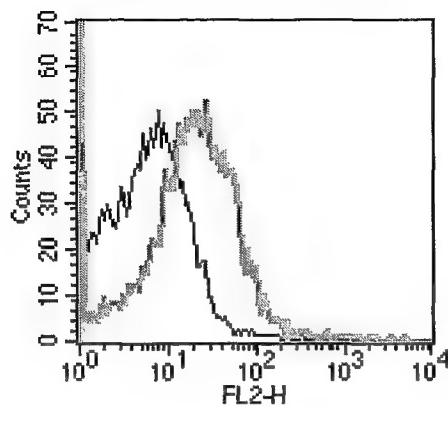
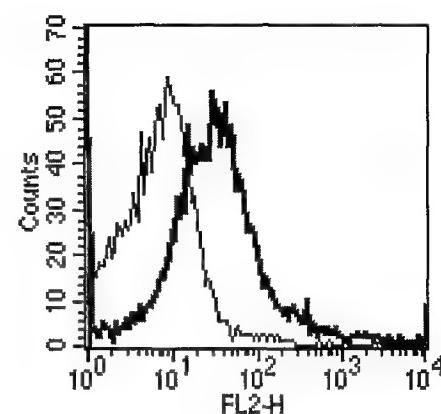
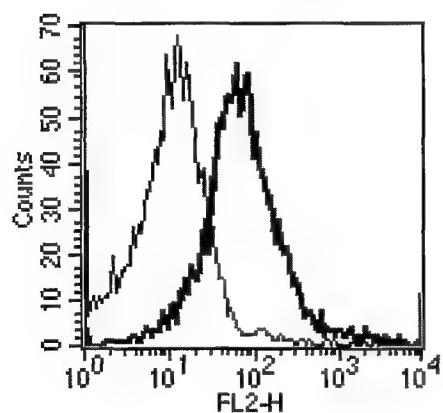
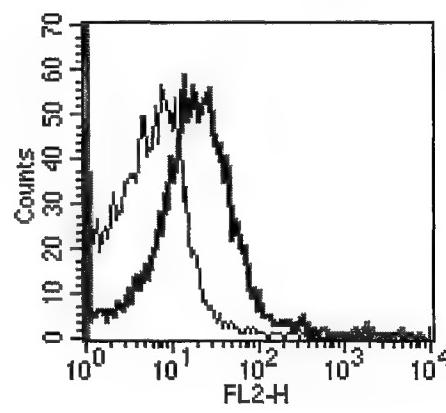
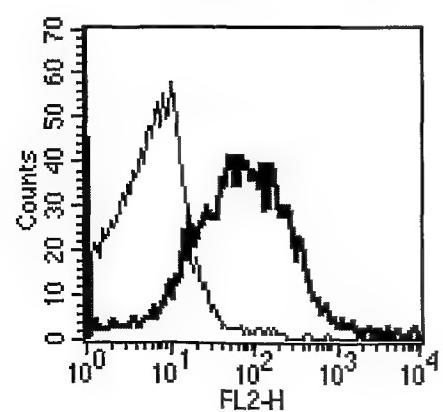
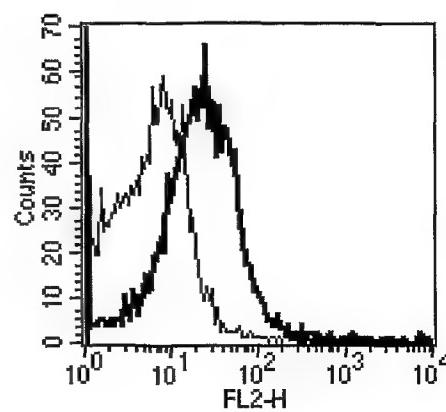
FIGURE 274**FIGURE 275****FIGURE 276****FIGURE 277****FIGURE 278****FIGURE 279**

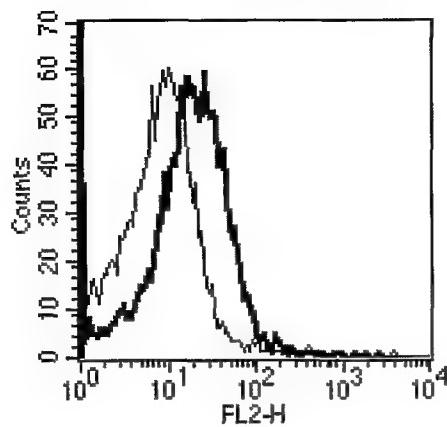
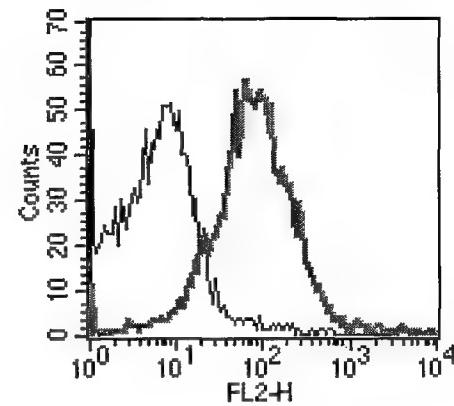
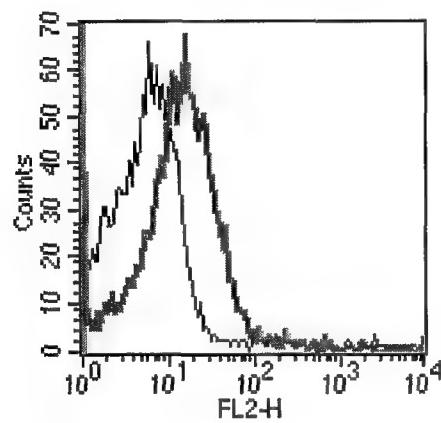
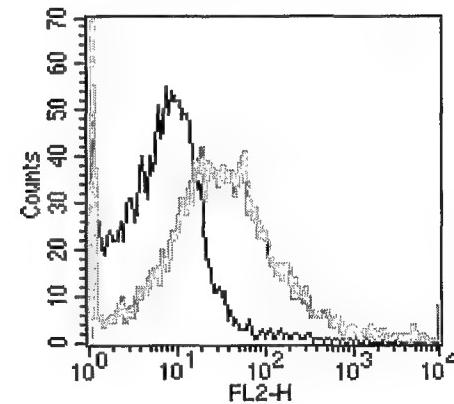
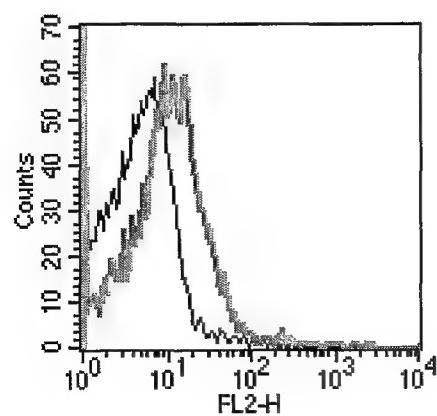
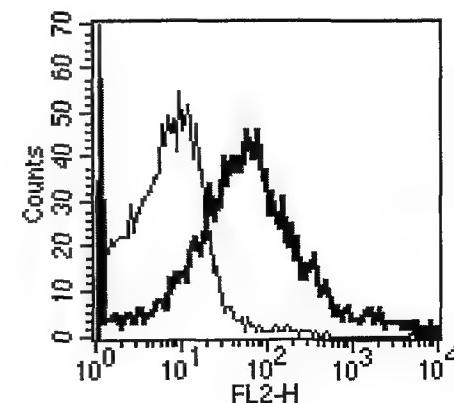
FIGURE 280**FIGURE 281****FIGURE 282****FIGURE 283****FIGURE 284****FIGURE 285**

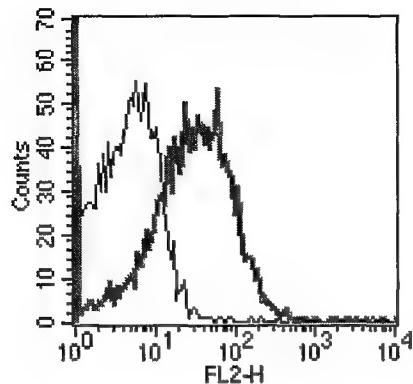
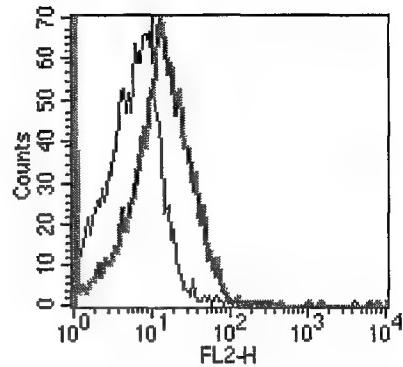
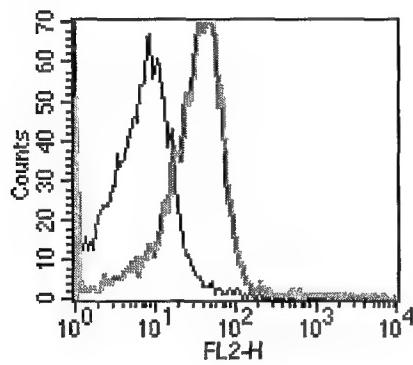
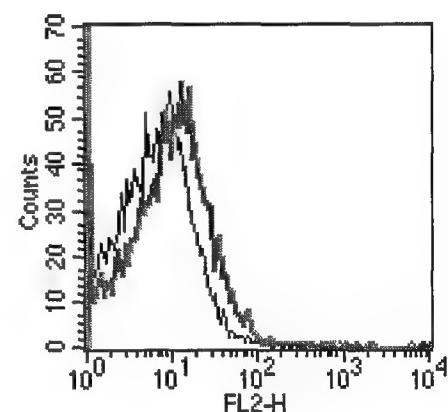
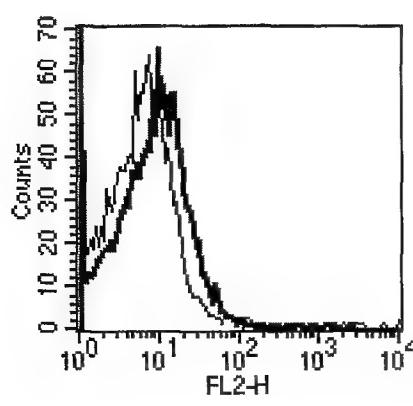
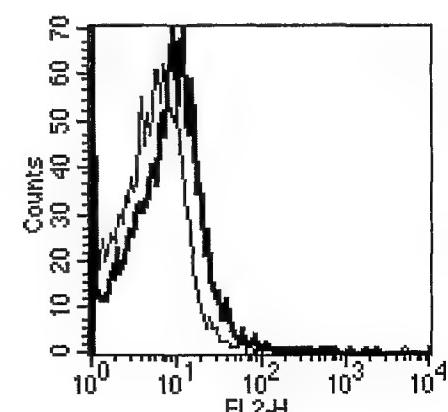
FIGURE 286**FIGURE 287****FIGURE 288****FIGURE 289****FIGURE 290****FIGURE 291**

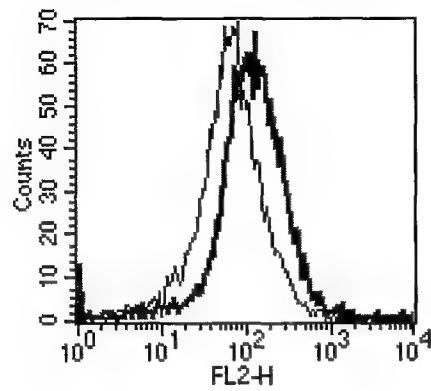
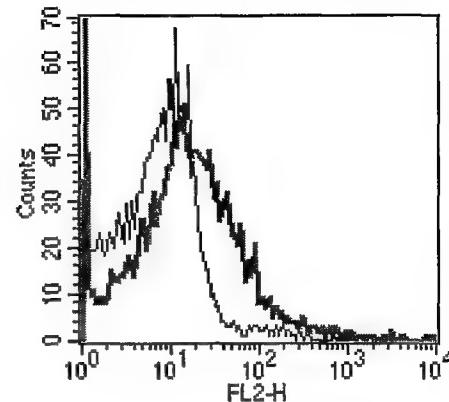
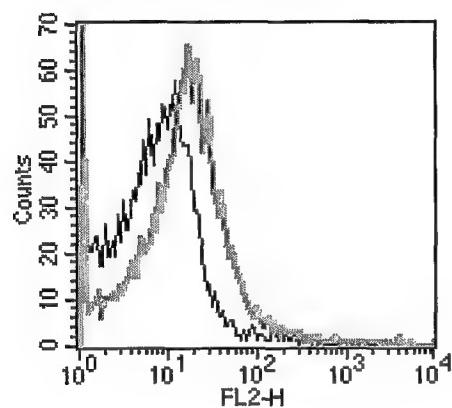
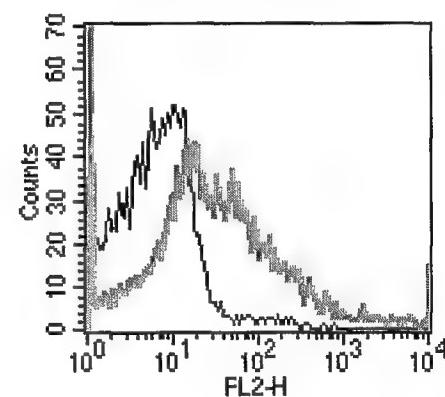
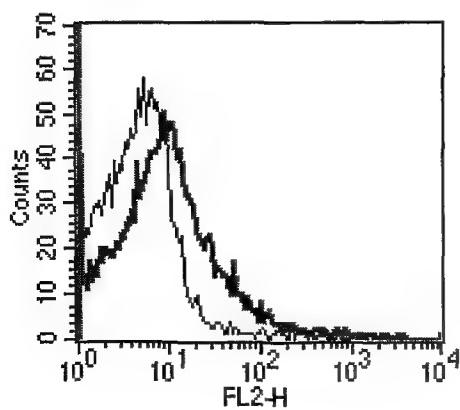
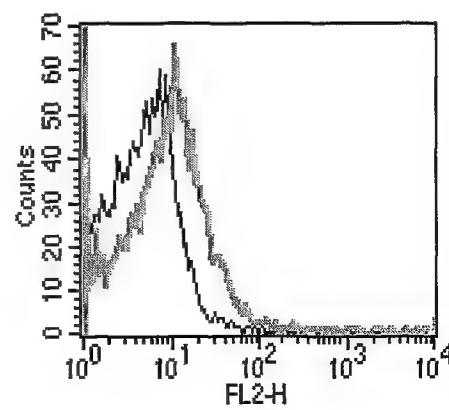
FIGURE 292**FIGURE 293****FIGURE 294****FIGURE 295****FIGURE 296****FIGURE 297**

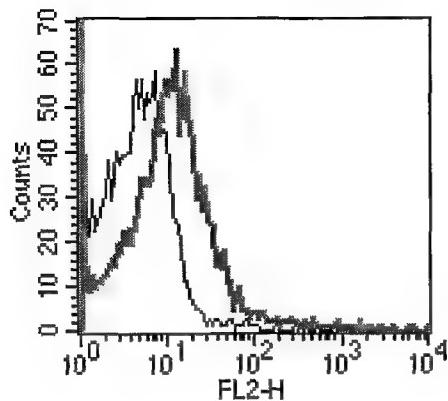
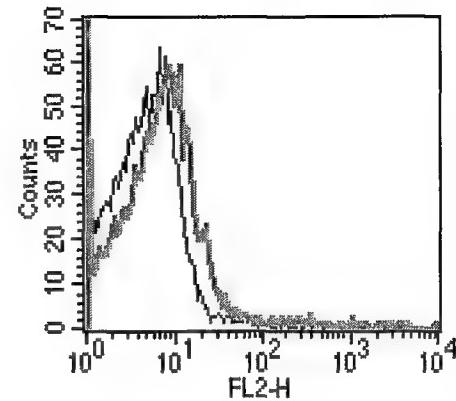
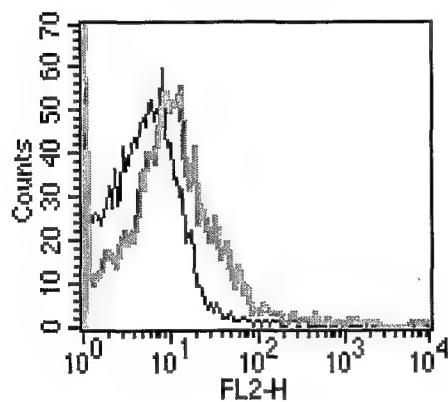
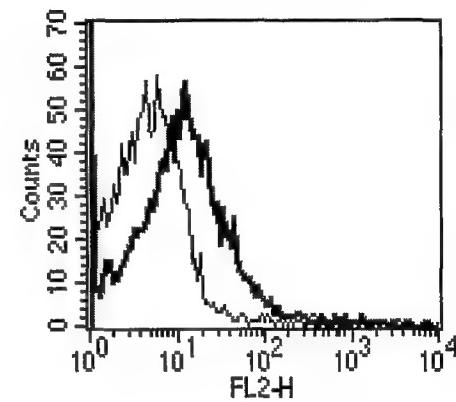
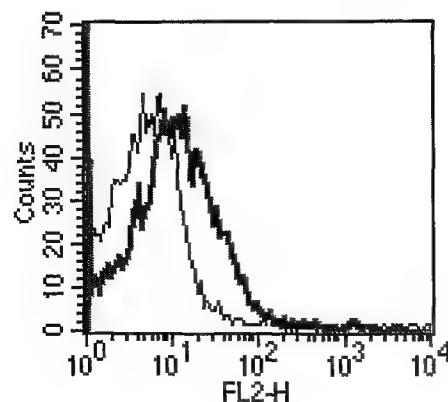
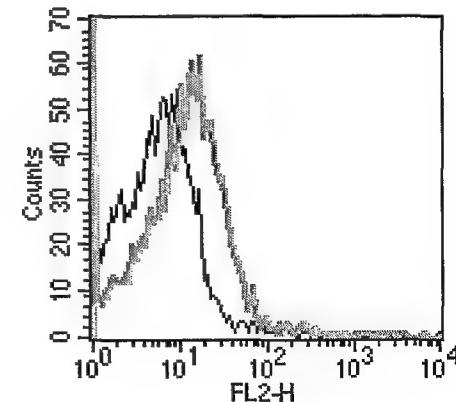
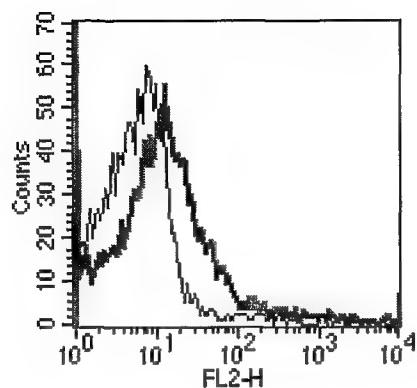
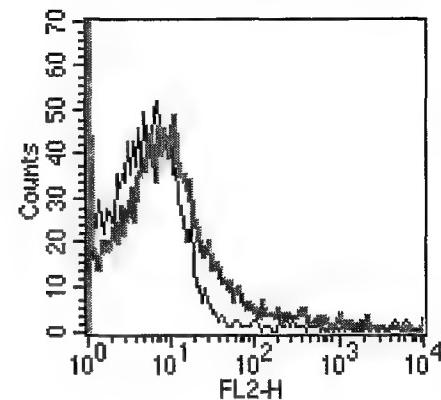
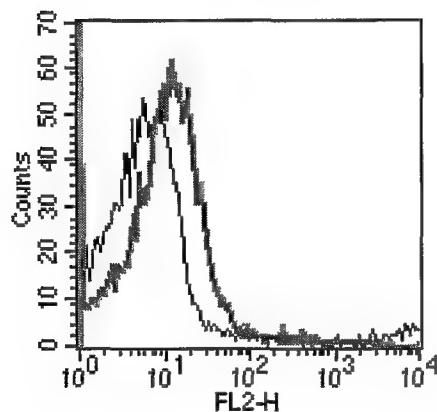
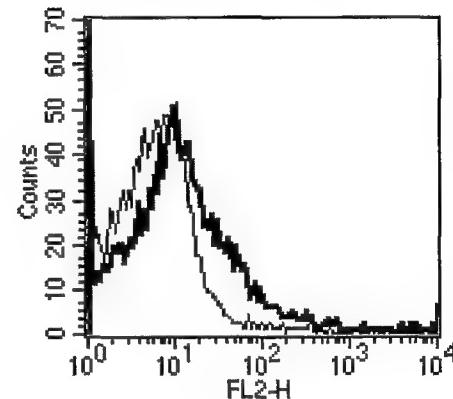
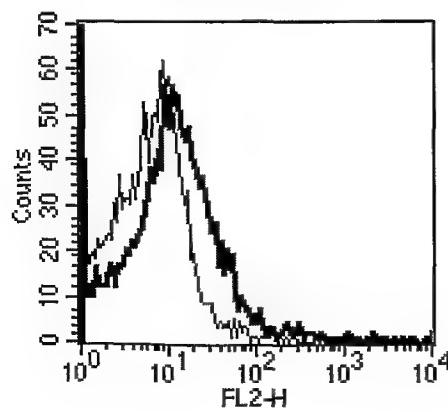
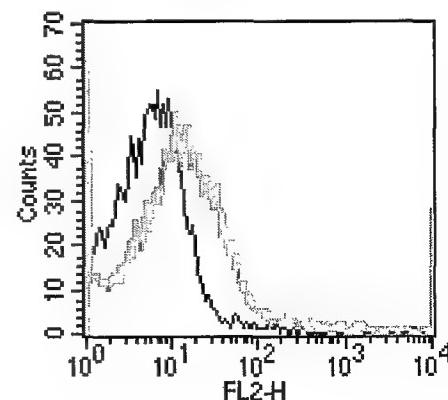
FIGURE 298**FIGURE 299****FIGURE 300****FIGURE 301****FIGURE 302****FIGURE 303**

FIGURE 304**FIGURE 305****FIGURE 306****FIGURE 307****FIGURE 308****FIGURE 309**

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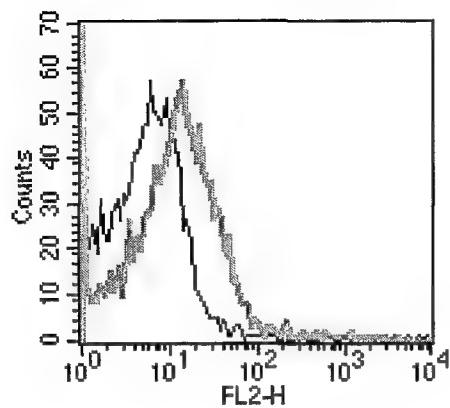
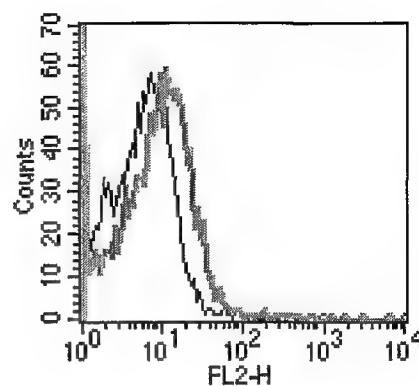
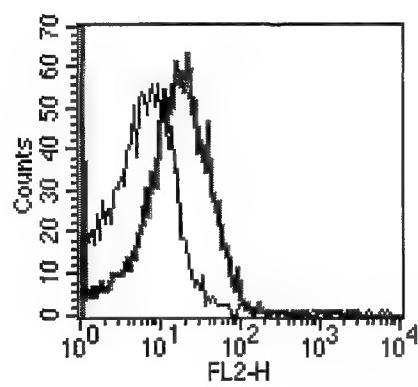
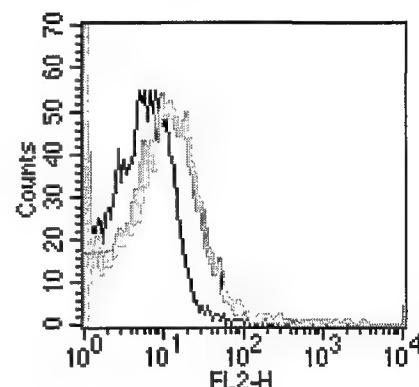
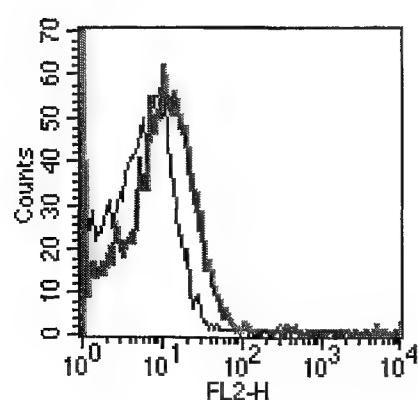
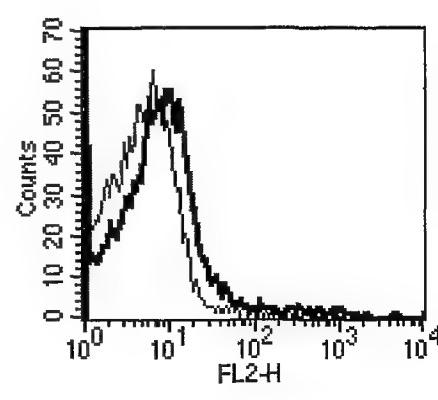
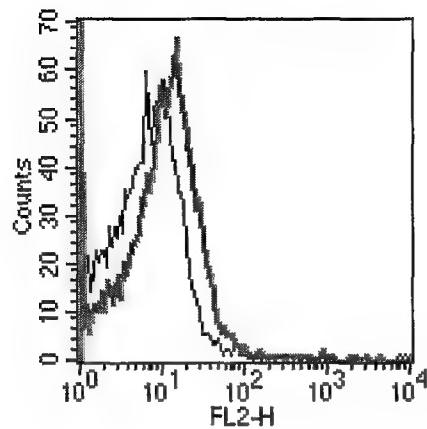
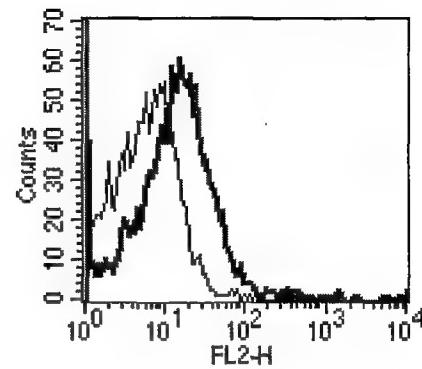
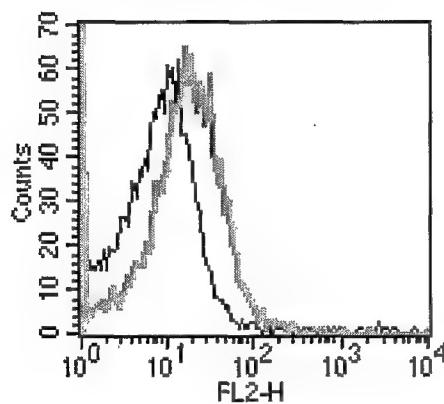
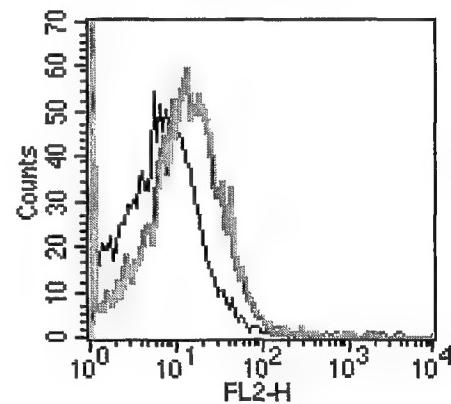
FIGURE 310**FIGURE 311****FIGURE 312****FIGURE 313****FIGURE 314****FIGURE 315**

FIGURE 316**FIGURE 317****FIGURE 318****FIGURE 319**

SEQUENCE LISTING

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SEQ ID 2

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SEQ ID 4

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SEQ ID 19

ATGAAAAAAATTATCTCTCAGTTAGTGCCTTACTTAATTGAGTGCCTGTAATCTGTTGACCGCGCTATAAAAGGCGATAATAC ATTGATGAAAAAAACTGCCAAAAGAAGAAAGCGAAGCAGCTCTAAAGCCTATGAAAGAAAGCATTCAAAAGCTCTCAAAGCTGATGCTAGCCAATT CCACAACAAACAAAGTCGGCAAAGAAGAAGCTAAGGTGTAATGAGGACAAGTCAGGGACATTACCTTAAAGTTATTCCTAAAGCTT CCCCCTAGCTGTTGAGAAACTCTCTACCCATGCTAAAAAGGCTACTATGATAACCTTACCTTACCTGTTGATCAACGACTTTATGATTCAATCA GGTGACCCAAAGGAGATGGCACAGGTGTTGAATCGATTGGGAAAGGCAAGGATCTTAAAGATGCTGGCAATGGCTTGTCAAGGAAATCTCT CCATTTTATATCATATCCTGGCTCTTGCCTGGCAATGGCTAATGCTGGTCTAACTAAGCTAGGCAATTTTATATCAACCAAAACAGAAAAT CAAAGCAAGGGATTATCAAGTACCAACTACCCAAAACCTATCATCTGCTATGAGCATGGCGCAATCCAAGCTTAGTGGCGTATACTGTA TTTGGTCAAGTCATTGATGGTATGGATGTTGTCGATAAAATTGCGCTACTTCTATCAACCAAAATGATAAACAGAACAGACATTACGATTACC TCAATTGACATTGTCAGGATTATCGCTTAAAC

SEQ ID 20

MKKLISLSLVAISLNLNISACESVDRAIKGDKYIDEKTAKEESEAASKAYEESTOKALKADASQFPQLTKEVGKEAKVVMRTSQGDITLKLFPKYA PLAVENFLTHAKKGYYDNLTFRVINDFMIQSGDPKGDGTTGGESIWKGKDPKKDAGNGFVNIEISPFLYHIRGALAMANAGADTNGSQFYINQNKKN QSKGLSSTNPKPIISAYEHGGNPSDLGGYTVFGQVIDGMDVVDKIAATSINQNDKPEQDITITSIDIVKDYRFKN

SEQ ID 21

ATGGTATTATGGCAAATAAGAAAAACAAAAGGAAAGAAAACCAGAACGACTACTAAGGCAGAAAATAGAGCGTCAAAGAGCTATTCAAAGGATG ATTACTGCTCTTGTAAACATTATCTCTTCTGGTATTATCAGATTAGGTATTGGTATTACGCTATAACGTCATCGTCTTATGCTA GGTAGCTGGCTACTTATTGCGCAACTTAAATCTACCTTATTGCTTAAATGGTGCAGGAAAGAAGATAGCTTAGCAGGGTTTTG ATAGCTCTTCTAGGATTATTGATTGAGTGGCATGCTTACCTTCTCAATGCTTATTGAAAGATAAAAGAATTTGCGTCAACTGCTCGATTAA ATTGTGTCGATTAAATGCAATTAAATCACTGTTTGCCTGGAGGTATGTTGGGTCTTGTATTACAAGCCAATTGCTTCTTCTCTTCTT AATATTGGCCTATATGATTGGTCTCTTCATCATTGGCTCTTCTTAAATGAGTTCTGGAAGTTATGACATCGTCAATTAGTGAAGT GCTTTTAAAGTGGCAGAGAACGAGCAGCAAATAAAAGGAGCGTTTGCTAAGCGAGAGATGAAAAAGCAATCGTCAACAGAGCGC ATAGAGCGCTCAAAGGATGCAAGAAGAAGCTTATTAGCTCGGTTAATGAGACCCCTGAAACCGGGTGAAGATTCTAGAGGATCAAGCTGAGGACAT TTGGATGTCGCTACCCACTGGAGGTAAAGTGAACATCAACTCGGTATTGGAGCAGAGATCCTGTTATGAGACATCGCTCAAATGATCCT TTACCACTGAGAGCGACAATTATTGAGAGACTATGATTGCGCTACTTCTTAATGAGAGAAAATGATGAGGAAAATGTTATGATGATGAT GATGAGTATGAGTATGAGAAATGTCGACTTTACACCTTAAAGCAGACTGGTTATAATTACCAAGATAGATTATTGCAACAGAACAG CTTAAAATCAATCCAAAAGAAAAGGATTAGTCCGAAAGAATATCAGAGTTTAAAGAAGAAACATTAGAAGTTGGTATGATGAAAGTAGAA CGTGTGAAATTGGACCATCAGTTACTAAATATGAAATTAAACCGCAGTTGGAGTCGCTGTAATCGTATTCACATCTGACGACCTAGCT CTTGCTCTGCAAGCAAAGATGTCGCTATGAAACACCAATTCTGTTAAATGAGTATTGAGTTCTAATGAGTTCTAATGAGTAACTCAGAAATTGCAACGGTT TCTTCCCGCAACTTGGGAAACAATCTGATGCCAATCCTGAAAACCTTAAAGTGGCTTAACGGCAATGCTCGCAGTTT AACTTAGCTAGAAATGCCGATCTTGTGAGTCGTTCAACTGTTCACTGTTCAAGTAAATCTGCTGAGTTAATGAGTAACTTCAAGTATTGATGATGAG GCACGTCCAGATCAAGTTAAGTTATGATGCCAATTGTTGAGTAAATCTGTTTAAATGAGTAACTTCAATCCCTGTTGTA ACCAATCCGCGTAAAGCAAGTAAGGCACCTCCAAAAGGTTGATGAAATGAGGAAATGAGTAACTGAGTTATGAGTAACTTCAAGTATTGCTGCTGTAATGAGTAA GCAGGTTATAATACAAGGTTGAAGGTTAAATGCTTCTCTGAGCAAAACAAATACCTTGGCTTAACTGTTGAGTAACTGAGTAAATTGCGTAAATATA GCAGGTTATAATACAAGGTTGAAGGTTAAATGCTTCTCTGAGCAAAACAAATACCTTGGCTTAACTGTTGAGTAACTGAGTAAATTGCGTAAATATA GACTTGATGATGGTTGCTAGTAAAGAAGTTGAAGGATGCTTATTGCTTGGGGCAAAAGCACGTGCTGAGGTTACATGATGTTCTGCAACT CAACGTCCATCGTAGTGTATTCTGTTGGGTTGAGTAAAGCAATGTTCCGCTGCTGAGTAACTGCTGTTCAAGTGGTACTGATAGCGTACG ATCCCTGATGAAAATGGTGTGAAAGGATGCTGGTTTATCAAAGACCAAGCCGAGGGTCAACTATGATGATGCTGCTGAGTAACTGAGTACAGACTACAAGGTTCC TTTATTCAGATGATGATGTTGAAAGGATGCTGGTTTATCAAAGACCAAGCCGAGGGTCAACTATGATGATGCTGCTGAGTAACTGAGTACAGACTACAAGGTTCC GAAACAGATAACGGCTCTGGTGGCGCGAGTACCTGAAAGTGAATGCTCTTTGAAGAAGCCAAGGGACTCGTTAGAGACGCAAAAGCA

AGTGCCTCAATGATTCAACGCCATTGTCTGGTTCAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGTATTGGTCAGCA
GAAGGAACCAAGCCACGAAACTTAAATGACTCCAACCTCGAGTGAA

SEQ ID 22

MVFMANKKTKGKKTTRPTKAEIERQRAIQRMITALVLTIILFFGIIRLGIFGITVNVIRFMVGSLAYLFIAATLILYFFKWLKDKDSLVAGFL
IASLGLLIEWHAYLFSMPILKDKEILRSTARLIVSDLMQFKITVFGAGMGLALIYKPIAFLFSNIGAYMIGVLFIIILGLFLMSSLEVYDIVEFIR
AFKNKVAEKHEQNKKERFAKREMKKAIEQEIERQKAEAAEYLAVNVNVDPETGEILEDQAEDNLDDALPEVSETSTPVFEPEIILAYETSPQNDP
LPVEPTIYLEDYDSPIPNMRENDEEMVYLDLDDVDSDIENVDFPKTTLVYKLPTIDLFAPDKPNQSKEKDLVRKNIRVLEETFRSGVIDVKVE
RAEIGPSVTKYEIKPAVGVRVNRISNLSSDIALALAAKDVRIFTPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSF
NLARMPHLLVAGSTGSGKSVAVNGIISIILMARPDKVFKMMDPKMVLSVNDIPHLLIPVVTNPRAKSKALQKVDEMENRYELFSKIGVRNI
AGYNTKVEEFPNASSEQKQIPLPLIVVIVDELADLMVASKEVEDAIIRLGOKARAAGIHMLATQRPSDVVISGLIKANVPSRIAFAVSSGTDSTS
ILDENGAEKLLGRGDMLFKPIDENHPVRLQGSFISDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGPVPESDPLFEEAKGLVLETQKA
SASMIQRRLSVCNFNRATRIMEELEAGVIGPAECTKPRKVLMTPTSE

SEQ ID 23

ATGGTTAAAAGAAATCAAAGAAAAAAAGTGCCTTAAGAACGGTTAACAAAAGCAGAAGTGGAAAAGCAACGTGCCATTAAAGAGGATGATTTTA
TCTGTTTAATGGCTTGTGTTATTTGCGATGCTTCGTTGGCGTCTTGGTGTGACAACCTTAAATATGATTCTGTTTTGGTGGTAGT
TTAGCCTATCGTTATGGCTTAAATGGTAACTTACCTTAAAGGGTACGGCAAAAGATGGAATGGCGGAGTGTGTTATTGCTCGCTAATTACA
AGAGATTACTAGCCCTGCGCGTGACTGAATTGTTGTTGGAGGAATGCTTGGTGTGCTTAAACCCATAGCCTTTTATTTTCAAGATATC
GGCTTACTTATTGGTTTTGGTATCTATTAGGATTATTCTAACTGACGCCCTGGGATATCTATGATGTGAGTCAGTGTGAAAGAGGCT
GTTGATAAACAGTGGCTTACGGAAAATAGAAAAGCCTGGTGTGATCAAAGAGAAGAGCACGGCTTACAAGCTGAAAAAGAGGCTTGGAG
AAACAAGCACAAAGAGGAAGAAAAGCTCTAGCAGAATTGACGGTTGATCCTGAGACGGGAGAGATTGTTGAGGATAGTCAGTCTCAAGTCAGCTAT
GATTGGCTGAGGATATGACAAAAGCAGAGATTCTGCTTATGATAGTCACCTCAAAGACGATGAGACAAGCTTATTGATCAAGAAGACTTG
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GAAATCAACCGCTGCTGGGCTCAGGTTAACCTGCTTAACTTGCATGATTGGCAGCTTGGCTCTGGCTCTGGCTCTGGCTAAAGATGTCATG
GCACCAATTCTGGAAAATCTTAATGGTATTGAGCTTCCAACTCAGGAAATGCAACGGGTTCTCCGCAATTGGGAAACATCTGATGCC
AATCCTGAAACCTTTAGAGTACCACTAGGTAAGCTGTTAATGGCATTATTCAAGTATTGATGAAGGCACGTCAGATCAAGTTAAGTTATGATGATT
GGTCAACTGGTCAGGTAAATCTGGCAGTTAATGGCATTATTCAAGTATTGATGAAGGCACGTCAGATCAAGTTAAGTTATGATGATT
GACCCCAAAATGGTGAATTATCTTTATAATGATATTCCACATTAAATCCAGTTGTAACCAATCCGCTAAAGCCAGTAAGGCACTCCAA
AAAGTGGTGTGAGGAAACCGCTACGAGTTATTGAGGAAATTGGTGTGCTAATATAGCAGGTTATAATACAAGGTTGAAGAGTTAAT
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GGACGGGGTGTATGCTTAAAGCCGATTGATGAAACATCCTGGCTTCAAGGGTCTTCTAGATCAGATGATGTTGAGCTTGGTGTGAAAGT
AACTTATCAAAGACCAAACGAGCGGATTATGATGACGCCCTTGATGAGAAACACAAAAGCTAGTGCCTCAATGATTCAAAGGCTTGTGGT
GCTGCTGAAGGTGATCCTCTTTGAAGAAGCAGGCTTGTAGAAACACAAAAGCTAGTGCCTCAATGATTCAAAGGCTTGTGGT
GGATTAAATCGTGCACCGCCTGATGGATGAATTGAGAAGCAGGTTATCGTCCAGCAGAAGGAAACAGCTCGTAAGGTATTGAGACA
AAC

SEQ ID 24

MVKRNQRKKSAPKKRLTKAEVEKQRAIKRMLSVLMLLIFAMILRLGVFGVTTYNMRFLVGSLAYPFMFAWLIYLFCFKWLQKDGMIAVVI
FLGLLVEWAHLFAMPRMLDQDIFLGTARLITRDLALLRVTEFVGGMGLALLYKPIAFLFSNIGSYFIGFLFILLGLFLMTPWDIYDVSHFVKEA
VDKLAVAYQENKEKRFIREEHRLQAEKEALEKQAOEEEEKRLAELTVDPETGEILEDVSDQSQVSYDLAEDMTKEPEIAYDSHLKDETSLFDQEDL
AYAHBEEIGAYDSLSALASSEDEMDMDEPVEVDFTPKTHLLYKLETLDFAPDKPNQSKEKNLVRKNIKVLEDTFQSGVIDVKVERAEIGPSVTKY
EIKPAVGVRVNRISNLADDLALALAACKDVRIEAPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPHLLVA
GSTGSGKSVAVNGIISIILMARPDKVFKMMDPKMVLSVNDIPHLLIPVVTNPRAKSKALQKVDEMENRYELFSKIGVRNIAGYNTKVEEFN
ASSEQKQIPLPLIVVIVDELADLMVASKEVEDAIIRLGOKARAAGIHMLATQRPSDVVISGLIKANVPSRMAFAVSSGTDSTS
GRGDMLFKPIDENHPVRLQGSFISDDVERIVNFVIFDQTEADYDDAFDPGEVSDNDPGFSGNGGAAEGDPLFEEAKALVLETQKASASMIQRRLS
GFNRATRIMDELEEAGVIGPAECTKPRKVLQTN

SEQ ID 25

ATGCATATTGAGACTGTTATTGATTTCAAAGAAATTAGGAAAAGATATGTTTAAAAACTCTACAAAAGAATTAATAGCTGATACTTTAGAACAA
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CATTTAAAGTTCTCAACAGAAAGTGGCTGGAGAACATCTAGCTTATTTCAGTACATAAGATTGTGAGAACGAGCTTCCCTTAAGTT
GAAAATGTTAGATTGAGATAATTGAGCTCTAATGTTCTGAGCAAGAAATCAAGAGGCAATTGCTAATATAAGAACATTAGACAAGGA
AATACTTATCAAGTAAATTATACACTAGAGCTTGGCAACAAATTATGCTCGGATCCTTAACTGTTTATGAGCCTAATGGTAGAACAAAGGAGCA
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CCAATGAAGGAAACAGCGTAGAAAGCCTATTATCAAGAGATGGCGGGAGGAGATTGTTGGCAATGATCTTAAACATGTTCTGAAAT
ATGATGATTGTTGATTATAAGAAACGATATGGCCGTTATCTGAGTGTGAGACAGTTAAGGAAAAACTATGTCAGTGGAGCAGTATGCA
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GACGGACAAGCTATTGCTAACGTTCTGAGTCAAAATGAGTGGGGAGGTTTACGGCTTCAATCAGGCTTGGTGGAGGTTACGTGGAGAGC
CAGACAGATCTGAGATAAGGAAACCGCTAAAATCAGCTGTTTAACACGGCTTCAATCAGGCTTGGTGGAGGTTACGTGGAGAG
GAAAATAACTCTCTCAACAAACATGTCGAGAGGATTGAGTGAATTGGCTTCAAGGAGGTTTACGGCTTCAATCAGGCTTGGTGGAGGTTACGTGGAGAG
GAAGTGAAGGTTTACCTTCATGAGTGAAGGAGGATTACGGCTTCAAGGAGGTTTACGGCTTCAATCAGGCTTGGTGGAGGTTACGTGGAGAG
CTAGTGAATTTATCAAAGGTTTACGGCAGAGGTTGGCTGAGACTACCCATTAAATTATCCCCTTTACTTATTGTTAAACACTCTTAT
CGCCCATATTATTGAGGTCAGAAAGATATTGTTGATCTCTGAGGGGTTGCTATTGAAACAGTATTGGAAATATTGTTAGAAAAA
AATGGAAGGTTTAAACCCAGATTATCAGAAGGAGGGTTGAATGGGATTATCGTCGTATCTCCTTAAACAAAAGTAATTGAGCACC
CTAACTTTAAAGATTAGAACATCAGCCGATCTATACGCCGTTAATGCTGTTAGAGGGCTTATCTCTAAACCTAAAG

SEQ ID 26

MHIETVIDFKELGKRYRFKNPTKELIADTLEQLEVLEVIKEVDYYQSQNYVVGVLYSEASAAFDHFVKSQQLAGEHLAYFTVHKDCNEAFPLSY
ENVRLADNWTAJVSEQEYQEAIANIKQIQRQNTYQVNTLELSQQLCSDPFPSVYERLMVEQAGYNAIAYDDKRILSVSPLEFFKKDEVLTTR
PMKGTSARKPTYQEDVAERDWLANDPKNRSENMMIVDLLRNDMGRICDVGTVKVKLCLQVEQYATVWQMSTIEVGLSPEVTLMSIFQALYPCGS
TGAPKISTMAINELEKRPRTGYCIGLCPMDPGQAIIFNVPIRTQVMKGQQAYVGVGGGIFTWESQTDSEYEETRQKSABLVRVNPKFQLITTGRV
ENKLLFSQHQVERLVESASYFAYSFDSKSFERELKKYLHQLDEKDYRLKIMLDKTKGVTFEVKQLVNLNSKFLTAEVVVDYPIKLSPTFYFKTSY
RPHIIEGQNEKIFVSPGLLLETSGNIVLEKNGRFLTPDLSEGGNGIYRRHLLKNQKVIAPLTLKDESADAIYACNAVRLGLYPLNLK

SEQ ID 27

TTGGGTATGCATAGAAAActATTGATTTCAAAGAGCTGGCAACGCTATCTTGTGATGAGCCATTAGTAGAATGGTAGCCAAGTCCTTA
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GACAATGCCCTACAAACCCATAATGACAGACTAGGCAACAGACTGGCTATTACGTGCAACAAAAGCCTACCTCTT
GATTATGACAGCAGCTTACCTACCAATGGTCAGCGCAACTCAGGAACTCAATGCAGCTGATAGTTAGCCATTACAAATAACTGTCGTTGAA
CAGGGCAATCTTACAGGTTAACATCAGGAACTCAATGCCTGAGCTGTTGCGTTATTACAGCTAGTCTGAAATTGTTAAACAGAGGGCAACAGGTTA
ACTACTAGGCTATGAAAGGACCACCAACAGGGGTTAATAGCTGGCTGGATCAACAAGAACATGACTGGCTCCAAGCTGACGGAAAACCGT
TCTGAAAACATGATGATTGGAATTGCTCCGAATGACATGGGAAAATTGCAAACAGGAGTGTGTTGATAGGCTCTGTGAGGTCGAG
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TGCCTACTCTGATGGTCGGCTTCTTCATAGTCCCATTAGAACCTCAGCTGATCAATAACAGGCTACTTATGGTGTGGAGGCGCATC
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ACCAGCTACCGGCCTATATTGAGAAAATCTTATGAACAGTATTCTATAACCAAGCGGGCAATTATTGAAACGTCCTGGCAATCTCTT
GTTCACTGGGTGAGACACTAGCTGATTTAAAGAGGCTAGCGCTATTGGAGGAAATGCTGTCGCTGGCCTTATCCTCTCACCTGAGCTTACT
CACCTGTGATGCCCTTAGCTAACAGTCAAGC
SEQ ID 28
LMGHRKTIIDFKELGQYLFDEPLVELVAKSLDQVGPVIEKVVOHYQQLGYVVGVLYSEAAFFDNALOTHNDRLGNEYLAYFTVHKTCKOKKDLPL
DYDSITIPNQWVSATQKEAYQKAIEIETIHRMOMQGNTYQVNYTLQLTQELNAADSLAIYNKLVEQAAGYNAYIAHDEFAVISASPELFFKQEGNR
TTRPMKGTTKRGVNSWLDQQEHDWLQADGKNRSENMIVDLLRNDMGKICQTGSVRVDRLCEVERYSTVWQMTSTIVGDLKADCILIDILKALFPC
GSITGAPVKSTMIAITSLEPKPRGIYCGSIGICLPDGRRFFNVIIRTIQLSHNQATYVGGGITWQSKWEDEYEVHQKTAFLYRHKQIFDLKTTA
KVEHKKIAFLEQHNLRLKEAATYFAPPNEKALQQLSTYLENKNAAYRMLMIRLSKDGKISLSDQPLELPSADFLTAQLSLQKKDVTASPFTYFK
TSYRPHIEQKSYEQLFYNNQAGQNLLETSIGNLFVQLGQTLTYPVAVGILPGLFRQELLATGQAAQEKEVTLADLKEASAIFGGNAVRGLYPLNLELT
HLDALLAKSQA
SEQ ID 29
ATGGTCACAGGAGGATTCGACTAGACCTCTTACTTGAGATAACTAAGATACTGCAACTTACTATTATCAACTAAAGAACTGAATAAACCA
AATAAAAGACAACAGCAATCAAATCTGACATTCAATCCATTATGATGAACATAGAGGAAACTATGGCTATCGTGGATTATTAGAACTGCGAAAT
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AAAGGTGAGGTTGGTAAGAAGGCTGATAACCTGATTCAACGCGAGTTGAGGGCTGAAAGCCCTATGAGAAGTGTCTACCGATGTCAGGGAGTTT
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CAGGGTCAACACCAGTGGCTGAGAGGGCTTCTGCGGCTTCATACAGCGAACACCTCTCCACAGCGAACAGCTGGCAGTACAGCACAAGTCC
TACCATCAATTCTGGAGGAAACAGGCAATTCTCCTCTATGTCAGCGAACAGGCTGACAGGTTATGAGAATCTTCTTGGGATT
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AAGCGAATCAAAGCAAACAAAGGACTTAGTCTGTGCAATACAGAACTAAACCTTCACT
SEQ ID 30
MVTGGFRLDLLLEITKIA RATYYYQLKKLNKPDKAIKSDIQSIYDEHRGNYGYRRIYLELRNRGFVINHKRVQGLMKSMGLTARIRRKRKYASY
KGEVGKKADNLIQRFEGSKPYEKCYTDVTEFALPEGKLYLSPVLDGYNSEIIDFTLSRSRSPDLKQVQTMLEAFPAASYSETILHSDQGWQYQHKS
YHQFLEDKGIRPSMSRKGNSPDNGMMESFFGILKSEMFYGLEKSYKSLDDLEQAITDYIFYNNKRIKAKLKGFLSPVQYRTKSFT
SEQ ID 31
ATGCTACTTGAATCCTGATTATCACGCTCCACCTATTACTATCAAGTGAAGCAGTACTGCTCAAGGAGATAAGGATATAGAACTAAAGCATG
ATTGAGAGATTATGATGAGCATAAAAGGAATTACGGTTATCTCGGATTCATATGGAGTTGCTAACCAGGAGATTGTTGTAAGAAGGCTGAT
GTTCAACGCTCTATGAAAGTCTAGGGCTTAGCAGCCGCATTCTCGGAAGCGCAAGTATTCTCTTACAAAGGAGGGTTGTAAGAAGGCTGAT
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TCACCTGTTCTGATGGCTATAACAGTGGAGATTATTGATTCTACTATCTCGGCTCTTAATTGAAACAGGTTCAACCATGCTTGAAGAAGACT
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TTTAGTCTGTCCAATACAGAACTAAACCTTCA
SEQ ID 32
MILLEILDLSRSTYYQVKRLAQGDKDIELKHWIRETYDEHKGNYGYRRIHMELRNRGFVNVHKVQRLMKVMGLAARIIRRKRKYSSYKGEVGKKAD
NLIKRHFEKGSKPYEKCYTDVTEFALPEGKLYLSPVLDGYNSEIIDFTLSRSRSPNLKQVQTMLEKTFPADSYSGTILHSDQGWQYQHQS
YHDFLESKG
ILASMSRKGNSPDNGMMESFFGILKSEMFYGLEKSYKSLDDLEQAITDYIFYNNKRIKAKLKGFLSPVQYRTKSFT
SEQ ID 33
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TCCCAATTAAAGAAAATGGTTACTATTGTTGAGAAAACAAGGGGAGACCGAGTAAAATGGGAGCTAAGCGTAAGGAAACTTGGGAGAAAATG
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SEQ ID 34
MKLSEYDKELEYLRKIGMSWSQISQRYDVRISNLKYMIKLMDRYGVEIVEKGRNEYYPPELKQEMIDKVLIHGCSQLSVSLDYALSNCSILT
NWLSQFKKNGYTIKEKTRGRPSKMRKRKTKTWEEMTELERLQEENERLRTENAFLKKLRLRLRDEALQSERQKQLEKWSQEDSD
SEQ ID 35
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GAGATAATAAAAGTCTCTGATTGACGGCAATCTCAGAAACACATCTTCTGATTATGCTCTCTAATTGTTCTATACTCACAATGGCTT
GCGCAATACAAGAAAACGGTTACTATTCTGAAAACCAAGAGGGAGACCGAGTAAAATGGGAGCTAAGCGTAAGGAAACTTGGGAGAAAATG
ACAGAGGTTGAACGCTTCAAGGAATTAGAAATACCCTAGAGCGGAGAACGCTTCTAAAGGTTGAGGGATTGCGCTTGAGGGACGAAGCC
AAACTCAAAGCAACAGAAATCATTCAAGCAT
SEQ ID 36
MKFNQETKVKITYELRQMGESIKSISKFDMAESDIKYMIRLIDRYGVTIVQKCKNHYYSPELKQETIKVLIIDGQSQKQTSLDYALPTSSMLSRWI
AQYKKNGYTIKEKPRGRPSKMRKRKKNLEEMTEVERLQKELEYPRAENAVLKKLREYRLRDEAKLKEQQKSFKH

-5-

SEQ ID 37

TTGAAAAATCAACAAAATTAACTAGAGACTAGAGCTATACTCAAACATCACTAAAGCCGTGCACACCTTTTATTCTAACCTTAC
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TATCTATTCTACCTAAAAGAAATTGATATGATTGAGCCTAAATGCCAAAGAACTATATCTCATCGTTCTGATAAAAAGGAGAAATCACACTT
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AATCAAAAATTCTGCAAACAATTGCTAGCAGTGATATTGACTAGCTGTTGGATGGCTCTATCCTTTATAAAGATGGAATTGATCAACC
ACTATTTCACCGCAGCAATTGTTTAACTGATACCTTACCCACGCCAACTCTAACAGCTGAAAACAGTGGACAGATTCTCTTTGAATATCCT
ATTTCAGTTCTAGAACATGAACCTTCTTACCTAACACCATTAGAGTACGGAAATTGGCAAAACAAATTCTTATGAGCTTACATCATGTCA
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CGCTATTGGATAAAGAGTGAATGCTACCATTTCTAAGAAATAAGTTATTTCAGAGTACATTATGATTATAAAAAGATGTTGAATTATCT
GGAATTGCTCTCTACTTTATAAGCTTTTAAACCAAG

SEQ ID 38

MKNQQKLMYLESIELYNSITKAALFISQPYLSVKIQKLENELEIKLISQSGHQTFLTYAGQRYLFYLKEIDMIERQMAKELYLIRSDDKGGEITL
GINSGLASSILANVLPKFNLEHPEISVKLLENNQNISEQLVASCDIDLAVGMAPILYKDGIASTTIVRDEFLMIPTSQLYNAEKRGQIIPFEYP
ISVLDNEPLILTPLEYGIGKTIAQFYELHHMSLNQMITTSTVPTAASLSLSGMGATFPQTLIHRYLDKECNVYHFHKNLFSEYIMIYKKDVELS
GIALLLYKAFLTK

SEQ ID 39

TTGATAAGACAAGGAGAATCCTATTGGATATTAAACAAATCGTATTTCATCGCAATCGTGAATCATTAACTTGAGCCAGGGCGCGGAA
CTGTTGTATGTGTCGAGCCGACACTAGCATGATCAATGATTGAAAAAGAGAAAATGTTAACGCTCTCAAACGAAAAGAGGTCGATT
ATTGGGTTAACCTATCTGGTATAATTATAAGGACGCTCAAAGGTTCTCAGTCTATGATGACATGTTTGAATTGCATGATCACAGT
AAAGGGTTAACGGAGTATCAATTGGTATTCCCTCTTATTTATCAGTTGTTTCTCAGAAGTAATGCCAAACTGATTAGAAAATCCG
GGGATTCAATTCAATGTTAAGGAGATTGGTGTACCAACTAAAAAAATGAACACTCTCGTGGAAATGTTGACGTCGAGCTTGTATTCCCAACAA
GGCAGCTGCTGATAATTGGTGTGAGATATTGAATTCAGAGATCAGAATTATCTGTATGCCCTGTCACGCCATCGTTAGCTCCAAAAAGTT
ATTCACTGGAGATTAAACAGATGAAACACTGGCTTATTTGATCCTAGTTCTAGGTTCAACCTATTAGTGTGAAGCTGGCAGGTCACCAA
GTCAGACCTAATTATTGGATTTGACGTCCTCTCCTGGGATTATTGATTAACGTTAACTGGAAAGATTAATCACACAGTCCTAACTATTGTCCCAACCT
ATTACAGAATTATAACCAATTAAAGGACATTAAGTGTATTCAATGGAACGTCCTTCTGGCGTGTGCTTAACAGCCTCCGGAAAAAGT
TATTCTGAATAGAGCCTACATCATGGACGACTTGTACAGTCCTTTTAAG

SEQ ID 40

LIRQGESYLDIKQIRYFIAVENHFNLSSQAAELLYVSQPTLSMMINDFEKRENVKLFKRKRGRIGLTLGDNYYDKAQVLSLYDDMFLKLHDHS
KGLKGSSINIGIPPLILSUVFSEVMPLILENPGIQFNVKEIGAYQLKNELLGVNVDVAVLLSPTGIADNLVETYEIQRSSELSVCLSPRHLASKKV
IQIWEDLTDEQLALFDPSFMVHHLVLEACERHQVRPNIILTSSSWDFMLNSTKINHNVLTICPKPITELYQLKDIKCIPMERPISWRVVLTLLRKKS
YSEIEAYIMDDLLQSFFK

SEQ ID 41

SEQ ID 42

MANASLRHQLFKEKLDQKCDQMVAIRRYLHENPELSFKETKTAAIYISDFYKGKDCHVQTQFGGMGVVVDIYGDKATDKPIKHALRADFDALPIQE
ETGLSFSKTAGVMHACGHDAHTAYLLILAESLIELKSEFSGHIRILHQPAEEVEPGGAKAMIEAGCLDGIDAVLGHVMSTMEEGTVQYHAGPIO
TGRATFKVILQGKGGHGSMPHRANDTIVAASSFVMAAQTIVSRRVNPFDTAVVTIGSFDGKGKSANVIKDSVTLEGDVVRMSEETRGVVEEFKRIL
DGIATQTYGVSYQLDYQNDDPVLVNNSEVTQKVANSLKSVAIKEILDVIDCDPQTSEDFAYYAQTIACFVFYVGAHEEGQPYPHHHPKFQIAESS
LMVSAKSMATAALAMLVEGE

SEQ ID 43

ATGTTAACGACAAAGGAAAATTCAAAGGAATAACAAATTATGGTGGGAATTGTACTCGCTGTACTATCATTTGGTTATTCACAGTCTATT
TTAAACATGGGACCAGATGTTCACTCATTAGGTATTTCATCTGGTGCATGGATTGGTGTCTCAAGTACGGCATGGTTCAAGGTTATT
ATTGGTGAACGGTGGTTAGCAGATAAACTTGGTCAGGTTAAATTACTTTATTGGTCTTGCTTAATATTGGTCTCTACTAATTGGT
TTAGCTAATGGAGCAGTGTCTATTATGGACGCTATTGGCAGGATTGGCAGCAGCTTATTATGCATCACAAATGGCCTGGTAAACG
TACTATGATGTTAAAGATAGACAACGGTCAGTTAGTCTGGTCAATCGGATCTGGGCTGGCTCAGGTCTATGGTCTATTGGTGGAGCGGTG
CGAACGACTCTAGGGTGGCTTATGCTTTTCAATCATCGCATCAGTAGTTCTATTTCAATGGTCTATGGTCTATTGGTGGAGCGGTG
GTTGGACAAAAAACTCACTTGATTACCTGGTTAATTATTTTATTATTCATGTTATCGTTAAATTGGATATCTATGGCTCAGGAACAT
GGATTGATGAACTGTTATCCATTGAGTCCTTACAGTGATGCTTATTGGATTGTTCTGTTTATTATGGTAAACAGTAAATCTAATAGTTT
ATTGACTTCTATCTGGTTGAAAATGATTACTTAGGTGCGACAATATCAAATTCTACTGAATGCACTGGAGGAACTGATTGTTATTAA
ACTTACATCGAACACAAGGTCGCCAGCTAACACAAAGGTTGCGAGCTGAAATGCTTTAGGCTATTGGTTGTACTAATTGCTATGGGTTGGT
GAGAAAATTTCACACGTTGGTGCCTGAAGCCATGCTTGGGAGCTATGAGTACATTGTTGGGATATTAACTGATTGCTCAATT
CAAGGACCTTGTATCTGTGTTAGTCCTTGGTTATGCTTATTGGAAACAGGCTGGGATCTATGGCAGACCATCAACAGATAAGCTATT
TCTAGTATTCTCTAATGAAAAGTAGGTTCTGCATCTGGAAATTACAAATGGCAAGTCTACTAGGTGGTCAATTGGTGTAGCAACTTCAATTGCG
ATTATCATGCTTTCTGGTAATGCAAGATTTCACAAAGCAGCTTGTGTGGATTAAATTAAACCTAGTTTTGTAGTCTATCGATCTTATCA
ATTCTTTTGTATCCCTAAGAAAATTGAGGATAAA

SEQ ID 44

MLTTKENVFGNNKLLVGIVLAVLFWLFAQSILNMGPDVQSSLGISSGAMDIGSSTALFSGFLFIVVTGLADKLGRVKFTFIGLCLNIIIGSLLIV
LANGAVLFIMGRIFQGLAAAFIMPSTMALVKTYDGGDKDRQARVSFWSIGSGWGGGLCSYFVGAVASTLGWRWYRVIIFSIIASVVSFLILLGTPESKN
VGQKTHFDYLGLIIFIISMLSNLNIGISMAQEHHGLMNVIPLSLFTVMLIGFVLFVVYETRKSNSFIDFHLEFNRFYLGATISNFLNAVAGTLIVIN
TMYQQGRQITVKGAVAGEMSLGYLVCLVIAIRVGKEKILQRFQARGPKMELGMAMSTFVGIFLMTLNVIQGPLYLVLFVFGYALFGTGLGIYATPSTDATI
SSIPNEKVGSASGIFYKMASSLGGAIGVATSAIYEHFGNADFHKAAALCGLILNLFVCSLSILSILSFVLPKIEDK

SEQ ID 45

ATGTCACATCATCAACAAACC GTTTCAAAAACAATTATGGCGATTATGCCATAGCACTCATTGGTTTCAGGAATTTGTCTGAAACCAGT
 ATGAATGTCACCTTCCCGACACTGATGTCAGTCTATCAGTTACCTTAAATAGCTTGCACATGGATGACGACCATTTACTAGCAGTGGCGATT
 ATGATGACCACTTCGGCTACACTGAAAAAAATGTGCGGAAAGACCCCTCTTTTATGCCACAGGTCTTTTACATTGGCACCATCTTGGCC
 GTTCTGACCCAGTCCTTGCGATCATGTTGCTAGCCCGCATTTTCAGGCTTGGTACTGGTCTGGTAATGCCAGATGTTAATTATTTTA
 GAGCGTGTCCAATGCAAGTAGGTCTATTATGGATTGCTGGTCTTATTAGCTTACCTGCTTTGGGCTACTTATGGGGCTTT
 ATGATTAGCCATTTAGTGGCAATGGATTCTGTATACTCCCTGTACACTGATTGAGGTATTCTACCTTATTAGCTATTACCTCGAAGATTCT
 CCAGTAAGGAAAAGTACCCCTTGACTGGTGGCATTATTGCACTATCGATTAGCTTAATTCTGCCTTATTAGCTATTACTAGCTAGAAAAC
 GGCAGTGTAAATTGTTACTTAGGGCTTTATTCTCAGCTTATCCTCTTACAAGAACATCTCACAGCTAACGAAACCTTCTGATATT
 CGCATTCCTAAAATCCCTCTAACCTTGGCCTGATTCCCTTTGTCTCCAGCTGATTAATTAGGCATAAATTCTAACGCCAAACTTT
 ATTGTCATGGAAAAGTGCATAGTTCTCAAGCTGGTACTACCTGGTACCTGGAGCTACTAGCACCCTGCTTGGTAAA
 CTTTATGATCAAAAAGGAGCAAGACTTCGCTTATTAGGAATGCCATTAGTTATGATTATGACACTTCAAACAGACATT
 ATGTTTACCACTCTTATATTATTCACTGGCGTAACTGGCTTAAATAGCTTACGGCTATTAGGAACTGCTATGGCATCACTGATGCAAAGTAGT
 CAAGCAGAATTCAACAGGGTGTCCAGTGTCTACCTCTTACTATTTGCTCTACTTGTATTATTTCTTGTATGTTTACCTTGGCATGTTTACCAT
 TTAGGAAAAAGGATTAGCC

SEQ ID 46

MSHHQQTVSKQTIMAI TIALIGFSGILSETSMNVTFPLMSVYQLPLNSLQWMTTIYLLAVAIMMTTSATLKKNRERPLFFMATGLFTFGTILA
 VLTQSFAIMLLARI FQIGITGLVMPQMFNIILERVPMHKVGLFMGFAGLIIISLAPAFGPTYGGFMISHFSWOWIFICILPVPLIAGILAYYYLEDS
 PVSEKVPFDWLAFIALSILSALLTLENSGVNLYYLGLFILFLYKLNLTAKQPFLDRIKLPISLTFGLIPFFFVQLINLGINFLTPNF
 IVMEKIANSSQAGMVLPGTLLGALLPAFGKLYDQKGARLSLYLGNALFSLIIMTLQTRHFMLLPFTLILFTGRNMGFNNSLATAIRELP
 AEKNADATAIFQMMQOFAGALGTAMSLIANSQAETSGVQSVYLLFTIFALLDFIFFFAMPYHLGKKGLA

SEQ ID 47

ATGAGTTATCCATCATGACAAAACACAAACACCTAACCTCTTAGACCGTAATGACATCCAATCTGGTTGGATAGAGGAGAACCTTAAAGCC
 ATCGGGCTTAATCTACTGAAACACCCACTACTATCGAAAAGAGTCAAACGAAATAAGCAACTAACCAAAGACTGCCTAGACTGT
 CCGCTACTAAGAAAAGCTCCCTATGTTGTAATGGGTGTCAGGAGGAGATCAACTGTGTTACAAGAAGACCTCTATCTGCTAAAGCAAGCT
 CAAAGAAAATATGAAACTTGTGAGAGGAATCCCTTGAAACAAAGAGACCTCTGGAAAATAGATAGGTGCTTCAATGG
 GTCAAGAAGGGCCAACGTCTATCATATCCTCAAACACGATCTAGAAGTGAGTTCTCAACCCTTATCGACACATCAAGAAAGGCTACCTA
 TCCATCACCAATCGACCTACCCAGAGCTGTGAATTCAAAAAGGCAGAACACTCCCTCTATTCAAAGCGATTAAAGAAGGGCGA
 CGGTACGAGGATTTATAGAACACATAACNNNNNTAAT

SEQ ID 48

MSLSIMTKKHLLTLLDRNDIQSGLDRGETFKAIGLNLKHPPTIAKEVKRNQLRESTKDCLDCPLLRKAPYVCNGCPKRRINCYKTFYLAQQA
 QRNYEKLLVESREGIPLNKETFWKIDRVLNSNGVKQRIYHILKTNDLEVSSSTVYRHKKGYLSITPIDLPRAVKFKRRKSTLPPIPKAIKEGR
 RYEDFIEHITXXN

SEQ ID 49

ATGGCTAAAAAGTTGAAAAACTTCAATTCTGCTGGTAACGCAACTCCACCACTGGGACAGCACTGGTCAAGCAGGA
 ATCAACATCATGGATTCACTAAAGGTTAACGCTCGTACAGCTGATCAAGCTGGTATGATTATCCAGTTGTTCTCAGTATATGAAGACAAA
 TCATTGATTTCATCACTAAACACCAACAGCTGCTGTTCTTGAAAAGCTGCAGGTGTTGAAAAGGATCAGGTAAACCTAACACTAA
 GTTGCAACAATTACTCGTGCAGTACAAGAAATTGCTGAAACTAAAGCAGATTAAACGCTGCAACACTTGTGAGTCAGTGTGATGAC
 GAAGGTACTGCTCGTTATGGGATTCACTGTTACTGAC

SEQ ID 50

MAKKVEKLVKLQIPAGKATPAPPVGPA LQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDIFITKTPPAVLKKAAGVEKGSGEPNKT
 VATITRAQVQEIAETKMPDLNAANLESAMRMIEGTARSMGFTVTD

SEQ ID 51

ATGCAATTATTGCTATCTGTGGGAGGTTAAAATCTCAATTACGCCAAAACACAAACAGGAGGATTTTAAAATGGCTAAAAAGTCGAAAACCTT
 GTAAAACCTCAATTCCCTGCTGGTAAAGCTACACAGCTCCACCACTGGGACAGCTCTGGTCAAGCAGGTATCAACATCATGGCTTCACTAAA
 GAATTAAACGCTCGTACAGCTGATCAAGCTGGTATGATCATCCAGTTGTTATCTCAGTTATGAAGACAAATCATTGATTTCATCACTAAACAA
 CCACCACTGCTGTTCTTGAAAAGCTGCAGGTGTTGAAAAGGATCAGGTACACCTAACACTACTAAGGTTGCGACAGTTACTCGTGCACAA
 GTACAAGAAATTGCTGAAACTAAGATGCCAGATTGCAACATTGAAAGCAGTGTGATGCAAGGTACTGCTGTTATGGGA
 TTCACGTGTTACTGAC

SEQ ID 52

MQYCISVGKGNLYRNQHNRRIFKMAKKVEKLVKLQIPAGKATPAPPVGPA LQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDIFITKT
 PPAVLLKKAAGVEKGSGTPNTTKVATVTRAQVQEIAETKMPDLNAANIEAMRMIEGTARSMGFTVTD

SEQ ID 53

ATGGCTAAAAAGTAAAAACTTACCGTCTGGTCTGCTCTTGAGAAAATTGATAGCATAAGCATACAGCTAGAAGAAGCTGAGCTCTTGCACAAAGAA
 ACTAACTTGTCTAAATTGATGCAACTGTTGAAGTTCTTATAACCTTAAACATTGACGTTAAAAGCTGACCAACAAATCGTGGTCTATGGTT
 TTACCACTGGTAAACTTCACGTGTTCTGTTCTGCTGGTCTAAAGCTGAGAAGCTAAAGCAGCAGGTGCAAGACTTTGTGCGGT
 GAAGATGACTTAGTTGCTAAAATCCAAGGTGGATGGCTGACTTTGATGTTGTTATCGCAACACCAGATATGATGGCAGCTTGTGGACGTCTTGG
 CGTGTCTGGACCTCGTAACCTGGCAAACCTTAAAAGCTGGTACAGTAACATGGACGTTCTAAAGCAGTTGAAGAGTCTAAAGGTGGTAAA
 ATTACTTACCGTGTGATAAAGCAGGTAACGTCCAAGCCCTTATTGGTAAAGTTCTATGATGATGCTAAATTAGTTGATGATAACTTCAAACGATT
 AATGATGTTATTGTTAAAGCTAACCGACTACTGCAAAAGGAACCTACATCACAAACCTTCAATTACAACACACAAGGTGGTATCAAAGTT
 GATCCTAACACTACT

SEQ ID 54

MAKKSKNLRRAALEKIDSTKAYSVEEVALAKETNFAKFDATVEVSYNLNDVKKADQQIRGAMVLPAGTGKTSRVLFARGAKEEAKAAGADFVG
 EDDLVAKI QGGWLDFDVIA TPDMMALVGRVLGPRLNPNTGVTMDVAKAVEESKGKITYRADKAGNVQALIGKVSFDDAKLVDNFKAF
 NDVIVKAKPATAKGTYITNLSITTTQGVGIKVDPNSL

SEQ ID 55

ATGGCTAAAAAGCAAACAAATCCGTGCTGCACTTGAAAAGTAGATAGCACAAGCGTACAGTGAGAAGAAGCTGAGCTAGCATTAGTAAAGAA
 ACGAACCTTCGCAAATTGATGCGCTGTTGAAGTTGCTTACAACATTGACGTTCTGCTGAAACATGACGTTCTGCTGAAAGCAGACCAACAAATCCGTGGCGAATGGTA
 TTGCGAAACCGGAACCTGTTAAAACACAACTGGTGTGTTCTTGTGCACTGGTCTGGTCAAGCTGAGAAGCAGCAACAAAGCAGCTGGTGCAGACTCTGTAGGG
 GAAGACGACCTTGTGCAAAATCAATGGTGGATGGCTTACTGTTGACGTTGTTATCGCAACGCCAGACATGATGGCTATGTTAGGTGCTAAGCGTTGAAGAGTCTAAAGGTGGTAAA
 ATCACTTACCGTGTGACAAGCAGGTAATGTTCAAGCTTATTGGTAAAGTTCTATTGATGCTGACAAATTGGTGAAGAGTCTAAAGGTGGTAAA
 CACGATGTAATGGCTAACAGCTAACCTGCAACAGCTAACAGGAACCTACATGGCAAACGTCTCAATCACATCACACACAAGGTGGTATCAAAGGTT
 GATCCTAACACTACT

SEQ ID 56

MAKKSKQMRRAALEKVDSTKAYSVEEAVALVKETNFAKFDASVEVAYNLNIDVRKADQQIRGAMVLPGNGKTQRVLVFARGAKAEEAKAAGADFVG
EDDLVAKINGWLDVDVIATPDMAIVGRLGRVLGPRNLMPKTGVTMDVAKAVEESKGKITYRADKAGNVQALIGKVSFDADLKENFKAF
HDVMAKAKPATAKGYMANVSITSTQGVGIKVDPNSL

SEQ ID 57

TTGGTAAAGGAGACGTAACATATTGGAGCATTACTTGTTATTGATGGTCACTCTGCATGCCATTACAGGATAGCAAAGTCATAAA
CTAAACAGTATAAACTACGCTTGGGGAGAAGACTTTGGTCACTGTTAATCCGCATCGCTATAACCTGTCACTTGTGTTATCAGGATATG
GTTTATGAGGGGGTGGTACGATATGGACAATGGAAAATTGAACAGCCTTACGGAGGAGCTTACGGAGGAGCTTACGGAGGAGCTTACACT
TTAAATTGAGAAATGCTAAATATTCTGATGGCAGTAACCTTAATGCTGCAATGTCACAGTAACTTTGATAGTATTTTCAAGTCTAATAGA
GGTAATCATAAATTGGTTAATTAAACGAAATATTGAGAAATTATCGTGCCTTGAATCAAAGTACTTTGAAATTAAACTGAAACAAGCTTATAGT
GCTACTTTATGATCTCTATGATCGACCAATTGCTTTTATCTGATAGCCTTCCCTAAAGCTGAGGAGCTTACGGAGGAGCTTACGGAGGAGCT
AAACCAATTGGAACGGGTCAATGGGGTGTGAGGAAATTAAAGCAAATGAAATATTACCTCCTAAACGTAATGAGAATTACTGGGGAGAAGAACCA
AAATTAAAAGGAGTAAACGTTAAAGTATACCGGATGCTCACGGCGTCTTACGGTCAACAGTATTGACAAGGTTCTATTGCTAAGAACACCTTACGGAG
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GCTAAGGAAAGTATTTCCAAGATAAAAAGTTCGTCAGGCAATGAAATCATGCTATTGACAAGGTTCTATTGCTAAGAACACCTTACGGAG
GAAAAGCCAGACACTATTTTCAAAATCAACATCTCAGATGCTAAGTAAACCTTATAGCTATAATGTTGATAAAGCAATCAGCTA
TTGGATCAAGCTGGTGGAGATGGGGAAAGATAAGGTTCTGAGGGAAAGATGTTAAACTCTAACCTTACGTCTTCTATATGCCACTAAGGCA
ACTGATAAAAGCCTGGTAACTTATTTCAAGGAGAATGGCGTAAATGGTATTAAATGTTCTTATTGCTATGAAAGAAGATGATTATTGGGCT
AATGCTAAAAGGGTAATTGATGATGTTAACTTCTGGGAGCACCATGGGACCTCTGCTGGATGTCGGCATTAACGCAAGGCA
GATCATGGACATCAGAAAATATAGCTTAAAGGATGAGTAACTTAAAGGATGAGTATTAAGCTAGCTAGTAGATCTAGGAA
GAAAATGTTAGAGAGACTATAAGGGTTCTGAAATTATTGATGAGGCTGTTATATCCATTAACTTATGTCATCGGTGATTCTGTTAT
AGGAAAGGTGATTAAAACCATGCGTTTGCAGAGAAAATTCTACGCTATAGAAAAAAACATGATCTAAG

SEQ ID 58

MVKMRRNILLSITCLLMVTLTACHSQDSKSHKLNSDLTLAWGEDFGDVNPFRYNPDQFVIQDMVYEGLVRYGDNGKIEPALAKSWSISQDGKTYT
FKLRLNAKYSDSGSNFNAANVKRNFDSIFSKSNRGNHNWFNLNTNQLENRYRALNQSTFEIQLKQAYSATLYDLSMIRPIRFLSDAFPKGDDTKKNVK
KPIGTGWWVSKKQNEYITFKRNEVYWGKKPKLKEVTVKVIPOAOTRALAFESGVDLIVYNGNIGLDTFAQYTKDKYVTAISQPMSTRLLLN
AKESIFQDKVVRQAMNHAIKVSIAKNTFRGTEKPADTIFSKSTHSDAKLNPSYNDKANQLLDQAGWKMGKDVKREKGKTLTLELPYIATKA
TDKDLVTVFQGEWRKIGINVSLIAMEDDYWNAKGNFDMMILTYSWGPDPHAWMSALTAKDHGHPEINTALENLATKTEMDRILIKSALVPKE
ENVDRDYKVKLELLHDEAVYIPLTYQSVISVYRKDFKTMRFPAPEENSFPLRYIEKNNVSK

SEQ ID 59

TTGATTGTCAAAATACCTAAAATACTCTCTATTACGCTTATTTGACTGGGCTTATTTAGTTGCTATGTCACAAACAAAAGCCTCAAACAA
AAAGAACGTCAGCGCAAACAACGCTAAAAGACGAACCTGCTTCTATGGGGCAAAGCTCCCTCATGAATTGATCAAAGGACCTTATGGA
GTCCACAATGAAGGAAATATCAGTCACTGACTTCTGAACTGATGATTAACTCTCAAAATGCTGAGGAGCTTACTGCTGATGTTAAAGTTACTTATGAT
GAAGATGGGCTGACTTGGCTGTTGACTTGCATGATGATTAACTCTCAAAATGCTGAGGAGCTTACTGCTGATGTTAAAGTTACTTATGAT
ATGTTGAAAGCAGATGGAAAGGCTTGGGATCTAAAGAATGCTGAGGAGCTTACTGCTGATGTTAAAGTTACTTATGCTGAGGAGCT
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TACATGGTAAAAGAATATAAGGCTGGAGAACAGCTATTGTTGTAACCCCTATTGGCATGGGAAAAAACCATCTTAAAGTGGACTTGG
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GGCACCCGCCCTCTTGTATTCATCAAATGATGTCGCGGCTTATCATTACCTTATGTTGAAAAGGGCTCATCACTGATTCTCTGATGGTTAT
CCTGTTAGGAAATGATGTCACTAGTGTACTGTCAGAACATCCGAAAAGCTTGTACTATTGTTTAAATAGGCAAAAGGTTCTGATACGGTTTAAATGGT
TATGGTAAACGCTTAACTTGTGATGTTAAACACCATTGGGATGCTTAAAGGATGCTTAAAGGATGCTTAAAGGATGCTTAAAGGATGCTTAAAGGATGCTTAAAG
TTGACAAAAGCGGGATGGAAGAACAGCAGCAGCTGGCTTGTGATCTGACTACCCCTACTATGATCAA
TTGCGAGCGAACCTAGCCGTTAGCTGAGCTGAGCAAGGCCAGGGCTTGGGATGTTACTTAAACTGAGCTTAAAGGATGAAATGGCAACG
AAAGTCACATGACTCAGCCTTACTTATGCGGGAGGACGTATCACCGCAGCAATTATGATGTCATCATCCAAGCTAGCAGGGAAAGGTTGG
ACCAATATTACGTTTATAACAATCTACCGTACTAAGTACCTGACAAAGCAATGACATCTCTGACCTTGTATAAGGCAAAAGCTAACGAATATTGGAAAG
TTAGCGCAGTGGGATGGAAAAAGGGCTTACTCTGGAGATTGCAATGTTGAGCTTAAACCATACTTATATTGGTGTGAACTAAG
CGTATCAATGTTAGGAAACAAGGCTTACAGTGTACTGACATGGTACTGTTAGGCTATTGACTAACATTGCGAGTGGACTTGGGATGATCAACTAAG
SEQ ID 60

LIVSKYLYKFSIITLFLGLILVACQQQPKQTKERQRKQRPKDELVVSMSGAKLPHEFDPKDRYGVHNEGNIHSTLLKRSPELDIKGELAKTYHLS
EDGLTWSFLHDDFKFSNGEPVTADDVFKFTYDMLKADGKAWDIFTIKNVEVVGKVNQVNIHLTEAHSTFTQALTEIPVFKHYNDKYKSNPIGSGP
YMVKEYKAGEQAIIFVRNPYWHGKKPYFKKWTWVLLDENTALAALESGDVDMIYATPELADKVKVKGTRLLDIPSNDVRLSLPVVKGVITDPSDG
PVGNDVTSDFPAIRKALTIGLNROQVLDLTVLNGYKGPAYSIIDKTFWNPKTAIKDNKVAKAKQLLTQAGWKEQADGRKKGDLDAAFDLYPTNDQ
LRANLAVEVAEQAKALGITIKLKASNWDEMATSHDSSALLYAGGRHQAQQFYESHPSLAGKGWTNITFYNNPTVTKYLDKAMTSSDLDKANEYWK
LAQWDGKTGASTLGLDPNVWLVSLNHTYIGDKRINVGKQGVHSHGHDWSLLTNTIAEWTDESTK

SEQ ID 61

ATGTATCTAAGTAGTTGTCATCAAAAAAATATTGTCAGCTTTGGCATTGTTTCTATCACTCTAACATTATTCTTATCAAACATCA
ACAGCTTAATTCAGCAGAAAATTACCTCTGTTTCTACAAAATAAGTGTAGTCAGCAGCTAAAGAAGCAGAGCACTATTAGGTTAGATAAG
CCATTATGGAAGCAGTACTGGCTGTGTTCTACAAAAGCTTAACAGGAGATTGGGATATTCTTATGTCAGGTTGCCAGTATTAGATTGGT
TTACAAAGCTTTGGCTACTTTATTGAGCTGAGTGCCTTCTGCTAATTGTTACCTTCTACCCGTTAGGTTGCTGGGCTGCTTACAT
GAATCTCGAGGAGTGTACTGTTGAGTTCTAGTGTCTATGCCAAATTGTTGGGCTTACTGTTGATGTCGCTATT
TCGGCAAATTAAATCTCTGCTGTTCTAGGAGGTAACGATTTACAAGGTTAAATGCTGAGGAGTATTACCTTAAGGTTCTACCGTAGGTCAA
TACATAGCCTTATTGAAAAGCTATTAGTCAAGAAAATAGAAGTTAAATGCTGAGGAGTAAAGAAGCTTATATTGTC
ACACATCACCTCTTACGAGCTTACCTGCTACAGACTGACAGACTTGTGACTGGGTTACTTATTAACAGGATCAATTATTGTTGAAGAA
ATTTTTCTGGAATGGAATAGGACGTTATTGAGCTGAGCTTAAAGAACTTACAGATCTTCACTGAGTGTGTTACTTATTAACAGGATCAATTATTGTTGAAGAA
TTATTGTTCTGACTAATAATTGACACAGTGTGTTATGAAATTGGGTTGATCTCGGTTACGAAAGTCAGGGAGAAAA

SEQ ID 62

MLSSSIKKILSAFLALFFISLLTFLILSTVNSAENYLRLSKISVSPPEALKAEHYLGLDKPLWKQYWLWFQKALTGDFGYSVRLPVLDLV
LQRFLATLFLGTSASFLLIVT1STPLGVWAGLHESARSDHLIRFLSFSSVSMPNFWVAYLLMLLFSAKLNLPLVSGGNDLQSLILPSITLFSFTVQ
YIALIRKAISQENRSLNVENARLRGVKEYIVTHHLLRNALPAIMTALSITWVYLLTGSIIIVEIFSWNGIGRLFVTSRLSDLPVIQACMLIFGT
LFLANNFMTCQCFMNWVDPRLRKSREK

SEQ ID 63

GTGAAACGTAACCTACATTATTCATCTGGAAAATCATCAGATGTCAGCCTTATTTGGGGTATCTGTTTGCACCTCGTTAAAGCAA
TCTCCAGTACGATCCAGTCATGCCAAGTGTCAATTATGACACATCACTAACCCCTGCTCAGTACAAAGCAGTGTCACTATGGCTTGGGATAAG
CCAGCTCTAGTCAAAATTATTGTTGTTGAAAAGATGTCAGGAGGAGTTAGGGACCTCGCTGTTCTGCGCAACCTGTTAGTGTATATT
AGATCACGGGAGGTGCTTCTTCTACATTGAGCTCTCTGGGATCTTATGGGTTCTATTGAGGTTATCTTACGGGTTATGGGACTTATCCGCTTAC
CAAGGAAATTACTTGACCGAGTTGTCAGGTGGTTCTACACCTTACAGATATGCTGAGTACCAACGTTTGGACTTACGGTACAGTAAAG
TCTGTCAGCTGGGGTGGTTCCGATGGTATTCTTCCCGATAGGCACTTGTGACTCAAGATATTACGTTAGCTGATCAGGTTAAGCACCTTATG

TTACCTGTTTCACGCTAACGTATTCTAGGCATTGCAATGTCACCCCTCATACGAGAACTAAAATGATGTCGGTCTTCTAGTGAATATGCTTA
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TTTGAGAATTGTTGGAGGATCTGTCTGCTGAGCAAGTTCTCATATCTGGCTTAGGGCTACCCCTCACTGAAGCAGGACTTAAAGTGTAT
ACACCGCTCTTCTAGTATTGTGATAGGGACATTATTGTTTGCAGGCAATCTATTGCGGATATTAAATAGCATCATCAATCCACAG
TTAAGGAGAAAAGTA

SEQ ID 64

VKRTTIIIIIWKIIRCVTLIFGVSVLTFVLLKQSPVDPVMASVNYSQTSLTPAQYKAIAHHYGLDKPALVQYFIWLKNVIQGDLGTSVLVYRQPVSDDI
RSRAGASFILMGLSWILSGLIGFILGTLSAFHQGKLLDRVWRFSYLSQISVPTFWIGLIFLFLISFSVQLGWFPICISSPIGTLQSQDITLADRVKHLM
LPVFTLSILGIANVTIHTRTKMMSSVLSSEYVLFARARGETQWQIFKHHCRLRNAIVPAITLHF SYFGELFGGSVLAEQVFSYPGLGSTLTEAGLKSD
TPLLLAIVTMIGTLFVFAGNLIADILNSIINPQLRRKV

SEQ ID 65

TCTGTTAGTAGTGGCATTTCGGCCCTATTCTATCTAGCTTGATCCAAATACGTAGATTATCACAAAATTATTGGCTCCAATAATGTT
CATTTGTTAGGGACTGACCAATTGGGTAGAGATGTATTATCTCGCTTGCTTATGGTGTAGATATTCACTGTTTAGCTATTATTAGCTTA
TTGGAATTAAACGATTGGTATGTTGTGGGCTTATGGTGTGGGATCAAGGAAAGTTAGAAAACCTTTTATGGATAGCTAAATTATTGTTA
GCTTTCGGAGCTTTGCTCTCTGCACCGGTGGAACTTCTAGGTCTAGGGAAATTAAATTGGCAATTGTCTTGTGGAAATGGGTT
TACTATGCTAAATTAAATGACCAATTAGTAAAGAGTCACAAAAAAAGGCTTATGTGTATAATTAGCAGCCTTCACTGTGGCAATT
TTAAGAAAACATATTTCCTTTGTGTATCAGGCAATCCTCGTTATGGTCCTTATGAATAATTAGGAAATTATTAAATGATTCTGGCTTTCT
TTCTTAGGGATTGGTGTGCAACCTAATGTCACAGAATGGGGATGATGTTGACAGTGTAGAGGATATTAGGACAGCTACTGGATGATGTTA
TCTCTGGAAATTGCGATTTCCTTAACAGTATTTCCTTAACTTTAGGGATGCCATAGATAAAAAGATTGAAACGACAATGGAACAGT
SEQ ID: 66

SEQ ID 66

MLVISIAIFAPILSSFDQPQYVDSLSQLLAPNNVHLLGTDQLGRDVLSRLLYGARYSLFLAIISLLELTIGMFVGLIVGWYQGKLENLFLWIANIIL
AFPSFLLSLATVGILGHGLGNLIFAIIVFVEWVYYAKLMTNLVKSACKEPYVINAQIMGLSVWHILRKHIFPFVYQPILVVMVNIGNIILMISGFS
FLIGIGVQPNVTEWGMMLHDARGYFRATWMMLSPGIAIFLTVFSFNTLGDAIDKKDWKRQWN
SEQ ID: 67

SEQ ID 67

ATGATATTGAAACGTCAACGATGGTTTATGCCAAGGGTATGCCATTCTCTCATTCTAGTATTCTAGCCTAAACCTTATTCCTATAGG
ACGCCATTGAAACCAATGCAGCTTACGCAACCTCGCTCCCTTAAACCATCTTTTGGAACAGATGGTTAGGTAGGGATATGTTGTCAGA
ACGATTAAGGGTTTATTCCTTACAAGTCGCTTATTAGGCCCTTATGGGAGTCCTTCTTGCACCGTTTGGAGTCCTGCAAGGCTA
GGAAAATAGCCTTATTGATAAAATAAGCCTGGTTGATTTGTTATTGGTATGCCCTATTGATTTATGATCTCATTTCTTTGTTGTT
GGGAAAGGGCTCAAGGGTTTATCATTGCAACAGCTTACCAATTGCCCTCTAGCAAGGCTTATGCCAATGAGTCATGACTAAAGAAT
AAAGCCTTGTCCAGCTCTAAAGCATGGGAAAAACGCCTTATTATATTGTGAGGCATCATATCCTGCTTGTATGCTCTCAATTTCATT
GGGTTTATCCTTATTCCGACGTCATCTGCATGAAGCATCCATGACTTCTTAGGATTGGCCTTCTGCCAACACCTCGGTTGGTATC
ATTTGTAGAGGCAGCTAACGATATCTCTTGGCAATTGGGTTGGTATTTCCAGGCCATTCTTATTTGGTGTCAATGCCATTGAT
ACTATCGAGAAATCTTAAAGAAACTCTTACCCAAACGGATCATTT

SEQ ID 68

MILKRRRTMVLWQLGIAISLILSILALNLYFYRTPLETAALRNLPALSNLHFGTDGLGRDMFVRTIKGLYFSLQVGLLGALMGVFLATVFGVLAGL
GNSLIDKIIIAWLVDLFIGMPHLIFMILISFVVGKGAGQVIIATAVTHWPSLARLIRNEVYDLKNKAFVQLSKSMGKTPYYIVRHILPLIASQIFI
GFILLFPHVILHEASMTFLGFGLSAEQPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTTIGESLKKLFYPQTDHF
SEQ ID: 62

SEQ ID 69

TTGAAACGACAATGGAACAGTTAGAAAATTGTCTTACAGATAGGAGAGGTCCTGACTAAGAGATTTAGTGTAAAATAGATATGGAGAACCTCTAATTATTGGTGAGAGTGGTCAGGGAAAACCCCTTGGCAAATTATTGGTTGGTCACATTCCAAGGTATGACAGTTAGA
GGAAACATATTTTAAGGGAGTTGATTAGGAAACTAAGTGAAGCAGTGGCAGAAATTAAAGGGAGCAGAGATATTGCCTATTAGTGCAAAATCCCATGTCTATGTTAATCCTTCAAAATTAGGAGCGCATTTTGGAAACAACTCTTAGTCATGAGAAATGTTCAAGAGAGTAGGCCATTCT
AAAGCGTTAGATGGTGAACAGCTTAAATTAGTGTGCGATATCCCTGTTAAAAAAACCCCTTGGAGCTTAGGGAGGAATGCTACAAAGAATTATGTTAGCCACTATATTATCTCTGATCCTCAGGTAATCATATTAGTGAAGCAGCCTCAGCGGGTATTGTCATAATTGTTCTACTATATCA
GCTATTTCAGGAATTGAAACATGGAAAACCTTGATTACTGTAAACGCACTGATTATCAGTTAGCTAGAGACCTGGGGGACAATTATTAGTT
ATAAGTGAGGGAGAAGTTGTTGAAACAGGGACAACCCAGCTATTAAAGCAATCCTCAACATAACTATACGAAAGCAGTGCACAGTGCAAATGGAG
TATGAAGGAGATATTCTTAATGTTGGTTG

SEQ ID 70

METTMEQLEIRKLSLQIGEVPVLRDFSCCKIDMGESLTIIGESGSGKTLLAKLLVGHIPOGMVTVRGNIFFKGVDLGKLTVKQWQKLRGRDIAYLVQNPMSMFNFPKIEAHILETILSHEKC SKRVALSKALEWMKRLNLDDAISLLKYPFELSGGMLQRIMLATILSLDPQVIILDEPTSAVDCHNCSTISAILOQELNNNGKTLITVTHYQLARDLGGQLLVISEGEVVEQGQTQAILSNPQHNYTKALT VQMEYEGDILNVGL
SEQ ID: 51

SEQ ID 71

ATGACAAAAGAAATAATGTAATCTTAAGTGGCTGAGATTGATGCGTGTCTTAAACAGCTATCCGTAACGCTCA
CTGGAACTTGTGAGGAGAAGTCCTCTGTTGAGGGAAATCAGGCTCAGGTAATCTGTTTAAACAAGACCTTACAGGGATGTTGGAGTCT
AATGGACGCATTGCTAATGGTCTATGTCAGTGGGCAAGAATTGACAGATTAAAAAACAAATAAAGAGTGGGCAAGAATTGCGGCTAAAA
ATCGCAACGATTTCACGACCAGCTAGGACAGTCTAGTCCCATTAAACTATCGTAGCCTAACAGAAGTGATTATAAGCACAAAAAGTA
AGTCATGCCAAGCTAAGAAATGGCCCTGATTACATGAATAAAGTGGGATCCTAACAGCTTGAAGATTACCCATTGAGTAT
TCAGGAGGAATGCGTCAACGTATTGTTATCGCTATTGCTTCTGCGCCAGATATTCTTATCTGATGAGCCTAACAGCCCTGAGTGTG
ACTATTCAAGCTAAATCGTGTAGTTATTGAACTGCTCAACGAGAATATCATTTCACCATTATCTTATTACGCAGATTAGGTGTTGGCA
AGCATGGCAGATAAAAGTGGCTGTCATGTTGAGGAAATTGTTGAATTGGAAAGCTGCAAGAGAATTTCATGATCCAAGACACCCCTATACA
TGGAGTTTGTGCTAGCTTACCGCAGTTGGCAGATGAATTCTGGTGAACCTTACGCTATTCCAGGAACGCCCTCATCATTATTACCAAAATTAC
GGAGATGCCCTTGCCTCGCTCAGAATATGCTATGGTTTAACTTGAAAAGCACCTCCGGCATTACGTTACGACTCATGGGCAA
ACATGGCTTTACACCCAGAGGCTCAGGAAAGTCATTCAAGATTGATCATTAAAGAAAATGTCAACACAGGAG
GAAGGAAATGTC

SEQ ID 72

MTKENNVLITAKDVVVEFDVRDRVLTAIRNVSLELVEGEVLAvgEsgsgksVLTktftgmlesngriangsIVYRQQLTDLKTNKEWAKIRGS
IATIATQDFMTSLSPKTTIGSQITEVIIKRQKVSHAKEMALDYMNKVGIPNAKKRFEDYPFEYSGGMQRIVIAIALACRPDILICDEPTTALDV
TQAQIVELLSLQREYHFTIIFITHDGLVVASIADKVAVMYAGEIVEFGTVEEIfYDPRPHYTWSLLSSPQLADESGELYAI^PGTPPSLYSPI
GDAFLRSEYAMVLDFEKAPPAINVSETHAWTWTIHLPEAPKVOKPEVTDIHLKHTLRKMSOOFGMV

SEO ID 73

TCCTTAAGTGGATTAGACCCAGTAACTCAAATTAAAATGCTACGTTATTACAAAAAATAAAACGCCGTATGAATTAAAGTTTATAATGATTCTCATGACCCTAAAATTGTCAGCTATCTGTAAACGGGTCTTCTGATAAAAATGGTTATTAGTAGAAAGATAATGAATTCTGAAGAGAGCGTGTCTACTAACTGTTGACCAATCTC

SEQ ID 74

MKEIFLMLVCNHNVKTFGRQEVLKDCHFHLKRGEIIGIMGKSGSGKSSLARLIIGLDSPTCGSIFYFQGKIYTPKGDKAQIILVFQDALS SVNPYFSIEEILNEAFYGKTTFELCQILEAVGLDGTYLKVKARQLSGQLQRVCIA RALLLPKIIIFDESLSGLDPTQIKMLRLQKIKRRYELSFIMIS HDPKICQAICNRVFLIKNGYLVEDNEFLKRACTNCLTNL

SEQ ID 75

ATGAATGAAGCAATAATTCAATTAGATCATATTGATATTACCTCCGTCAAAAAAACGGTTATCGAAGCTGTTAAAGATGTCACGGTTCATATC AATCAAGGAGATATTATGGCATTGGGGATTACGGTGCAGGAAATCAACTCTTGTGCGTGTGATTAACCTGCTACAGGCACCAACAAACGG AAAATCACTGGTGTGACTGGGGATGTGACTTTTGACCAAGGGAAAATTCAATTGTCAGCTGATGCCCTCGCCAAAACGACGTGATATTGGTATGATC TTCCACATTTCAATTGATGGCCAAAACAGCCAAGAAAATGTAACGATTGCGCTCCCTCATTGCGCTTAAGTAAGACTGAGAAAGAACAC AAAGTTATCAGACTGCTAGAAGCTGAGTTATCAGAGCGAGAGAAACTACCCCTGCCAGTTACGGTGGGGCAAAAACAAAGGGTGGCTATT GCGCTGCTCTAGCTAACATGCAAAATTGATGGCCACATCAGCAGACTAGATCAGAAACAAATTGCGCTTGGCGCTCTTGAAGAATTTGCGCTTGG CAAGAATTAAACCGCAAATTGGCCTTACCAATTGTTATGATTACTCATGAAATGCAATTGTTAAGGATATTGTAATCGTGTGTTATGCAA AATGGTGTGTTGATTGAGAAGGGTCTGCTTGTGATATTTCAATCAGAAAGCCTGACACAGGAATTATCACAAACAGCTACAGGATT GATGAGGCTTGTGTTGAGAAAATTAAACCAACAAGACATTGTTAAACATTGCGCTAACATGCCCTCTAGCTAGTGAATATGCAGGAACCTCTACG GATGAGCCTCTACTTAATAGCATTACCGTCAGTTGAAGTGCAGCTAATATTGAGGCAATTGAGATTAGATCATATCCAGTGGT GACATGATGTTGCTTGGAGGGCAAGCTGAAAATTCTGCGGCTGAGAAAGCCTGATGAAGCTGGTGTGATGTTAGTATTAAAGAGA GGAGCC

SEQ ID 76

MNEAIIQDHIDITFRQKRVIEAVKDVTVHINQGDIYIGIVGYSGAGKSTLVRVINLLQAPNTGKITVDGVTFDQGKIQLSADALRQKRDIGMI FQHFNLMAQKTTAKENVAFLRHSSLSKTEKEHKVIELLELVGLSERADNYPQLSGGQKQRVIAARALANDPKILISDEATSALDPKTTKQILALL QELNRKLGLTIVMITHEMQIVKDIICNRVAVMQNGVLIEEGSVLDIFSNPKELTQEFITTATGIDEALEKINQODIVKHLPanallaQQLKYAGTST DEPLLNISIYRQFEVTANILYGNIEILDHPVGDMIVVLEGQAEINILAAEKALHEAGVDVSILKRG

SEQ ID 77

GTGGAACCTAAATATCAACGTATATTAAAGTTATCTGGTGAAGCATTGGCGGGAGATAAGGGTGTGGTATTGACATTCCCTACCGTTCAATCT ATTGCAAAAGAAATTGCGGAAGTACACAATTGCAAGCTGTTCAAATAGCGCTTGTCAATTGGTGGAGGTAATCTTGGCGTGGAGAACCTGCACTGAGCAA GCAGGGATGGATCGTGTCAAGCTGATTACAGGGATGTTAGGGACAGTAATGTAATGCTCTGCTGATAGCCTCAACAAATATGGGTA GATACTAGAGTTCAACAGCTATTCAATGCAAACCTGTTGCTGAGCCTTACGTGCTGCTTACGTCATAGAGAAAGTGTGTT GTCTTGGAGCGGGTATTGGTTCGCCATTATTCTCACTGATACAACAGCAGCGCTTGTGCTGAGATTGAGGGCAGAAGCAATTAAATGGCT AAAATGGAGTAGATGGTGTATAATGCTGATCAAAGAAAGATGCAAATGCTGAAATTGATGAAATTAACTCAGTTGAAGTAATAAAAGCA GGGTAAAAATCATGGATGCAACCGCATCAACTATTCAATGGATAATGATATTGACCTGTTGTTCAATATGAATGAGACTGGTAATTAAG CGTGTGTTCTGGAGAACAAATCGGAACAAACTGTTCAAACAAAGCATCTGAA

SEQ ID 78

MEPKYQRILIKLSGEALAGDKGVGIDIPTVQSIAKEIAEVHNSGVQIALVIGGGNLWRGEPAEEAGMDRVQADYTGMLGTVMNALVMADSLQQYGV DTRVQTAIPMQTVAEPYVGRALRHLERKNRIVVFGAGIGSPYFSTDTTAALRAAEIEAELMAKNGVDGVYNADPKKDANAVKFDELTHVEVIKR GLKIMDATASTISMNDIDLVVFNMNETGNIKRVLVGEQIGTTVSNKASE

SEQ ID 79

GTGGAACCTAAATATCAACGTATATTAAAGTTATCTGGTGAAGCATTAGCAGGTGAAAAAGGAGTTGGCATTGACATTCAACTGTTCACTGAGCT ATTGCAAAAGAAATTGCGGAAGTTCATGTGTCGGAGTACAGATCGCTTGTATTGGTGGAGGCAATCTCTGGCGTGGAGAGCCTGCACTGAGCAC GCTGGAATGGACCGTGTCAAGCTGATTACACTGGCATGCTGGAAACGGTGTGAAATGCCCTAGTCATGGCTGATAGCTTCAACATTATGGTGT GATACCCGTGTGCAAACAGCTATTCTATGCAAATGTAGCAGAAACCTTATATTGCGGAGCTGCCCTGCGCCATCTAGAAAAAAATCGGATTGTT GTTTTGGAGCTGTGTTGGCTCGCCATTATTCTCAACAGACACCACCGCGGACTCGCTGCTGAGATTGAGAGATGCTATTAAATGGCA AAAATGGTAGTGGATGGGTCTATAATGCTGATCTAAAGAAAGATGCTAATGCGTTAAATTGATGAAATTACACATGGTGAAGTGTCAAACGT GGTCTCAAATCATGGATGCAACGGCATCGACCTTATGATGGATAACGATATTGATTTGGGTTTCAATATGAATGAGCTGGCAATATTCAA CGTGTGTTCTGGAGAACATATTGAGACTACTGTATCAAATAAGTTGTGAC

SEQ ID 80

VEPKYQRILIKLSGEALAGEKGVGIDIPTVQSIAKEIAEVHNSGVQIALVIGGGNLWRGEPAADAGMDRVQADYTGMLGTVMNALVMADSLQHYGV DTRVQTAIPMQNVAEPYVGRALRHLERKNRIVVFGAGIGSPYFSTDTTAALRAAEIEAELMAKNGVDGVYNADPKKDANAVKFDELTHVEVIKR GLKIMDATASTLSMDNDIDLVVFNMNETGNIKRVLVGEQIGTTVSNKCD

SEQ ID 81

TTGATTGATGATTATCAAATGGTAAATTAAAAGAACACGAGCTCAGGTACAGTAATAGAAGCTAATTGTTAAGGGGGTTGGCGCTCCA

SEQ ID 82

MIDLDSNGEIKRTRASGTVIEANWLRCVGAP

SEQ ID 83

ATGACTAAGGAAATCGTACAAAAGCTCAAGAGCGTTTGAGCAATCACACCAAAGTTATCAAGAGAATTGCAAGGGATTGTCAGGACGTGCT ATTGCTAGCTTGTGATCGTATTCAAGTTGAGTATTGAGGCGCAACCCCCCTAACCAATTGCTTCTATTACTGCTACCTGAGCTGTT CTTTAATTTCACCAATTGATAATCATCAATCAAAGATATTGAGCGTGTATTACGAATTGAGTTAGGTTATTACCTGCAATGATGGTCA GTTATTGCTCTGTTATTCCAGCTTGTGAGAAGAACACGCTGCTGATTAGGTTAAAGAAGTGAAGGAGAAATGCTAAGATTGCTATC CGTAATATCGCGGTGATGCTATGGATGAGCTAAGAAGCAAGAAAGATAAAGAAATTACAGAAGATGACTTGAATCTCTTGAAGGAGATT CAAAAGGCTACTGATGATGCTGTAACAAACATAATTGAGAGATGACTGCTAATAAGAAAAGAATTGTTGAGTT

SEQ ID 84

MTKEIVTKAQRERFEQSHQSLSREFAGIRAGRANASLLDRIQVEYYGAPTPLNQLASITVPEARVLLISPFKSSIKDIERAINESDLGINPANDGS VIRLVI PALTEETRRDLAKEVKVGENAKIAIRNIRRDMDEAKKQEKNEITEDEDLKSLEKDIQKATDAVKHIDEMTANKEKELLE

SEQ ID 85

ATGGCAAATGCAATTATTGAAACTGCAAAAGAACCGTTTGCAACATCCCACAGTCTTATCACGTGAATATGCCAGCATCGTGCAGGGCTGTGCAACGCTAGTCTTTAGACCGTATCAAGTTGATTATTACGGGGCACCGACACCATTAAATCAATTGGCTTCAATCACGTGCTACCTGAGAGCGCTGCT TTATTGATCTGCCCTTGTGATAATCTTCTATCAAAGATATCGAGCGCCTTAAACGCTACAGATTAGGCAATTGAGTGAAGGAGAAATGCTAAATTGCAATC GTCATTGCTTGTGTTCCAGCTTGTGAGCAGAAACACGTAAGAAGATTAGGCAAAAGAAGTGAAGGAGAAATGCTAAATTGCAATC CGTAATATCCCGCGCATGCTATTGAGTGAAGCAAGAAAAGCAAAAGAAATCACTGAGATGAGTTAAAACACTTGAGAGAAGATATC CAAAAGCAACCGATGATGCTATCAAAGAAATTGACCGCATGACGGCTGAAAAGAAAAGAATTGCTCTAGTG

SEQ ID 86

MANAIETAKERFAQSHQSLSREYASIRAGRANASLLDRIQVYVGAPTPLNQLASITVPEARVLLISPFKSSIKDIERALNASDLGITPANDGS VIRLVI PALTEETRKELAKEVKVGENAKIAIRNIRRDMDDAKKQEKAKEITEDELKLEKDIQKATDAIKEIDRMATEKEKELLSV

SEQ ID 87

TTGGCAAGTAATAAAATGATTATGGAGGTAACGTGATAGAATCAAACAGATGGATTGGTTGCGTTACCTTTAAAAGGAGAAAATGAAT
 ACATTATTAGCGACAGTCATAACAGGCTTAAGTCACTGATGAAAACAAAGATTTACTTTATCCAAAAGATGGCTTACCTTGCAATTATCAAAG
 TCAGAAGGAGAGCATCACATTGGTAAAAGGATTGGCTTACAGATATGCAACAAAAGCAGCTCTACAACAAAGATGGCTTACCTTGCG
 ACTCGAGATCATTATGGTGGGGACAGTTACTGAGGTAACGTTAAAGACTGGGAGTATTCTTGATACTGGTCTCCAGATAAGCAAGTGGCTTGC
 TCTTGAGATGTTCTCCTGAATTGAAAGAACCTGGCCTAAAAAGGTGATGCCCTACGTTTAGTGTGATAAAAAGATGCTCTGG
 GCTCTCCCTGAGATCCTGAAGTGGTCAAGCAACCCCTGCATATAACAAATATGCAAATCAAATTGGCAGCAATCGTTATCGCTTA
 AAATTGTCAGGAACCTTGTTATCTACCAGAAAATAATATGCTGGCTTATTCCAGCTAGTGAACGTTACAGTGAACCTCGTTAGGGCAAGTG
 CTGGATGCAAGCAGTTATTGGCTTCAGAGAACGTTGATAGAACCTTAAATTATCATTAAAGCCTGTTTGAATGTTAGAAAATGACGACAA
 ATGATTTAACGTATTAGAAAGTAACGGAGGATCATGACTTTAAATGATAATCTCTCCAGAGGAAATTAAAGCTACTTTGGAATTTC
 GGTCAAGTTAAAAGCACTGGAGGACTCATGAAAGCTAAAAGATCAAACAAAGATCAGTAGGTACAGAATTATTA

SEQ ID 88

MASNKMIMEVTDRIKTRWIWFGYLFKRRKMNTLLATVITGLVDENKDIFYFIQKDGFTEALKSEGEHHIGEMVKFAYTDMQQKARLTTKETFA
 TRDHYGWGVTEVRKDLGFLDTGLPKDQVVVSLDVLPELKEIWPKKGDRLVYCLVDKDRWLAPADPEVFQRMATPAYNNMQNQNWPALIVYRL
 KLSGTFVYLPENNMLGFIHPSERYSEPRLGQVLDARVIGFREVDRTLNLSPRSFEMLENDAMQILTYLESNGGFMTLNDKSSPEEIKATFGISK
 QOFKKALGGLMKAKKIKQDQLGTELL

SEQ ID 89

ATGAATGATTTACTAGCAACAGTCATTACTGGCTTATTAAAGAAGAAAACGCTAATGACTATTTATCCACAAAGAAGGGTTACCTTACCTTG
 TCTAAAGCAGAAGGAGAACGCCAGATTGGTATGGTCAACAGGCTTGCCTATACAGACATAGAGCAAAGGACGCTCACAACCAAAGAGATC
 CGTTCAACACGGACAAGTTGGCTGGGGAAAGTGCACAGAGGTTCTGCTGACCTAGGGCTTGTGATACAGGAATTCCAATAAAAGAAATT
 GTGGTTCTTGGACGTGTTGCTGAGATGAAAGAACATGGCTTAAAGGAGGATAAACTTACATTCTGGGATGTTGAGATGTTGATAAAAAGACCGT
 ATTTGGGACTTCCAGCAGAGGCTTCTCAAAGATGGCTAGCCCTGTTACAATAACATGTTGGCTTATTCACTCAAGTGAACGCTACGAGAACCGCCTT
 CGCCTAAATTAAACAGGAACGTTGTTACCTGCTGAAACACATGTTGGCTTATTCACTCAAGTGAACGCTACGAGAACCGCCTT
 CAGGTTTAGATGCCGTGTGATTGGTTAGAGAGGTCGATCGTACCTGAAATTATCGTGAATTGAGATGTTGAGATGTTGAGAATGAC
 GCTCAGATGATTGTTACTTATCTGAAGCCAATGGTGGTTCATGACTTTAAATGACAATCAAGTCCAGAAGAGATTAAGCAAGCAGCTTGGTATT
 TCAAAGGCCAGTTAAAAGCCTGGTGGATTGATGAAAGCTAAAGCTAACACAAGACGCCACAGGAACCTGAATTAGA

SEQ ID 90

MNDLLATVITGLIKEENANDYFIKEGFTLKSKEGERQIGDMVTGFAYTDIEQKARLTKEIRSTRTSYWGEBVTEVRRDLGVFVDTGIPNKEI
 VVSLDVLPEMKEIWPKKGDLYIRLDVDDKDRIWGLPAEPFQKMASPAYNNMQNQHWPALIVYRLKLTGTVYLPENNMLGFIHSSERYAEPRLG
 QVLDARVIGFREVDRTLNLSPRSFEMLENDAMQIVTLEANGGFMTLNDKSSPEEIKASFCISKGQFKKALGGLMKAKRIKQDATGTELIG

SEQ ID 91

TTGGCTTTTTGTTATAATGTATCTATTAAAGAATGGAGAACGATATGGAACGTCGATTTGCTGGAGGTTGTTGGTGTATGGTACAA
 CCATTGAGAAGAATTAGATGGTATTGAATCTGTTTATCTGGATACACTGGAGGACATGTTGAGAATCCAACCTTAAAGAAGTTGAGTAAACT
 ACTGGACATACAGAACGCTGTTGAAATTATCTGAAACAAATCTTATGCAAGATTGAGTTGAGTTATATTGGCACAACAGATCCAACA
 GACGCTTGGTCAAGTGTGAGGATCTGCTGGGATAATTATGCTCTGTCATCTTATGAGAATGAAGAGGACAGTCAGATTGCTAAACATCAA
 GATAAGCTACAAGCTCGGGTAGATTGATAGACCAATTGTAACCAGCATTGAGCCTGCTGATACTTTTACCCAGCAGAACAGACTATCATCAAGCA
 TTCTATGCACTAACCTGCTCGTTACGCCCTGAGTAGTGCAGAACAGATGCAATTCTAGAGGAGAACCTGGCAT

SEQ ID 92

MAFFVIMYLLKRMENDMERAIFAGGCFWCMVQPFEELDGIESVLSGYTGGHVNPYKEVCSKTTGHTRAVEIIFNPEKISYADLVELYWAQTDPT
 DAFGQFEDRGDNYRPIFYENEERQRQIAQSKDKLQASGRFDPIVTSIEPADTFYPAEDYHQAFYRTNPARYALSSARRHAFLEENWH

SEQ ID 93

ATGGAAAGAGCCATTTCAGGAGGTTCTGGTGTATGGTCAACCTTTGAGGAGAACGAGGTTATTCAGTCAGTCAGAACAGTGGCTACACA
 GGTGGGCATCTCCAAATCTAGCTATGAAACAAGTTGCTGCCAAAACACAGGACATACAGAACGCTTGGGCAATTGAGATCGTGGGACAACCTACCGTCTGTC
 GCTTATAACAGATTGGTAGAGCTCTTGGACGGAGACGGATCAACAGACGCCATTGGGCAATTGAGATCGTGGGACAACCTACCGTCTGTC
 ATTTCATACACAGGAAAGACAAAAGAACATTCAGAGGATTATCAGAACGAGGTTTATAAAAGAACATCCAAGCAGGGTATGCACAAAGCAGTGCATTGCT
 CATCAGTTTAGAGGAGAACATTGGTCA

SEQ ID 94

MERAIFAGGCFWCMVQPFEQAGILSVRSRGYTGGHLNPNSYEQVCAKTTGHEAVEIIIFDPKQIAYKDLVELYWTQDPTDAFGQFEDRGDNYRPI
 IYYTTERQKEIAEQSCKNLQASGRFDQPIVTTIEPAEPFYLAEDYHQGFYKKNPKRYAQSSAIRHQFLEENWS

SEQ ID 95

TTGAGAAAATCATTACAGTTGGTGTAGACACAAAGAAATCAAAATGAAACAGTAGCAATCTAGCAGATTACGCTTTGATGAAAC
 ACTTTTCCAAAACATAGTTCGGATTGAAACAGTTAGTCGCTATTAGAAGATGAGGAGGCTTTCCCTTAATTAAACAGATTGATGAT
 TGGAGATTATCTCAATCAT

SEQ ID 96

MRKSFYSLMTQRNPKSNEPVAILADYAFDETTFPKHSSDFETVSRYLEDEASFNLTDFFDIWEDYLNH

SEQ ID 97

TTGGTCATGAGAAAATCATTACAGCTGGCTGATGACACAAACGTAACCTAAATCAAATGAAACCTGTGGCATTAGCAGATTGCTTTGATGAAAC
 GACACCACCTTCCAAAGCATAACATGATTGAAACTCATTAGTCGCTATTAGAAGATCAAGCTAGTTTCCCTTAATTAGGTCAATTGAT
 GAAATCTGGAGATTATCTAGCACAT

SEQ ID 98

LVMRKSFSYSLMTQRNPKSNEPVAILADLVFDDTTFPKHTNDFELISRYLEDQASFNFNLQFDEIWEDYLAH

SEQ ID 99

TTGTTATGAGATATAACAAATGGAAATTGAGCCTTGCAGACCTCGAAAACCTGAAGGGTGTGAGATAAAAATCCGCTTATATTGTTGGTCT
 GTTTAGCAGGATTAGCTGCCGTCTTTTAATACGTGACGGTCAAATGGATGGTCAACGTTATTCTATATTGAGATAAGGAAACTACCTTTCTGGA
 GGATCACTGACGGTGTCAAACGACCTGATATCGGTTTGTAAAGCCTGCTGGTGTGAAATGGAAAATCTTCAGAAGGATGATCCAAATTCTA
 ACTGTCGCTCATTCCAAACATTCCAAAGAGTTAGCTAAGCTAGTCATGGAGACTGAAGAG
 TCTTCTAGGTGCTAACAGCAGATTGGAGGTTTCAAAGAACATTGGTAAAGTAACTGGACTTATGGGACTATGTTGCTTGGAGAAA
 TGGCATTGAGGATTGAAATGCTGCTGATATGCTATGCTTATCCATATTGGTGTCTGCTGATTTCACTTCATTAAATTAATAAAATAT
 AATCAATATGATTGTTAGTGTAAACCAATCATGAGTTAGCTCATAATGAGTGTCAATTGAGTAGCAAGCTAACTAATCTCCGTA
 GACTTAAAGAACGGTCAAGGCTGAAACAGCTCATCTCACAGTGGTGTGAAGCAAACAAATGATCTTACTCCAAATGATTGTTGTTT
 GTAACGAATGTTCTATCACTGAAAGTACGAACATGGTAGCTGATAGTGTAGCTAAACCTAATGGCATTGGGGAGGTTCTGGAAATTTG
 GAAAACCTAGCTGCTCAATCTGATGAAATTGGACATCCTAAAGTCTTACAAAGATATTCCAAAAGACTCATGGTTTCTGCTACTGCAACAA
 ATAAAGATCCAGTATTGAAACCTTATAGAGCCTTAACACATCGTGCACCTCCATGATGGTAAAGTAAACACCGGAGGCATTGTTACAGTTACA

GATTCTAACTGGATGAGTTTGTATCCATGCCAACCGCACTTCAGAGAAAATGAAACAATTGTTGGATTATGGACTTAT
TCAAATGTTGAAGCTAATTATATAAAAACCAATTGAGAATGTACTGGTCGAGAAATCAGAGAGTGGTTATCATCTTAGGTGTTCTGAA
ATGAAGATTCATGATTATCTGATAAACAAATATGTAAGTCAGCTCTGTTTATATGCCTTACATTACTAGTTATTCATGCCTCGAGTTAAAGGT
GACCAGCACAGATGTTATCCCACAAAGGACTGTTAACAGCTGGCTTACATTGGAATTTCAGAGATACTAGTTAACACGGAA
TATTCTATTAGAACCTGCTATGGAACTGTTTATCTTCTTAAATTGAGCTGGTCTCAGAAGTCTTAACTCAGCATTGATAATTGTC
TTGTTGCACTTTATACTATCTAACAGATAAGAAATCTGTTGAAGATATGGATTACCAATACCTGCCTTAATGCGTAAGTAGGCATGAAAAAA
ATTAGAGGAACCTATTAGAAGATTACTTCGAGAAGCTCATCTTTA

SEQ ID 100

MFMFRYTNNGNFEEAFARPKPEGVDKKSAYIVGSGLAGLAAAVFLIRDGQMDQRHFEELPLSGGSGLDGVRKPDIGFVTGGREMEMHFECMWDMYRSIPSLEVPDASYLDEFYWLKDPPNSNCRLIHKGQNRLESQDFLTGLTHSKELVKLVMETEESLGAKTIEEVFSKEFFESNFWTYWTGMFAFEKWHSAIEMRHYAMRFIHHIGGLPDTSLKFKNYNQDSMVKPISYLESHNVNDVFQDFSKVNTNISVDFKNGQKLAKAIHLTVGGEAKTIDLTPTNDFVFTVTNGSITESTNYGSHDTVAKPNTDLGGSWNLWENLAAQSDEFHGPKVFYKDIPKESWFVSATATIKDPAIEPYERLTLRDLHDGKVNTGGIVTVTDSNWMSMSFAIHRQPHFKEQKENETIWYIGLSNVEGNYIKKPIEECTGREITEEWLYHLGVPEMKIHDLSDKQYVSTPVVYMPYITSYFMPRVKGDRPDVPIPGQSVNLAFIGNFAESPSRDTVFTTEYESIRTAMEAVYTFLNIERGVPEVFNASFDIRVLLQSYLYNDKKSVDMDLPIPALMRKVGGMKKIRGTYLEELLREAHLL

SEQ ID 101

GTGATGATATCACTTGTGACTATTCAAGGAGGCTTGAAATGTATTATACTAGTGGTAATTACGAAGCTTTGCAACACCTCGAAACCCGAA
GGGGTAGATCAGAAAATCAGCTTATATTGTTGGTACTGGTTAGCTGGTTAGCAGCAGCTGTTCTTATTGCATGGGATATGGCTGGGAA
CGCATTCATCTGTTGAGGAATTGCCCTTAGCAGGGTTCTTAGATGGTATTGAAAAGCCTCATCTGGTTTGTGACCCGTGGTGTGAG
ATGGAAAATCATTGAGGTATGGGACATGTATCGGTCTATTCCCTCACTGGAAAATCCTGGTCTTATTAGATGAATTATTGGTTG
GATAAGGGATGATCTAACATCAGCTGGTATTGACAAGAGAGGAATCTGTGGATGACGCCAGTACGCTCGTAACAGTC
AAAGAATTAATCCATTAACTGAAGACAGAAAGATCTAGGAGACCAAAACATTGAAGAGTCTTCTCAGAAAGATTCTTAAAGATTAATT
TGGGTGATTGGCAACCATGTTGTTGAAAATGGCATTGCTGTAGAAATGCGACGTATGGATGAGGTTTACCCATATTGATGGT
TTGCCAGATTTACCTCCCTCAAGTCAACAAATAACCAATATGACTCTATGGTCAAACCGATTATTGTTACCTAGAATCACACAGCTTGTGAC
ATCCAATTGACACAAAGTCACTGATATTCAAGGGAGCAACAGCTGTTAAAAGGTAGCAAAACCATCCATATGACGGTGTCTGGGAGGCT
AAGGCAGATTGAGCTAACACCTGATGATTGGTTTGTGACCAATGGTTCTATTACTGAAAGCAGCACATACGGTAGTCATCAGAAGTGGCTAAG
CCAACCAAAGCGTTAGGTGGTTCTGGAAATTATGGAAAATCTAGCTGCTCAATCAGATGATTGGTCATCCTAAAGTGTCTTACAGGACTTG
CCTGCTGAAAGCTGGTTGTGCTCAGCAACCCATAAAACACCCAGCTATGGCCTTATATAGAACGCTTGTGACCCACCGTGAATTGACGAT
GGCAAAAGTGAACACTGGCGGCATCCTACTATTACAGATCTACTGGATGAGCTTGGCATTACCGTCACCTTAAAGAACAAAAAA
GAAAATGAGAACACTGTCGGATTACGGTTCTTATTCCAATAGTGGGCAATTACGTCACCAAGAAAATTGAGGAGTCAACGGTCAGAAATC
ACAGAAGAACATGGTGTACCCACCTGGGTTACCTGGTGTGATAAAATCAAGGACTTAGCAGTCAGGACTATATCAATACAGTCTCTGTTACATGCT
TATATTACGAGGTTACTTTATGCCACCGCTCAAAGGAGACCGTCCAAAAGTTACCCAGATGGTCTAGTCACCTGGCTTATTGGTAATTGCG
GAATCTCATCTCGAGATACGGTCTTACGACTGAGTATTCTATTGCTACTGCCATGGAAAGCAGTGTATAGCTCTGTAATGTTGAAACAGGGCATC
CCAGAAGTCTTAATTCAAGCCTATGATATTGCTGAAAGCTTTATTACCTTAATGATAAAAAGGCAATCAAGGATATGGATTGCA
ATTCTGCACTGAGAAAATGGACATAAAAAGTCAAGGATACCTTATGCAAGAATTGCTCAAAGATGCTAATCTTATG

SEQ ID 102

VMISLCLTIQGGLEMYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGLAAAVFLIRDGHMAGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGRE
MENHFECWMDDMYRSIPSLEIPGASYLDEFYWLKDPPNSNCRILIHKGRRNVRDDDCQYTLGKQSKELIHLIMKTEESLGDQTIEEFFSEDFFKSNF
WVYWATMFAKERWKHSAVEMRRYAMRFIIHIDGLPDFTSLKFKNKYQDSMVKPIIAYLESHDVQIFDFTKVTDIQVETAGKKVAKTIHMVTSGEA
KAIELTPDDLVFVTNGSITESSTYGHSHHEVAKPTKALGGSWNWLLENLAQSDDFGHPKVFYQDLPASWFSATATIKHKAPEYPIERLTHRDLDH
GKVNTGGITITDSNWMSMSFAIKHQPHFKQEKENETTVWIYGLVSNSEGNYVHKKEECTQEITEEWLYHLGPVDKIKDLASQDVINTVPVYMP
YITSYFMPRVKGDRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVSYFLNVERGIPEVFNSAYDIRELLKAFYYLNDKKAIKDMQLP
IPALIEKIGHKKIKDTFIEELLKDANLM

SEQ ID 103

ATGAAATTGGTATAATGAGTCACCTACTGTAGAAAAGGAAGAATAATTGCAAGAATACTCTATCGAAATTACTTTACAACATCCAGATGAT
ATGATGTCACTCTTGGCAGCAATGAGGCCATTAAATTAAATCGAAGAAAATTAGATGTTATCATTGCTAGAACGTGTTAGGTA
TTAGGTGACTCTGAAAGAAGCAGTAGAAACCGCTCGTTAACCATGAAAGCATTATTAGTGTGTTAACCGCGGGATGACTGTGAATACTCAGAT
GTTGTAAACAGCCTTATCATGGCACAAAATGGTCAATTGATAAAATTGTTGCCCTTATGAGGAAGAAAATTATAAGGATAGCTATGTAAGCCT
ATCCGTGTTAAGACTTTAGGCAAAAATATACTGTAGTGTTAAAAATCATGATGTTGTTTGTATTGGGCTCTGGAACGGAAAAACT
TTTTAGCAGTCACTCTAGCAGTAACCGCCTAAAGCGTGGTCAGTTAAAGCAATACTTAAACGAGACCCAGCGGGTGAAGCTGGTAAAGCCTT
GGTTTCTGGAGGAGATCTAAAGGAAAAGTGTACCTTATTGAGGACAGGTTATTTAGTGTGCCCTATACCAAAATTAGGTAAGGCAAAACAGT
GCCTTAATGGAGCGTGAATCATCGAAATTGTCCTATTGGCTTACATGCGTGGTGTACTTTAGTGTGCAATTGTCATTAGTGTAAAGCGCAA
AACACCACTATAATGCAATGAAAATGTTCTAACACGCTTGGCTTCAATTCTAAAGTATTGTAATGGCGATTTAGGCAAAATTGACTTACCA
AAGAATGTTAAATCTGGTTGATTGATGCTGTTGAGAAAATTAGGAAATATCAAAAGATTGACTTTATTGTCATTAGTGTAAAGGATGTTGTAAGA
CACCCCTGTCGTTGCTGAAATAAAATGTTATTGAGATTGAGAAAGTACTGACAAGCTACAATCTGATAAGGAC

SEQ ID 104

MKFCYNNVVTYCTKRKNLQEQSIEITLQHPDDMMSLFGSNERHLKLIEENLDVIIHARTERVQVLGDSEEAVETRLTIEALLVLVNRGTMVTNTSD
VVTALSMQNGSIDKFVALYEEEIICKDSYGKPIRKVTLGQKIIYVDSVKNHDVFGIGPAGTGKTFLAFTLAVTALKRGQVKRIILTRPAVEAGESL
GFLPGDLKEVDPYLRPVYDALYQILGKEQTSLMEREIIIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMINVNGDVSQIDLP
KNVKSGLIDAVEKLRNIKKIDFHIHLASKADVVVRHPVVAEIIINAYSDSESSHKLQSDKD

SEQ ID 105

TTGAAGAGTATTCTATTGACATTACCTAACCCATCCTGATGATGTTTAGCTCTTTGGTAGCACGAGCGTCATTGAAGCTAATAGAAGCT
CATTTAGGAGTTATTGTCACGCAAGAACCGAGCGAGTCCAAGTGATGGGTGATGATGAAGAAGCTGTGAAATTGGCTCATTGACCATCAAAGCC
CTACTGGTTCTAGTGGGTCGTGCATGGTGGTCAACACATCAGATGTGGTGCACAGCTTATCTATGCCAGAACTCATCAGATTGACCAATTATG
GCGCTTTATGAAGAAGAAATCATTAAGATAACTATGGTAAGGCAATACGAGTCAAAACATTAGGTCAAAAAACCTATGTTGATAGTGTCAAACGT
CATGATGTTGGTTTGGTGTAGGACCTGCAGGGACAGGTTAAAACCTTCTAGCTGTTACGCTTGCAGTCACTGCTCTGAAAGAGGACAGGTAAG
CGTATTATTTGACGCGCTCTGGGTTAGAAGCTGGCAAGGCTAGGTTTACCGGCAGTTGAAAGAAAAGGTGGATCTTACCTCAGACCT
GTTTACGATGCCCTTATCACATTAGGCAAGGAAACAAACACCAGCGTCATGGAAAGAGATGTGATTGAGATCTGCTCTGGTAGCTTATATGGCA
GGTGTGACTCTGGATGACGTTTGTATTCTTAGATGAGGCTCAAAACAGCAGGACCATCATGCAAATGAAGATGTTTGTGACCGCTCTGGTTTAAT
TCTAAAATGATTGTCATGGAGATACGAGTCAGATTGACCTCCCTGCAAATGTCAGTCTGGTTTGTGATGCTACTCAGAAATTACAAGGCATT
AAACAGATTGATTGCTATTCTCTGCTAAGGATGTTGCCACATCCTGTTGGCTGATATTATCAAGGCTTATGAAAGCTCCTCAGAGGAG
ATGAAGGACTACTAAACCTAACGCTAGTGACGTTGAAAGCTGATTACCAAGCCAGGCTTGACAAAATACCTGATCGGTCAAGGAC

SEQ ID 106

LQEYSIDITLTHPDDVLALFGSNERHLKLIEAHGLGVIVHARTERVQVIGDDEAELARLTIKALLVLVGRGMVVNTSDVVTALSMABSHQIDQFM
ALYEEEIIKDNYGKAIRVKTLGQKTYDVSVRHDVVFVGVPAGTGKTFLAFTLAVTALKRGQVKRILTRPAVEAGESLGFPLPGDLKEKVDPYLRP

VYDALYHILGKEQTTRLMERDVIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMINVDTSQIDLPRNVKSGLIDATQKLQGI
KQIDFVYFSAKDVRHPVADIKAYETSSEEMKDLLKPKASDVEADYQPGLTKYPVIGQEH

SEQ ID 107

ATGGACCATTTCACAAAACCTGGCAAGATTCTCAAACCTTCAAACTGTGTTGCTATAGCAGTCCTGGTACAGTTTGAC
CAATCTCCGATTATGATTGATGTTATTGTCAGCAACTCTGATATCACTAGTCGTAACAGTATCCTAACAGACTGTCATTACATTGAA
CTTAAACAATCATTACTGGGAGCTGAACATAATGGTACCTTAAACGACGAACTGATATTGATATTCTATCGTAACATAGATAACTTTTATCA
GACTTAGAAGATGCTGTGAACACCACAATTCTCGAATTGGATACACTACTTGTGTTGGCATAACCTCATCAATTGCAAATACTCTATGATCCT
GAAAATCAATTACAATCACTCAAAGAGAGATTCGAAGTTCTATCCCAGTCAGTACAAAACAAATTATCATTCAAATCGTAACCTTATTAAACT
GGCAAGCTCCCTCTTACGATAAAACAAATTATAAAAGCCCTAAACGCCAGACTTGTGTTAGTACTCACCAGATAACTACTGCTTCTTAGATTCC
TACTTGTGATATTATTTTGTGACTTAAGTTGACACATCCTGGCAGAAAAGAATGATTCTATGCTAAGAAGATGCTACATTGCTTCTCAA
CATTGAAAGAAAATATCATTAAACTATGTCATCACAACTCCAACGAACACACTGTTAAAGAAACATTAACGATATAATGCATCTGACGTC
ATGCTTAAAGAAAATTTCACACATTATAGGT

SEQ ID 108

MDHTKWLWQDFSKLPNVAIALGGSRSGDSFDQSDDYLYVYCAATPDITSRKRLNKHCHYIELNNHYWELEDNGTLNDGTDIDILYRNIDNFLS
DLEDVVEHHNSRIGYTCFWHNLINQCILYDPENQLQSLKERFEVSYPSQLQKIIIONRMLLTGKLPSYDQKIIKALKRQDFVSTHRTTAFLDS
YFDIIFALNLKTHPGKERMISYAKKNATLLPKHFEENIILKLCCHNSNEHTVKETLNDIIMHLDVMLKENFQHFIG

SEQ ID 109

ATGAAACAAAGATTATTTCTACATTAGGTCAAAAGTTGGACATGAGACTATCTTTAACATATTCTGGTGTATTTGACAGATGGTAAGGGA
CGTGTCTTACTCCAATTAAAGAGCTGATAAGAATTCTTGGGAAATTATTGCTGGATGTATGGAGTTAGGTGAGTCATCAGTAGATAATTGAAAAGA
GAATTTTCTGAAGAACACTGGATTGAGAGTGGACCAATCAGACTGTTAAATCTACTTCAACTCTTCAAGACTCTTACATGCCAATGGCATAAAGGCA
CAAACCTCGGTTTATTATGAGTAAGCTGTCACAAACAGGTTAATAGAAGGTTTCTATAATGAGGAACATTGCAATTGGACTATTCT
AAAGAAGACGTCAAAATATTACGATGTTAAATGAACACACCAATTAAATTAGATGAATTCTACAAACATTCCAAATGGGGCGT

SEQ ID 110

MKQDYISYIRSKVGHETIFLTYSGGILTDGKGVRVLLQLRADKNSWGIIGGMELGESSIONVDTLKREFFEETGLRVEPIRLNVYTNFQDSYPNGDKA
QTVGFIYEVSCKPKVNPINEGFHNEETLQLDYFSKEDVKNITIVNEQHQLILDEYFSQTFQMGR

SEQ ID 111

TTGGCTATAATGAGAAAGAATACTAACATAGTAAAGCGAGATCATATGCCAACAGACTACATTCTTATATCCGCTCCAAAGTTGGGCATGATAAG
ATTATTCTTAATTGCTGGTGGGATTTGACCAATGATGACGCCAGGTGCTGATGCGCTGGTGTGATAAGAAAACCTGGACTATTCTGGT
GGCAGACTTGAACGGGGAGCTTTAGAGACTTGCACAAACGTGAGTTCTAGAGGAACCCGGAAATTGAGGTTGAAGCTGTTGCTACTGAAT
GTTTACACTCATTGAGGAAGTTTACCCAAACGGTGTGACTATTGCTTTATCTATGACTAACCGGCTGTTCTGATATGGCTATT
GATAACTTCATAATGAGGAACGCTCAAGTTACAAATTCTCATGAGGAGATAGCAGAGTTAGAGAGTGTCTCAGGCCAACATGCCCTGATG
TTAGAGGAATATTAGTGTAGCTTGTCTATGGGGCAT

SEQ ID 112

LAIRKNTNIVKRDHMPQDYISYIRSKVGHDKIIINFAFGILTNDGKVLMLQRLGDKKTWTIPGGTMELGESSIONVDTLKREFLEETGIEVEAVRLLN
VYTHFEEVYPNGDAVQTIVFYELTAVDMAIDNFHNEETLKLQFFSHEEIALESVSAKHLMLLEYFSDSFAMGH

SEQ ID 113

GTGACTGTTTTTAGAAAGCATAAGAAGTACAGAAAAGAAAATTATGGAATATTGATGGTGGGGATATGCTTACTTACGGTATTGGAATGAT
ATACTTAAAGAAAATCCAGTT

SEQ ID 114

MTVLELSIRSTEKENYGFDDGDMLYLRYWNDILKEIQF

SEQ ID 115

ATGAAAGATAACATTACACGGCGTTGCTAAACGTTATTAAATCACCTTATATATTAGGGCTAAAGATGCGATGGCTAAACATCCGATACCTAATGAT
AAAAATCCTAGCAATTGTTGAACAGATAGAATATGATTTGATAAAATTGATAATTCAAGACTCTTTTATGCAACATTAGCTAGAATTGCG
GTTATGGATAGAGAAATCAAAAATTATTAGAGAAAATCCAATAGTCAAATCCTTCAATTGGTTGGACTTGATAACAAGGTTGAAAGAGTC
GATAATGGACAAATAGGCTGATAACCTTGATTGCGAGAGTTATGGAGATAAGAAAATTATTTTTGAGAGCATGAAAGAGTTACTAATA
GCAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAACCTCCAAATGCCCCCTTTCTAATCGTGTGAGAGTTGTTAATGTTCTAAA
GAAGATGACGTAGAGACTTTCTCATATCGACAAATTGATGAACTTGGCACAATTATGATTGTCATAAGGAAATGATTAATAAAA
GGAAAGCAACATGATAACGTTAAAGTATGGATAACGAAATTGAGCTTGGTACAGATGTCATGAGATTGTTAGACCCCTAAATTAAAG
CAAATAATCTGATTAACCTTACAGATGAGATGAGCAATTGAGTTAGGCACACTCGCTTTACTTCCAAACATTGTAATTAAATTGTT
TTAGGTGTGACGATAATAAGCATCTGAGAAAAG

SEQ ID 116

MKITLHGVAETLLITLYIRAKDAMAKHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDRREIKKIRENPNSQILSIGCGLDTRFERV
DNGQTRWYNLDPVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQAPFLIVSEGVLMLKEDDVETFLHILTNFSQFMAQFDLCHKEMINK
GKQHDTVKMDTDFQFGITDGHEIVDLPDKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYKEYKASEKK

SEQ ID 117

ATGTACGTTGAAATGATTGATGAAACTGGACAAGTTGAGATATCAAAAGCAAACCTTGTATTTGTTAGAGTTGCGACACAAAAACAGGT
AAAGAGAATAAAAGAAAATGGCTGTAACGTTGTCACAAATGAGCTAGCATGATGAAATTGAGATATGCGAGATACCGATCGTCCGACTGATGTT
ATCAGTTAGAATATAAGCCTGAGGGTGTATTTCTTGTGATAAGGCTAAAGAACAGCAGAGAGTACGGTCACTCTTATGAGCTGAAATGGTTTTAGCT
TCTTATATTGGTGAACCTTTATTCTATTGATAAGGCTAAAGAACAGCAGAGAGTACGGTCACTCTTATGAGCTGAAATGGTTTTAGCT
GTACATGGTTTTGCTGATTAACGGTTATGATGATTACACCCGAAGAAGAAAAGAGATGTTAGCAGTTACAGGAAGAAATTAACTGCTT
GGACTTAAACGACAA

SEQ ID 118

MYVEMIDETGQVSEDIKKQTLILFEEAAQKTGKENKEMAVTFVTNERSHELNLEYRDTDRTPTDVISLEYKPEVDISFDEEDLAENPELAEMLEDFD
SYIGELFISIDKAKEQAEEYGHYSEREMGFLAVHGLHINGYDHYPPEEEKEMFSLQEEILTAYGLKRQ

SEQ ID 119

GTGCCAACATACCAAAATGAGGTGGCAGCCCTTCCCTAACACATTACACCTTATGTTATGAGATGTTGACGAAACGGGACAAGTTGCGAAGAG
ATTATGGAGCAAACACTGATTGCTCAATTGCTGCTCAAAGACGGGCAAAGAAGAAAAGAAAATGCTGTCGACCTTGTGACCAATGAAAGA
AGTCATGAACCTAGAATACCGAGATACTGATGTCACAGATGTTGAGTTCTCTAGAAATATAAGCCAGAAACGCCATTATTTATTAGTC
GAGGATTGGCTGCTGATCCTAGTTGGCAGAGATGAGTCAGAGTTGATGCTTATATTGGCAATTGTTATTCTATTGACAAGGCGCTGAG
CAGTCCCAAGAATATGGCACTCTTGGCAGAGTGGATTGGCTGTTATGAGCTTACATTAATGGGATGTTAGCAGTTACAGGAAGAAATTAACTGCTT
GAAGAAGAAAAGAGATGTTACAGGAAGAGATTGACTGCTTATGGCCTAACAGCACAA

SEQ ID 120

VPNIPNEVGSPSLTINLMIYIEMIDETGQVSQEIMEQTLNFAAQKGTGKEEKEMSVTFVTNERSHELNLEYRDTDRTPTDVISLEYKPETPILFSQ
EDLAADPSLAEMMAEFDAYIGELFISIDKAREQSQEYGHFSEREMGFLAVHGLHINGYDHYPPEEEKEMFTLQEEILTAYGLTRQ

SEQ ID 121

ATGTCAGAAAATCCTGATGCCATATTATCGTAGTCAAAATTGCAATAATCAGGATTTCCAAGTAACCTCAAAGCTATTGCTAGGGCGGGTGCA
GGAACAAATAATATTCTATTGAGAGGGCAAGTGCACAGGGAAATAGTCGTGTTAATACCCAGGTCAAATGCTGTAAGGCGGTCA
ATTGCTGCCATTACTTCAGCTGTGATTATTAGGAGCTAACCGATGGGTTAATACTCTAATCTGAAACAGATAATTCCAACAAATGAGCA
GGAAAGAAAGCTTCTGGTAAATGAGGAAAAAAATTGGGAGTTATCGCCCTTGGCATTGGAGCTAGAATTGCGAATGCTAGA
CGCTTAGGAATGACAGTTCTGGTTATGATCCCTATGTTCAATTGAAACAGCTTGGAAATATTCAAGGCATGTTCAAAGGGTTAAAGAGATTAAG
GATATTTTGAACACTTGTGACTATATCACAAATTGTTCCCTAACAAATGAAACACTAACGATACATTGATGCGAAAGCTTTCAATCATGAA
AAAGGAACATGATTACAACCTTGCTGTCGAGAATTAGTCATAACCAAGAGCTATTGAGCGATAGAAACTGGTGTCAAGCGCTATATT
ACTGATTTGGAGACAAGAAATTATTAACCAAAAG

SEQ ID 122

MSENPDAYIIRSNQLHNQDFPSNLKAIARAGAGTNNIPIEEASAQGIVVFNTPGANANAVKEAVIAALLSARDYLGANRWVNTLTGTDIPKQIEA
GKKAFAGNEIAGKKGVLGIVLGAIGARTANDARRLGMTPVLDYPIVSIEAWNISHVQRVKEIKDIFETCDYITIHVPLNETKHTFDAKFSIMK
KGTTINFARAELVNNQELFEAIETGVVKRYITDFDKELLNQK

SEQ ID 123

TTGATGAAAATTAAAATTATAATGTTAGAGGCCAGAGAACGACTCTTAGCAAAAAATGGGCTGATGACAATGGGATTGAGATTTCCTGACGGAG
TCTCCCTTAACCTCTGAAACGGTTAAAGAACGCTGAGGCCAGGGATTGCCAATGCCAAATTGGCTCTTATAGTGTGCGATTATCCTCTC
TTAAAGGAATGGGATTAAACAAATCGCTCAGCACAGTGTGATATGTATAACCTGATTGGCCACCAGAAAATGACATTATTATCACA
AATGTTCTAGTATTCTCAGAATCATTGCAAAATTACGGTTACTATTGCTTAATTAACTGTCATGTTGGAGTTGATTGAAATGTT
AAAAAAACAAATTCTCAGTGGGACTCCCTATCCGGCCGCTTTAGGTGATATGACAGCTGGCATTATCGGAACTGGACGTTGGCTAGCT
ACTGCTAAATCTTAAAGGTTGGCTGCAAGGCTGGTGGATATGATATTACCAAAAGCGATGCTGCCAACAGCTGTCTGGACTATAAGGAATCT
GTAGAAGAAGCAGTAAAGATGCTGATCTTCTTCATACATGCCAACACTGAGAACACACACCTTCAATTGATTTTAAATCT
TTCAAAAAAGGGCTATTGATGAATATGGCCGTTGGCCTATTGAGACCAAGATTACTGATGCTTGGATGCGAGGCTACTGAGCGGA
GCTGGTATTGACACTTACGAATTGAGACCTTATACCTAACGAAATTGAGGTCAAGAAATTACAGATTCACTATTAAAGCTTGTGATTAAAC
CATCCTAACGTTATTATACACCTCATGCAGCTTATACGATGAGGCCGTTAAACCTAGTTGAGGTGCCCTAATGCTACAGTAGAGATT
ATCAAAACTGGGACAACGACAACCTGTTAAC

SEQ ID 124

LMKLKLYNRGEAVLAKWADDNGIEISLITESPLTPETVKAEGFDGIANAQIGPLDDAIYPLLKEMGIQIAQHSASVDMYLNLDLATENDIIIT
NVPSYSPESIAEFTVTIVLNLRHVELIRENVKKQNFWTGLPIRGVRVLGDMTVAIIGTRIGLATAKIFKGFGCKVVGDIYQSDAAKAVLDYKES
VEEAIKDADLVSLHMPPTAENTHLFNSDLFKSFKGKAILMNMRGAVIETQDLLDALDAGLSSAGIDTYFEGPYIPKNFEGQEITDSLFKALIN
HPKVIYTPHAAYTDEAVKLNVEGALNATVEIIKTGTTRTRVN

SEQ ID 125

ATGCTTTCATGAGAGATAATTTAGATTCTTGATTCAGCCTGTTATTGATGAGATGGCTAACATTATCAATGGCTGATCAAGACAAAACCTTC
TATGAAGAAGAATTACATGAGACTCTAAAGACAATGACTTGGCAGCTTGAANNNNNTAAT

SEQ ID 126

MLFMRDNLDLSLIQPVIDEMAKHYQWSQDKTFYEEELHETLKNDLAALXXXN

SEQ ID 127

ATGGAATTTCAGAGAAAACAAGCCTTAGCTCTCCAAAAAATGCAAGAAAGAGATTAGACCTACTGATTATTGGGGAGGTATTACGGGTGCT
GGTGTGGCACTTCAGCGGAGCTAGTGGCTAGATACGGGCTGATTGAGATGCAAGGTTGCTCAAGGAACCTCTAGCCGTTCAACAAATTG
GTTCACGGGGGCTTCGTTACTGAAACAATTGATGTTGGAGGTGTTCAAGATCGGTGTCAGAGGGCTGTTGCAACAAATTGCCCCAC
ATTCCAAAACCAGACCCATGTTATTACCTGTTATGACGAACTGGCAGTACCTTACGATGTTGCTGTTGAAAGGTGCTATGATTGATGAT
CTTTAGCAGCGTGTCCAATACGCCAGCGCCAACAAGGTGTTACCAAAGAAGAGCTTAAACGAGAACAGACTAAACAAAGAAGGCTTG
CTTGGTGTGGGTTTACCTTGATTTCCGCAATAATGACGCAAGGCTGTTATTGAAAATATCAAACGAGCTAATCGTGTGAGATCAAGAACATCATTATC
AGTCATGAAAGCAGAAGATTCTTGCTAGATGACAATGGTAAGGATTATTGTTGAGGCTGAGGCGCTGATCTGCTGAGATCAAGAACATCATTATC
AAGGCTAAATTGCTCACACACCAGGTGAGTGGAGGTTCTGCTCAATTCTCTCATAAAGGGCAACCCGATTCTCAAATGCCCTTACA
AAAGGGGTGATCTGGTAGGGCTGCAAACCGGACACGGACTACACTGGAGACTTGGAGACCCACAGGTTAAATGTCGTTGAGATGGGCTT
TTGCCACGTGAGGAAAAAACTTATTGGAAACACGGACACGGACTACACTGGAGACTTGGAGACCCACAGGTTAACTCAAGAAGATGTTGAGGTT
TTGTTAGGCGTTGTCATAACCGCTTCCAAATGCCAACCGTGTGACATTGATGATATTGAAAGCAGTTGGGCTGGCTTCGCCCTTGTATTGAGG
AATAGTGTCTGACTACAATGGGCAACAGCGTAAAGTCAGTGATGATGTTGATCACTGGGCTGATCTGCAAAGCCTATTAACAC
GAAGATAGCGAGAGCTGTTGAAAAGCTTAAAGCAGGTTGAAACCAGCACATCTGAAAAGAATTGGATCGCTGAGTGTGAGGGTTCA
AGTTTGAGCGTGATGAGAATGGACTCTTACCTGGCAGGTGTTAAGGATTACCGACTATCGCAAATGGCTGAGGAGCATTGACAGGGATTATT
CAAATCCTCAAAGAAGGTTGGCAAATCCTCAAGCTTATCAATTCTGAAAACCTATCTGTTTCAAGGAGGTGAAATCAATCCAGGAAATGAGAT
TCGGGAAATAGAAGCCTATGCTCAATTGAGGACTCTAGTGGTGTGATGGTGTAGGTTATTGGGCAACACCTTATGGTTCTAATGCCCA
AAAGTCTTCCTTAACGCTGCAATTACAGCGTCAAGGGTTAGTTGCTGAAACCTTGTCTTACATTATGCGATGGATTATGAGGCT
CTTAAACCGACAGATTATTCCTGAGAAGAACAAATCACCTTATTATGCGAGATAGCCTAGATGCTTGTGATTGACCCAGTGTGATTAAAG
GCTAAACATTGAGATGGCTGATCAGGAAAGAGTGGCACAAGAACGATCTCGTGTGAGTGCAGACAATGATTGAGTCCTTAAAGGC
CATCAGGAGGT

SEQ ID 128

MEFSRTRRLALOKMOERDLDLIIIGGGITGAGVALQAAASGLDTGLIEMQDFQAQGTSSRSTKLVHGGLRYLKQFDVEVSDTVSERAVVQQIAPH
1PKPDPMILLPVYDEPGSTFSMFLRKVAMDLYDLLAVSNTPAANKVLTKEEVILKREPDLKQEGLLGGGVYLDFRNNNDARLVIENIKRANRDGALIA
SHVKAEDFLDDNGKIIIGVKARDLSSDQEIIIIKAKLVIINTTGPWSDEIRQFSHKQPIHQMRPTKGVLVDRQKLPVSPVYVDTGLNDGRMFV
LPREEKTYFTTDYTGDLEHPQVTQEDVYLLGVVNNRFPNANVTIDIESSWAGLRLPLSGNSASDYNNGNSKGVSDDSFDFHLVDTV
EDSREAVEKAIKQVETSTSEKELDPSAVSRGSSFERDENGLTLAGGKITDYRKMAEGALTGIIQILKEEFGKSFKLINSKTPVSGCEINPANVD
SEIEAYAQLGLTLSLSMDDARYLANLYGSNAPKVFAUTRLTAAEGLSLAETLSSLHYAMDYEMALKPTDYFLRRTNHLLFMRDSDLALIDPVINEM
AKHFEWSQDQERVAQEDDLRRVIADNDSLALKHQEG

SEQ ID 129

ATGGTTCGTCACAACACTGCTTAAAGGTAAAGGCCGCTATTGTTAATATGATTGGCTTTTTGAAGGTGGCTGTGTTTAGACCTT
TTTCTGGCAGTGGTAGCTATTGAGGCCATCTCAAGGGAAATGGCCAAGCTGCTCTAGTTGAAAAAAGATAGGCCGTCGCCAGTCGTTATT
CAAGAAAATATTGCAATGACTAAGAGTCCGGAGCAATTCAATTATTAAAGGCAACCGTGTCTTGAAGAACATTAAACGGGACAATTGAT
TTGGTCTGTTGGACCCGCTATGCTAAGGAAGAAATTGTAAGCAAATCCAATCATGGATAGCAAGGGTTATTAGGCGATGATCATGATT
GCTTGTGAAACGGACAAATCAGTTGATTACCTGAAGAAATTGCTTCTTTGGGATATGAAACAGAAAATTATGGCATTCTAAAGTAACGGTC
TACGTTGCT

SEQ ID 130

MVRTRPTTDKVKGAIFNMIGPFEGGRVLDLFGSGSLAIEAISRGMDQAVLVEKDRRAQVVIQENIAMTKSPEQFQILKMEANRALEQLTGQFD
LVLLDPPYAKEEIVKQIQIMDSKGLLGDDJMIACETDKSVDPPEIASFGIWQKQIYGISKVTYVVR

SEQ ID 131

ATGAGAGTTGTATCAGGTGAATTGGGGCGTCCTTAAAGACGCTCGATGGAAAAGATAAACACGCCACTTCAGACAAAGTTAGAGGTGCGATT
 TTTAATATGATAGGACCTTACTTTAATGGGGCGTGTGTTAGATTGTTGCAGGTTCAAGTGAGCTTACCTGCTGGGATG
 TCTGCTGCAGTTGGTGAAGAAGAACGCTAAAGCCAGCTATTATCAAGACAATTATAATGACTAAAGCTGAGATCGGTTACCTGTTA
 AAAATGGAAGCTGAGCGAGCTATTGATGCTGACTGGTCGATTGACTTAGCTTTAGACCCCTTATGCCAAAGAACATTGTCGAACT
 ATTGAAGCTTAGCAGCTAAAACATTGAGTGAACAGGTTATGGTGTGAGACAGATAAACAGCTTGTGCAAAGAGATTGCAACG
 TTAGGTTAGGAAAGAAAAATTATGGAATTAGTAAGGTAACAGTTATGTTAAC

SEQ ID 132

MRRVSGEFGGRPLKTLGKTRPTSDKVRGAIFNMIGPYFNGGRVLDFLAGSSGLAEAVSRGMSAHLVEKNRKAQAIQDNIIIMTKAENRFTLL
 KMEAERAIDCLTGRFDLFLDPPYAKETIVATIEALAANLSEQVMVVCETDKTLLPKEIALGIWKEKIYGISKVTVYVN

SEQ ID 133

ATGACAAAGAAAAGCTTATTTACAGGTTCATTTGATCCTGTTACTAATGGACATTAGATAATTGAGCGGCCAGCTATCTATTGATCATGTT
 TACATTGGTTATTTATAACCTTGAGAAGCAAGGTTACTTTGATTGAGTGCCTAAAAAAATGTTAGAAGAAGCTATCCGTCAAGTTAAAGAAT
 GTTTCAGTTTAGTGGCGCAAGATAGACTGGCTTGACTTAGAGAAGGGAAAGGGAGCAAAATTTGTCGAGGCTGCGTAATAGCAGGAT
 TTTGATTATGAAGCCAATTGGAGTTTTAATAAACAGTTGGCAGATGATATTGAGACAGTTTATTATCAACGTCGCCATCTTGAGTCCGATA
 TCATCTAGTCGCATCCGTGAATTGATACATTAAAGGTTCTGTGAAGCCTTTGTTCAAAGAGTGTGTTAGAGAAGTGGAGAAAATGAGTGA
 GAA

SEQ ID 134

MTKKALFTGSFDPVTNGHLDIIERASYLFHDVYIGLFYNLEKQGYFSIECRKKMEEAIRQFKNVSLVAQDRLAVDLAREVGAKYFVRGLRNSQD
 FDYEANLEFFNQLADDIETVYLSTSPSLSPISSSRIRELIHFKAJVVKPFVPKSREVEKMSEE

SEQ ID 135

ATGTTAACTAAAATAGGACTTTATACAGGGTCATTGATCCTGTTACAAACGGTCATCTGATATTGTTAAACGGGCAAGTGGCCTATTGATCAA
 ATATATGTTGGATTTTGATAATCTACCAAAAAAAGCTATTAAACTAGAAGTTCGTAAGCAATGCTTACTCAAGCTCTGGCTATTAC
 AATGTAATTGAGTAATTCCGACGTTAGCTATTGATGAGCTAAAGAATTACGAGTAACACTGATTAGAGGCTTGCAGAATGCAACT
 GACTTTGAGTATGAAGAAAATTGGAATATTAAATCACCTTTAGCTCAAATATTGAAACCGCTATTGATATCAAGAAATAATGGCAGGCC
 CTTAGCTCTAGTCGTGAGAGAGCTAATTCTAGTTCTAGAAGGTTGGTCTCAGTCGGTTATTGCTCAAGTGGAGAAAATGA
 GAAAAGACT

SEQ ID 136

MLTKIGLYTGSFDPVTNGHLDIVKRASGLFDQIYVGIFDNPTKKSYFKLEVRAKMLTOALADFTNVIVVTSHERRLAIDVAKERVHLIRGLRNAT
 DFYEENLEYFNHLLAPNIETVYLISRNKWQALSSSRVRELIHFQSSLEGLVPQSIAQVEKMNEKT

SEQ ID 137

TTGGATCTCTATTCTCACTCATTTCTCCACTTCTCAACAAACACTCTTGAAACAAAGGCTTCACAGAACGCTTAAATGTTAGTCAATTGACGG
 ATGCGACTAGATGATATCGGACTCAAAGATGGCAGCTTGTGATAAAA

SEQ ID 138

MDLYSSLIFSTSLLTFLGKGFTEALKCINSRMRLDDIGLKDGVDK

SEQ ID 139

GTGAAGAAAGAGATCCAAAAGAAAACATAAAAGTTACTAGGCTGCTTAAATGGGGATTATAGGTTTGCTTTTATTGTTAGTATTAGCA
 AGCCTTGTAGTGGACTACCTTATTGGAAATGCCCAGGTGGAGCTTATGATATCCGTTGGTATTGAAAGTGAATAAAAGGCTGATAAAAGCT
 AAGGGTTGTCACATTGGTGTAGCGGTATCTGTCAGTCAGAACGCCAGCTCAGGTTCTTATGCTGGTTAACTCCTTACAGAATTATCTAGT
 AAAGAGGAGAACACAGGTGGCTTGTAGTATGAGCTTATCTCAGGATTATCTCAGGATTATCAATTCTACATGGAGACTTCTCAAATGAGTCCATCTACAGCT
 TAAAGTTAGCTAATAAGCAAGTATCTCTTACTTAAAGGAGTTATGCTTAAACTTACGTTCAACTTACGTTAAAGATAGATTACATTAA
 GCTGATAACAGTCACAGGAGTTAATGGAAAAGTTCAAAAATTCTCTCAACTTACGTTAAAGTATTAAACTATCAAACGGTAAAATGGTATTGGTATCGGTTGACAGAC
 GTACAATACACAAGTCAAGGAAAAAGAAATCAGTTGGTAAAGTTATTAAACTATCAAACGGTAAAATGGTATTGGTATCGGTTGACAGAC
 CATAACAGAAGTATTATCTGATGTTCTGTGGACTTTAATACTGAAGGTGTTGGAGGACCAAGTGCAGGTTAATGTTACTTAGCAGATTACGAC
 CAATTGGTTAAAGAAGATTACGTAAGGACCTAAGGATTGCGAGTACTGGTACTATTGAGCAAATGGCATGTTGGGATATTGGTGGAGCAGGT
 TTGAAAGTTGTTCTGGCGCTAAAAGGAATGGATATTCTTGTCTTAAATCCGATCGATAAAAATGCTAAAAGGCAAACAAAGGTT
 CAGACGAATTATCAAGAGGCAAAGCAGCAGCTAACGCAAGGATTAGGTACGAAGATGAAAATTGACCAGTTCAAAATGTTAGCAGCAAGCTATTGATTAT
 TTGAAAAAAACAAAA

SEQ ID 140

MKNRDPKRHKHSLLGKLWWIIGFAFLLLVLASLVRLPYYLEMPGGAYDIRSVLKVNKKADAKGKSYNFVAVSVSQATPAQVLYAWLTPFTELLSS
 KEETTGGFSNDYLRINQFYMETSQNESIYQALKLANKQVSILTYKGVYVLNLAKNSTFKDRHLADTVTGVNGKSFKNSSQLIKYVAALHLDGVK
 VQYTSQGKKKESVGVIKLSNGKNGIGIGLTDHTEVLSLPDVDFNTEGVGGPSAGLMFTLAIYDQLVKEDLRKGRKIAGTGTIEQNGHVGDIGGAG
 LKVVSAAKGMDIFFVPNNPIDKNAKKGKTKVQTNYQEAKAAAKRLGTMKIVPQNVNQQAIDYLKKT

SEQ ID 141

ATGAAAAGACTAAAAAAATCAAAATGGGGTAGGGCTGCTAGCTTAACTCTTTGCTAGCTTACCTTCCGCTACCTTATTATATT
 GAAAATGCTGGAGGCGCTTACGATATTGCGACTGTCTACAAGTCATGGCAAGAACAGAAAAGGAGCTTACCGAGTTGTCAGTGGC
 ATTAGTCGTGCCAGCCTCGTCAGCTATTATGCTTGGCTGACACCGTTACTGAAATTAGTACAGCAGAAGATAACACAGGCGGATACAGCGAT
 GCTGATTTCCTTCGAATTATCAATTTCATGGAAACATCACAAATGCAAGCTTATTCAGGTTACCTGCTGGAAAACAGGTTACATTA
 GATTATAAAGGCTATATGTTAGACGTTAACAGAATCTACTTTAAAGGAACGCTACACTTAGCAGATACTGTAACAGGTGTAATGGTAAA
 CAGTTTACTAGTCAGCAGAACTTATTGACTATGTTCTCACCTAAACACTAGGGGATGAAGTTACGGTTACAGTTACAGGTTGATAATAAGCTAAA
 AAAGGAGTTGGCGTATTATCAAACGTTAAAAGGAAAATGGGTTAGGATTTGGCTGAGCTTACGTTACAGGTTGATAATTCAAGCAGACAGTGT
 ATCTTCTAGTACTAAGGAGTAGGAGGACCTAGTGTGCTTAATGTTACTCTGATATATGATCAAATAACTAAAGAAGATTTCAGCAAGGGC
 CGTACAATTGAGGAGCTAACGTTAGGAGGACCTAGTGTGCTTAATGTTACTCTGATATATGATCAAATAACTAAAGAAGATTTCAGCAAGGGC
 CGAGATATAATTGTTGTCGAATAATCTGTTGAGGAAATTAAAAAGGTTAATCCAAATGCTAAAGTAATTACAGAAGAAGCCAAACAGGGCA
 GCCAAACGACTAAAGACCAAAATGAAGATTGTTCTGTTACGACTGTTCAAGAGGCACTGGTTATCTCGCAA

SEQ ID 142

MKRLKKIKWWLVGLLALISLLALFFPLPYIEMPGGAYDIRTQLVNGKEDKRKGAYQFVAVGIRSASLAQQLYAWLTPFTEISTAEDTTGGYSD
 ADFLRINQFYMETSQNESIYQALKLANKQVSILTYKGVYVLNVNESTFKGTLHADTVTGVNGKQFTSSAELIDYVSHLKGDEVTVQFTSDNPK
 KGVGRIIKLNGKNGIGIALTDHTSVNSEDTVIFSTKGVGGPSAGLMFTLDIYDQITKEDLRKGRTIAGTGTGKDGEVDIGGAGLKVAAAEG
 ADIFFVPVDPKEIKKVNPNNAISNYEEAKRAAKRLKTMKIVPVTQVQEALVYLRK

SEQ ID 143

ATGACAGAGCTTATAAGAAACTACATTAAATGATCTGCACTCTCATTTGAGAATTTCCTAAGGTAACAGGTTTTTCATGACAATCAAGCG
 CAGCCAATAGAGACGATTCACTTGACTTGGGGATAATATTGATAAAAGCCATCTTGCAGAGCAAGCAAGCTCGGGAAAGGCTAATGTC
 ATGAAATGAACTGGGTATTGAGCTTGCTACTATTGGAATAATGAAGGAGTTGGTTATCCAAAAGACTTGGACCAAGTCTACAAAGATTCAAGAT
 TTACGGTTATTGTTGGCAATTAAAGATAACATAATCGAACCGAGTTGGGAAAACCTTACATTATTGAGACGCAAGGACTAACAGCTT
 GCCTTTAGCTTATACTTTCTTATTATAACCTATGAACCTAATGGGGAGCAGATAGAAGATCCTAAATGCTTAAATGCCATTACAA

ATAAATGAGATAAAAGAGGCAAATTGTCGATTTGAGTCATTAGGTATTGATACAAGGATTGCTAAGAATTTCAGAAATTGAC
CTTATTATAGGTGCACATACACACCATTGAGGAAGGGAGCTAATTACGGTACATATCTGCAAGCAGCTGGTAATATGGTCGCTTGGT
GGGAGTATTGATATAACTTTGATAATCATAACTAAAAGATATTAACTCAACATGTGATACAAAACAACTAACGGTTATCCTCGGACAGT
GACTGGCTAACAGATTGAGTCAGAAGGTAAAGAACAGCTTAGAAAAGAAAGTT

SEQ ID 144

MTELIRILHNLHSHFENFPKVKRFFHDNQAQPIETISLDLGNIDKSHPLTEASSGKANVQLMNELGIELATIGNNEGVGLSKKDLDQVYKDSD
FTVIVGNLKDNIIEPSWAKPYIYIYETQQGTLAFLAYTFPVYKTYEPNGWTIEDPIDCLKCHLQINEIKEANCRILMSHLGIRFDTRIAQESEID
LIIGAHTHHLFEEGELINGTYLAAAGKYGRFVGSIDITFDNHLDILISTCDKQLTGYPDSDWLRRLSQVKVNSLEKKV

SEQ ID 145

ATGGATGCGATGCTGTTTACGCAGGTCAGATGTTGCTATTATCAATTCTGGCTTAATTGTTAGCCATTGAAAAAGACTTTGAGGAAAAAT
CTCCACGAATCATTACCTCATCAAATGCCCTCGCTAAATTGACAGTGAGTCAGAAGAACTTTAGAGATTATGAAACTATTATCAACAAGGT
CAATTTTAGCGAACAAAAGATTCTGGTATGGGCTTCTGCGCAAGTGCTTGGAGAAGTTTACATTGGGATTGATTACAAAATGGAAA
ATAGTGTAATGAGAAAGATATTGATGCCAAGAAGAAGTGATTCTGTTAATCGTGATCAGTATTATTGATCGTATTGAGTGTAAAAA
ACGAAAAGTAGACTTGCTTCTGAATTACTCAGAGATGTGGCAGCAGATTATT

SEQ ID 146

MDAMLFYAGADVAIINSGLIVQPFEKDFSRKNLHESLPHQMRMLAKLTVSSQELLEIYETIYQOQFLAQOKIHMGMFRGKCFGEVLHSGFDYKNGK
IVYNEKDIDAKEEVILVIVDQYYFASYFECLKTKVVDLLFLNYSEMWWQOII

SEQ ID 147

ATGCGAAAAGAAGTGACACCAAGAGATGCTTAACATAATAAGTATCCTGGCCACAGTTCAATTCACTTTGAAAATATCGTTAAAAGTGATGATATT
GAATTTCACCTGTTATTAAATGAAAAAATCAGCTTTGATGTCAGTGTCTTGGACAAAGCTTTCTGAGATTATTAAATATGATTATCGTT
GGCAGTTGGGTAACAGGCAAGGCTTGAGGCTTACAAAGAGTCTAGTACAATTAGAAAATAGCGGATTTCACGTTAGAGATTAT
ATTAAGAGTATTGTAACCTGGGTTGCTTATTGTTGGAGAATCCAATCTAGAGATTATTGATGATGAAAGACCTCATAGCGT
CGTAGTCAAGATCCAATCATAACTCAAAGATAATCGTCTCCAGTCATGCCATGCTATTACAGTAAAGAAGCGT
AAAGACACAAAAGCCGTCAAGAACGTATTAAGAAGAGCAAGATAAGGAAATGACCTCTGCAAAGCAGCATTGTTATTGTAAGAAAAA
SEQ ID 148

MRKEVTPEMLNKYPGPQFIHFENIVKSDDIEFQLVINEKSAFDVTVFQRFSEILLKYDFIVGDWGNEQLRLRGFYKDASTIRKNSRISRLEDY
IKEYCNFGCAYFVLENPNPRDIKFDDERPHKRRRSRSQSNSRNRQTSKRNRSQNSNANHTSKRKDTKRRQERHIKEEQDKEMTSAKQHFVIRKK
SEQ ID 149

ATGGATTTTCAGAAAGGTGTCAAATGAAAAAGAAAATTGCGAGAAATGTCACAACTATAATAAATTTCAGGTCCCCAATTATTATTCATTTGAA
GAGCAAGTTAGGCTGAAGGCATTGATTGTTACTCTTAGAAGTGTAAAGAACGCTTTGATAGACTAGCTTGGTCACGTTATAAGAAGTT
CTCCTAAAGTATGACTATATTGTCGGCATTGGGAAATGAACAGCTTCGCTTAAAGGGTTTATAAGGATAGTGACGATATCAAGAAAAGAAT
CGCATCTCACGTTAGAAGATTATATAAGAATTGCAATTGGGTTGCTTATTGTTAGAAAATCTCATCACAAGATATTAAATT
GAAGAGGAGCGCAACCAAGACGAAAGAAATCACCTAAATCAAATCAATCGCGAACGCAAACATTCAAATCAGCAGCCGACACCTAAG
AGCAAATCGAAGCGGGCATAAAAGAAAAGCAACCTGAAAACCAAGCGTTACAGTCAAAACGCTGAAGTAATACTAAGCATAAAAGAAAAGTCA
AAACGTAATCAGACTAGTCACCTAACCAAAATTAGTCATTATCATCAGAAAGAAAGATAAA

SEQ ID 150

MDFSERCQMKKEISPENYNKFPGPKFIFHEEQVKAEGIDLLLEDVKNADFDTTSFGQRYTEVLLKYDYIVGDWGNEQLRLKGFYKDSDDIKKT
RISRLEDYIKEFCNFGCAYFVLENLPQDIKFEEERQPRRKSPKSKNRRKPNSNQQPATPKSKSKRASKEQOPENQAFTSQKRRSNTKHKEKS
KRNQTSOLNTKISHFIIRKKD

SEQ ID 151

ATGAAGAAAAGAAAATATTATGCCCTAAAAAAACTGATACACCCGCTATAACCCCTCTATTATAGCTTAACCGCATGAACTAATAGCTTGGGCT
ATTGAACATGGAGAAAAGAAAATTCCGTGCTTCACAAATCTGGACTGGCTATAAAAGCGTGTGCAAAGCTTCGATGAAATGACTAACATT
AAAGATTTTATTGCACTTTGAACGAGAATTGTTGTTAATCCTCTAAAACACGTATTGTTCAAGAATCTGCTGATGAACTGTTAAATACCTT
TTGAAATTACCTGATGGCATGCTGATTGAGACGGTTTGATGTCACATTGTTCAACATTGTTTACAGTATGTTGTAACGACTCAAGTTGGTTGTAACATT
GGTGCACCTTCTGCAAGGTTGTTAAAGAACACCGTGTCTAGTCACATTGTCAGGTTGATGAACTTACAGTCTACTTCAGGTTAGCACA
CGATTTGTTGCAAGTAACTTAGCAGTATCTCTCATGCTCCAAATAACGATTACAGTCAGTATCATGCTGTTAATCGTCTTCCCTCTGAAAG
GGTGTACAAGTTAACTTAGCAGTATCTCTCATGCTCCAAATAACGATTACAGTCAGTATCATGCTGTTAATCGTCTTCCCTCTGAAAG
TTGTTGCGGCTATTGAAATTATATTGAGACGACTAACCGTGTGTAACATTGAGTATTATGTTAAATGGTGTCAACGATACCCAGAAAAT
GCTCAAGAGTTAGCAGATTAAAGAAAAGATTGCAAAATTATCTATGTCATTAAATTCTTACAATCTGCTCAGAACATGACAGTATAGT
CGTAGTCTAAAGAGCGGTGAGAAGCTTCTATGACGTTGAAAGAAAATGGAGTTAATCTGTTGCTCAAGAACATGGTACGGACATTGAT
GCAGCTTGGGCAATTACGTTCAAACACAATGAAACCGCAGTCAAAAGCGAAGGTAGGGCAG

SEQ ID 152

MKKENIMPKTDTPAYKPSIYSLTRDELIAWAIEHGEKKFRASQIWWDLYKKRVSFDEMNTNISKDFIALLNENFVVNPLKQRIVQESADGTVKYL
FELPDGMLIETVLMRQHGYGLSVCTTQVGCNIGCTFCASGLIKKQRDLNNGEITAQIMLVQKYFDERGQGERVSHIVVMGIGEPEFDNYTNVLKFLR
TVNDDNGLAIGARHITVSTSGLAHKIREFANEQVQVNLAWSLHAPNNDL RSSIMRINRSFPLEKLFIAIEYYIETNRRVTFEYIMLNVNDTPEN
AQELADLTKKIRKLSYVNLIPIYNPVSHEHQYSRSPKERVEAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSNTMKRDRQAKVGQ

SEQ ID 153

ATGAAACCATCGATTATAGCTTAACACGCGATGACTGATCGCGTGGCAGTTGAAACCGGCCAAAACAGTTAGAGCTACTCAAATTGGGAT
TGGCTCTATAAAAAGAGTTGATGAGGAGATGACGAAATTCTTCTGAGGAGATGACGAAATTCTTCTGTTCTATTGAAACTGTTCTGTCATCCT
TTAACACAGCGAGTTGATGAGGAGCTCAGCTGATGGCTACAGTAAATTGTTGAACTGCTGTTCTGTCATGTTGAAAGCTTAAATGCT
CAACATTGTCATTCTGTTGTCAGGCTCAAGCTGATGGCTACAGTAAATTGTTGAACTGCTGTTCTGTCATGTTGAAAGCTTAAATGCT
TTAACACAGTGGGAAATTACAGCTCAATCATGTTAGTCACATTGCTGTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTTGAAAGCTTAAATGCT
CTAACACAGTGGGAAATTACAGCTCAATCATGTTAGTCACATTGCTGTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTTGAAAGCTTAAATGCT
GGCATTGGTGAACCTTTGATAATTACAAAATGTCATGTTAGTCACATTGCTGTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTTGAAAGCTTAAATGCT
ACAGTCTCTACCTCAGGGTTAGCTACAAGATTGGGATTGTTGAAACGAGGGAGTACAGGTTAATCTGCTGTTCTGTCATGTCACCAAATAAT
GATTACGTTCAAGTATTATGCGAGTAATCGCTTTCCGCTGAAAAGCTTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTCACCAAATAAT
GTCACCTTGAATACATGCTAAAGCTGATGAGTCAGTCAGGTTAATGCTGTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTCACCAAATAAT
TATGTTAACTCTGATCCGTTAATCTGTTGAGTCAGTATGAGTCAGTAAAGCTGCTTAAAGAGCGAGTTAGCCTGTTCTGTCATGTTGAAAGCTTAAATGCT
AAAAATGGAGTTAAGTGTGGTGCCTCAAGAGCAGCGAACAGATATTGATGCAAGCCTGTTCTGTCATGTTGAAAGCTTAAATGCTGTTCTGTCATGTCACCAAATAAT
GAAAGCTTCAAGCGACAAAA

SEQ ID 154

MKPSIYSLTRDELIAWAVERGQKQFRATQIWWDLYKKRVSFDEMNTNISKDFVSIILNDSFCVNPLKQRVVQESADGTVKYL FELPDGMLIETVLMR
QHYGHGSVCVTQVGCNIGCTFCASGLIKKQRDLNNSGEITAQIMLVQKYFDERGQGERVSHIVVMGIGEPEFDNYTNVLKFLR
TVTSGLAHKIRDFANEQVQVNLAWSLHAPNNDL RSSIMRINRSFPLEKLFIAIEYYIETNRRVTFEYIMLNEVNDSIQKAQELADLTKTIRKLS
YVNLIPIYNPVSHEHQYSRSPKERVELAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSNTMKRDRQAKVGQ

SEQ ID 155

ATGCTTAAAGATTACTTACTGAAGATGGGAATTGACAAAGATTAGTCGCGTTCGTTGGATGTTAGTGATTATCTATTGTCTTATTATTGTC
AGGATCTGTTGGCCTCAAATTATGATTGAGGGGATCAACTCCGAATGTCAGCGCTTCGGAAGAATGCTAGCTCTTACTACCATTTAAT
TCTTTCGCTAGTTAGATCAGCTAACAGCTTAAAGAGATTGGTATTGGTCAAATGTAATTTACTGCTCTCTCCTCATT
ATAGGGTACTATCCTAAAGCCAAGTTCAGGAAATAAAAGCTTATATTACTGCTCTTGTATTTCATAGAGTGTACTCAAGTT
GTTTAGATATTAAAGATGCTAATCGGTTTGAATCGACGATCTATGGACAAATACCTAGGCGGCCCTTCGCCCTATGGACTTATCGA
AACATAAAAGGTTGGCTCAACTATTAGAAAA

SEQ ID 156

MLKRLTEDGELETKISRRFVWMLVIYCLIVRMCFGPQIMIEGVSTPNVQRFRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVNILLFPLI
IGLLSLKPSLRKYKSVILLAFLMSIFIECTQVVLIDILANRVEIDDLWTNTLGGPFALWTYRNKWLTLIRK

SEQ ID 157

ATGCTTAAAGATTAACTTGTGGTGTGTTAAAGGAAGAAAAGAACGGCTATCTTATTGAAATTGTCATTAAAGTTGCTTGCCTGTTAAAT
CTTATCCCTCAAATCATGGGATCAGTTATGATGCTATTACAACGGAAAATTAACAAGACCACAAATTGCTCTGGATTATTAGGTTGGT
TTGTCAGCTTAGCTATGTTAGGGCTCGTTATATTGGCTATGTTAGGGACTTCATACAAATTGGGCTAAGTTGTCAGATACCGGTT
TTGAACATTTCACAAATGTCCTTCTTTATCAGAAATATGTCAGGTTATTAATGGCGCACGCCAACGACATCAATTCTCTAAC
CGTCTGCAGGAGGAGGTTATGTCAGCAGTGGATGCCCTATCACAGCATTAGTAACGCTTACCATGTTCTTACTATTCTGGCAAATG
ACATTAATTGGCTTACCCCTTGCCCTTAATGGCCTTAGCAACTAGTAAATTGGGCGAAAACCCATGAAACACCTTCAAAGAAATCTCAGGCC
TTTCAGAATTAAATAAAAGTGCAGAAAGTGTCTCTGGCTCAAAGTGAATCATTGGTTATCAAGAACAAAGAAATTGCTTCTTTCAA
GAGGTTAACATGAGTACTTCGTAAGAACATGCCGACCATGACTTATGATGTCATGTTGACTGGTACCTGGTACATTGACGTTAGGAT
GTATTAAACATGGCTATGGAGCTTTATGATTTCAAAAGGTCAGTTACTGTTGACTGGTACCTGGTACATTGACGTTAGGAT
TGGCCCTGATGGCATTGGCTCTGGTCAATATGGTACAGCTGGTACTGGTACATTGATTTCTTAAACGGTATTAAAGCCTACTTGGTAC
ATAACTGACCTTAAATCTATCAGACCTGTTGTCATGGAAACATTAAAGATGATAITGATTCTTAAAGATACGACAATGAAAGAACCTTGG
GATATTCACTTCACCTTAAAGGTCACACCTTAAAGGTTAGGTTGGTAGGTCAAACGGGATCAGGAAAGACAAGTCTTATTGCTACGTGAA
CATGATGTAACCTGGGAAATTACTTAAATAAACATGATATACTGATTATGCTGAGTTACGTCACAACTCGTTATGTCCTCAA
GATCAGTTTATTGCTACAGTATTAGAAATGTCGTTGGAAATCCAACCTATCATCAATGCTTAAAGAACACTAAATTGG
CATGTTTACGATGACATTAAACAGATGCCAGCAGGATTGAGACTCTAATTGGAGAAAAGGAGTCTCATTCTGGTACAAAAACAAAGGATT
GCGATGAGTCGTGCGATGTTAGTCCAGATATTCTTGGATGATTCTCTATCAGCAGTGGACGCTAAACGGAACATGCCATTATTGAA
AATCTTAAACGAATGTCAGGGAAATCAGCTATTATTCAGCACATGATTACGCTGTTGACCGAGACCTTATCTTAGTTATGCAAGAC
GGCAGAGTCATCGAGCGAGGTCAAGAGTGTCTAAATAAGGTTGGTATGCTGAAACAGTATGCCACAGCAATTAGAAATGGAGGAA
GCATTGATGAGTC

SEQ ID 158

MSIIKNLWWFFKEEKRYLIGILSLSIVAVLNLIIPPKIMGSVIDAITGKLTRPOLLWNLLGLVLSALAMYGLRYIWRMVLGTSYKLGQVVRYL
FEHFTKMSPSFYQKYRTGDLMAHTNDINSLTRLAGGGVMSAVDASITALVTLITMFFTISWQMFTLIAVPLPLMALATSKLGRKTHETFKESQA
FSELNNNKVQESVSGVKVTKSFGYQEQQEIASFOEVNQMTFVKNMRTMTYDVMFDPLVLLFIGASYVLTLAMGAFMISKQVTVDLVTFTYLDMLV
WPLMAIGFLFNMVQRGSVSYNRINSLEQESDITDPLNPIRPVNGLRYDIDFFRYDNEETLADIHFTLEKGQTLGLVGQTGKTSLIKLLRE
HDVTQGKITLENKHDIRDYRLSELROLIGYVFPQDFLATSILENVRGNPLSINAVKKATKLAHVYDDIKQMPAGFETLIGEKGVSLSGGQKQRI
AMSRAMILDPDILILDDSLSAVDAKTEHAIIENLKTNRQGKSTIISAHRLSAVVAHDLILVMQDGRVIERGQHQLLENLKGGWYAETYASQLEMEM
AFDEV

SEQ ID 159

GTGATGAAAACAGCACGTTCTGGTTTATTAAACGCTATCGTTCTCATTACTGTCATTGCTGCGCTTATCTTAGCAACCTATTAA
CAAGTAAAAGCTCTGCTCTTAGGAGAGTCTGACTGAGTTGGAAAATCGGTCTAGGTTATTACGTTGCTAAGATGAGTGGCAGACACAT
TTAGCCCTGATTATCAGCTTTAATGCCGTGATGTTAAAGCTTACTGTTAGGTTACTGTTGCTAATCTAATATAGTTCTTA
CTTACACGTTGCTCAGCTACCGCAAGGGCTTATGGTAAATTAGAACCTGCTGAAACATTCTTGATTCAAGTGGTACTAATATTGCCC
GATGGGGAGATTCTCTCGTTTACAGGTTAGGATAATTACCAACGTTACCGCTGAAACATTCTTGATTCAAGTGGTACTAATATTGCCC
TACATCGCTGGCTGATGTTAGGCAAGATAAGCCCTTACCGCTGAAACAGTCACTGCTTAAATGCTTTATGGTAAACCCAGTTGCTCTATT
AACATCCGTTGGCAAGAAAATACCAAATACCAACAGCAAGAAGTCAGTGTCTTAAAGCTTTATGGTAAACCCAGTTGCTCTATT
ATTATTGTCACAGGTGCTCAAGAAGATAACGATGACAGCCTTTAAAGCATAATGAAAGGGTTCGACAAGGCCACCTTAAACGCCGCTGTTCTCA
GGACAATTATTCCAGTCATGAATGGAATGAGCCTTATTAAACAGGCTATCGTATTGTTGCGTTCAACATTGCTCTAGTGCACAAATCTATG
CCAGCAGCGGCAGCGCTGGTTAGTGTCTGAAATTACCAACCCATATTGCAACATGCAAATCGCTCTAGTTGGGAGAA
TTGCACTGGCTTACCGGTCTCAGCTTACCGTATTCAAGAAATGTTGATGAAACCGAAGAAGTCTGCTCACAATGCAACAGCGCTCAGCGCTT
AAAGAACAGCTGGCGATTAACACAGTCGATTTGGTATCTCTGGGAAAAGTATTACGATGTCATCGTGTGAGTGCAGGTTGATTACCTT
ATTGCGTGTGGACGCCAGGGTCTGAAAGACACTATTATGAACTTGTGTTACCGTTACGATGTCATCGTGTGAGTGCAGGTTGATTACCTT
GGCGTGTATTCTGACTACGATTGGTAGTCTCGTAAAGGTTAGGGATTGTTGCAAGAGTCAGTTCTTGTGAGTGCAGGTT
AATATTGTTGGTAGCAGCATTAGTCAGAACATGGTAAACTGCTGCGCTGCGACCCATATTGACTTTATCATGCTCTACCAAAA
GGGTACAATACCTATGTCAGATGATGACAATGTCCTTCAACAGGTAAAGCAGTTGATTCTATTGCTAGGAGCTACTGACTGACCCCTGA
GTGTTGATTGGTAGGAGGCCACTTAAATGTTGATACGGTTACGAAAGTAAATTCAACGGGCCATGAAAGCTATGTTGAGGTCAGGTT
TTTGTGATTGCTCACCGCCTAAACACATTAAATGCGATCACATTGTTGAAAGATGGCAAGGTCATTGAGCAAGGAAATCATCATGAG
CTATTGCACTAAAAGGCTTTATGCGAATTGTCATCACATTGTCATTGCTT

SEQ ID 160

VMKTAARFFWFYFKRYRFSFTVIAVAVILATYLVQKAPVFLGESITELKGKIGQAYYVAKMSGQTHFSPDLSAFNAVMFKLMLTYFFTVLANLIYSFL
LTVRVSHSTNRMRKGFLGKLERLTVAFFDRHKDGEIILSRSFTSDLDNINQNSLQNSLIQVVTNIALYIGLWVMMFRQDSRLALLTIASTPVALIFLVI
NIRLARKYTNIQQQEVSAALNAMFDETISGQKAIIVQGVQEDTMATFLKHNERVRQATFKRRLFSGQLFPVMNGMSINTAIVIFVGSTIVLSDKSM
PAAAALGLVVTFVQYSQQYYQPMQIASSWGELOLAFTGAHRIQEMFDETEEVRPQNAPAFSLKEAVAINHDFYLPQKVLSVDIVAPKGK
IAVVGPTGSGKTTIMNLINRFYDVDAHSITFDRDIRDYDLDLSLRQKVGIVLQESVLFSGTTDNIRFGDQTISQDMVETAARATHIHDIFMSLPK
GYNTYVSDDNDVFSTGQKQLISTARTLLTDPEVLLDEATSNVDTVTESTKIQRAMEAIVAGRSTSIVIAHRLKTLNADHIIVLKDGKVIEQGNHHE
LLHQKGFYAEELYHNQFVFE

SEQ ID 161

TTGATGAAAGTCTAATCAATGGCAAGTCTTAAAGAGATTAACTCTTACCGCCCTTATAAATGGTTACAGTATTAGCTCTATCTCTTATTG
TTGACGACTGTTGTTAAATATTCTCTTAAATGCTTACACTATCTGCTAATCTGACAAATGTTAATCAAACAGCAGTCTTATT
GTGGGATATTATTCAATGCTATGCTTGCAGACCTTAACTCAATTGTTGGAAATCTCTTGTGCGCTGTTCTTATAGTATTGTTAGAGATATT
CGTAGAGATGCTTTGCTAATATGGAAAGGCTTGGCATGTCATTGTTAGGACACCGGAGGATCTATAGTGTCTAGTACACTATGTTGATGTCAGAC
GAAGAACATATCTGATATTCTGGTATTGAGCTTATCTGGGATATTATTTACAGTTACTCTGTCACACTATGTTGATGTCAGAC
ATTAAACTAACAGGACTGGCTCTTATTACCTGTTATATTAGTGAATGTCATCGGAAAATCAGTCATGTCATTGCTAAACG
AGAAGTTTACTAGTGTATGACAATGAAAGTATTGAGGAATTCGCAATTGCTTGTGAGTCTCTTCTTGGTCAAGAAGAGCGCTTGAAGAC
GAATTGAGGAAATTAAACAAAGAGCATGTTGTTGATGCAATTGCTTGTGAGTCTCTTCTTAAAGCAGGGCAGGATTGATGTTTATT
CTCCTAGCATATGCTGTTCTTATGGCTTATTGGATTACAGGAGTTAAAGGAGGCTTACGGCAGGATTGATGTTTATTGAGTACGTT

AATCGTCTCTTGACCCCTTAATTGAAGTAACGCAAATTTCAACCTAACACATCAATGGTATCAGCAGGGCGTGTGTTGATTGAT
GAAACAGGTTTGACCAAGCBBBBBACAGAAGCTTTGTGAGAGAAGGAAATATCGAATTAAAAATGTCATTCTCATATGATGGAAA
AAACAAATCCTTGATAATGTTCTTTAGTGTAAAAAGCTGAAACGATTGCTTTGTAGGAGCGACAGGTTCTGGAAAATCATCTATTAAAT
GTCTTATGAGGTTTACGAAATTCAATCTGACAAGTTTATTAGATGGAAGGATATTAGGGATTACTCACAAGAACATTCAGGACAGGAA
GGACTCGTCTTACAAGACCCCTTTATATCATGGCACTATTAAATCTAATCTAACAAATGTACCAAGACATCACCGATCAAGAGGTACAGGACG
GCAGAGTTGTTGATGCTGATCAATTATTAGAAGTTGCCAGATAAGTACGATGCAGCTTTCAGAACGTTGCAAGTTTGTGACTGGACAA
CGCCAACTATTGGCGTTGCCAGAACTGTGGCTAGTAAACCTAAATTAACTTAGATGAAGCAGACAGCAAATTGATTGCGAACAGAGCAG
ATTGTACAGAGATCGTAAAGCTCAAGGTCGACAAACATTGCCATTGCTCACCGTTATCAACCATTCAAGATGCTAATTGATCTAT
GTTCTTGATAGAGGAAAGATAATTGAAAGTGGGAATCAGAGTCTTATTAGACCTAAAGGGACTTATTATCGTATGTACCAATTCAAGCTGC
ATGATGGAGTC

SEQ ID 162

MMKSQWQVFKRLISYLRPYKWFVLAISLSSLLTVVKNIIPLIASHFIDHYLTNVNQTAVLILVGYYSMYVQLTIQYFGNLFFARVSYSIVRDI
RRDAFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGIILSSFISAIFIFTVTLYTMILMLDILKTGLVALLLPVIFILVNVRKSVTVIAKT
RSLLSDINSKLSSESIEGIRIVQAFQEERLKTEFEENIKEHVVYANRSMALDSLFLRPAMSLKLLAYAVIMAYFGFTGVKGGLTAGLMLYAFIQV
NRLFDPPLIEVTQNFSLTQTSMSAGRVPFLIDETGFEPQSQNTAEFVREGNIEFKNVFSFYDGKKQILDNVSFSVKKGETIAFVGATGSGKSSIIN
VFMRFYEFQSGQVLLDGKDIRDYSSOEQLRKNIGLVLQDPFLYHTGKTSNIKMYQDIDTDQEVQDAAEVDQFQIKLPDKYDAAVSERGSSFSTGQ
RQLLAFARTVASKPKILILDEATANIDSETEQIVQDSLAKMRQGRITIAAHRLSTIQAQNANCYVLDRGKIIIESGNHESLLDKGTYYRMYQLQAG
MMEV

SEQ ID 163

GTGTATAATGAGGTCAAAGTGCAGGAAAGGTCTATAAAATGTTACTATTGGTAGATAATTACGATTCTTACCTATAATTAAAGCAATATTAA
AGTGTCTATAAAGAGGTATTGCTCATAAAAATGATGTTCTAACCTTTTATTAGTGTAGAGCGCAGAACCCATCGTCTTACACCTGGACCA
GGACACCCAAAGGATGCTGGAAAATGGTAGAATTATCAATCAGTTATAGGAAAGAACCTATTCTAGGTATCTGTTGGGCATCAAGCCCTT
CCCGAGTGTGTTGGTGGCGATTAAATTAGCAAATCAGTTATGCTGTTAACAAAGTGGTAACAATAACGACCATACTAGTTGTTAAG
GGAATTGATAGTCCAACCCAAGTTATGCTTATCATTGTTAGTACTGATTTACAGAGAATTGCTGTTATTGCAAGTCAATGAGGAT
AATGAAATCATGGCATTCATTGCCAGCTTAAAGGTATATGCGATGCGATTCTGAGTCAATCAGTTGCTGTTACCGTCAATGGAGTATTGATGAAATGAGGAT
AAAAACTTTGACCTTAAATTATGAC

SEQ ID 164

MYNEVKVQGVYKMLLVDNYDSFTYLNQKYLQVLSVYKEVFKVAKNDVPLFLLAESAEAIVLSPGPVHPKDAKGVELINQFIGKKPILGICLGHQAL
AECLGGRLNLANHVMHGKQSWTINDHTSLFKGIDSPTQVMRYHSLVTDLPENIAVIARSNEIMAFHCPSLKVYAMQFHPESIGSIDGMKMI
ENFLTLIND

SEQ ID 165

ATGACTACTCTTAATTGATAATTACGATTCACTTACCTAACCTCGCCAAATATTAAAGTGAATTGACGGAGACGATTGCTTGATAACCAAGAC
CCAAACACTTATGACATGGCBBBBBAAAGCTAACGCTCTAGTCCTCACCTGCTGGTGGCCCAAGGAAGCCAACCAATGCCAAACACTCATT
CAAGACTTTACCAACAAACACCTATCTTAGGAGTGTCTGGACCCAAGCTACGCTGAAACTTTAGGGGAAACCTTACGCTTGGCCAAACGC
GTCATGCTGGAGACAAAGCACCATTGAAACGCAAGGCCCTGCTAGTCTTGCCTCCCTGCCAACAGAGATCACCGTACGCTTACCCATTCC
ATCGTTGTTGATCAGTACCAAAGGTTTACCGCTAGAGACTGACGATCAAGAAATCATGCCATTGACCATGATTGCCACTTCATGCCAGCCATTCCCCGT

SEQ ID 166

MILLIDNYDSFTYNLAQYLSEFDETIVLYNQDPNLYDMAKKANALVLSPGPWPKEANQMPKLIQDFYQTKPILGVCLHQIAETLGGTLRLAKR
VMHGRQSTIETQGPASLFRSLPQEITVMRYHSIVDQLPKGFSVTARDCCDDQEIMAFEHHTLPLFLQFHPEISIGTPDGMTIANFIAIIPR

SEQ ID 167

ATGAAACAAAGAACACTACCTATATTGCACTCATGGTTGCACTACTTATTGTTTATTAGGTTTATCCAGGGATCCCATTAGGTTTCACTCCAGTC
CCAAATTGTTTACAAACACTTGGTGTATGCTGGCAGGTGCTCTGCTGGTAGTAGGAAGGGTTCTAGCTGTGGCTATTCTGCTCTTAGTT
GCTATTGGTGCACCACTTTACCAAGGAGGACGGTCAGGTCTGTAACGCTGTTGGCCAAACAGCAGGCTATCTGCTGACTTATCCATTGCAAGCT
TTTTTATCGGCCCTAGGGCTTACAGGAAAGTGAACAAACAAACACTCTGGTTCAATTCTTATTGATATTGGCTACTATTGATGATT
TGTGGTAGCATCGTCTTCCCTTCAACACTCTAACCTTAACAAATCACTATTCTAACCTTATTGATATTGCTGGGATACCTTAAAGCA
TCCATTGCTTGTGATTATTATCGTAAATTGCAACAGATTAACATCTACACAAAC

SEQ ID 168

MKTRTTTYTALMVALLVLFIPGIPLGFIPLVQLNLGVMLAGLMLGGKGTLVFLFLVIGLFLPVFSGSRRTIPVLMGPSAGYVIAYLLVP
FFIGLGLEVKVTTKLWVQFLIIWIFGVLLIDICGSIVLFSQTSIPLTKSLSFNLIPIPGDTLKASICLIIYRKFANRLTHLYN

SEQ ID 169

ATGTTTACACAAAGAACACTTGTAAAGGTGGCTATGACCACTTTGATTATTAGGCTTATTCTGCTATCCCGCTAGGCTTATCCCA
GTCCTTCTTACCTGTTCTCAGGCTCAAGAACACCATTCAAGGCTATTGATGGGCCATCTGCTGCTATGTTATTGCTACCTTGTGCCT
ATTGCTTTCACTACTTACCGCAATTGGTCTCAAAAGCACGCCATTAGCATTCTGCTAGCTTAACTCAGGAGTGTACTGGTGTGTT
CTGGGTGCTATCTGGTGTGAGCTACACTGGCATGCTCTGTGACATCGCTTTATCAAACCTGGTCTTATTCCAGGAGATACCATCAAAGCA
ATCATTGCCACCAATTATCGCTTAAACACAGATAGTTTGAATACAAACAG

SEQ ID 170

MFTTKEVLKVAMMTTLLIIILGFIPAIPLGFIPVPIVLQNLGVMLAGLMLGGKGTLVFLFLVIGLFLPVFSGSRRTIPVLMGPSAGYVIAYLLVP
IVFSLLYRNWFSKSTPLAFLALLISGVVLVDLGAIWLSAYTGMISLTSLLSNLVFIPGDTIKAIATIIVAVKYKDSFLNTKQ

SEQ ID 171

GTGACTAAATGATTCAAAATTCTCAAAATGGACCTCTCGTCCAGCCCTTAATCTTAATTCTGAAAGGAAAACAAACGCAACATGCCATAATT
TTAACGACTTAATGGGAGTCAAA

SEQ ID 172

MTNDSKFSKWTSPALNLSLKGKTKRNMAIFFKHLMGVK

SEQ ID 173

ATGCTATTATTAAATTCTGTTAAAGGAGGCTATCATGTCATTCAACAAATTATCCATTGGCTGACGAAATATTATCTGAAAGACTAGCATT
CTCTTATGAAACAGCCTGGAAATTCTAAATAGCGATGAGAACTCGTGGGAAATCTACGCTGCTGCCTTATACCTTAAACATCAAGTTAGCCGAAAT
AATATTGCGCTTAAAGCTTATTAAAGTGTCAAGCAGGACTTTGTGCAAGGAAATTGTTGTTACTGCTCTCAATCTAAAGAAAGCACTCTGACATT
GATAAATTGGTCTGCTCTCAAAATGTCATTCTAAACAGGCTATTGTCGCTCATCAAATGGTGTAGCGCTTCTGGTATTGCGATGAGTGG
ACTAACGCTAGCAAGAGAAAATTGAGCAGTATTGTCAGTCATTCCCTGAAATCAAAAGGCCCTCTGAGAAATTGCTTACCGCTGGTTT
TTGGATAGAGAACAACCTCATCAGTAAACAGCAGGAATTGACCGTATCATATACTCATAATCTAACACCCCCGAGAAAACCTACCCCAACATTGCA
ACGACGCTAGCTCAAAAGATCGTTGATACTTAGAAAGAATTCAACATGAAGACATTGATGTTGTTCTGGATTCTTGTGTTAGGGAGAG
AGCGATGAGGGCTCATCACATTAGCTTCTGAGCTAAAGAGCTGGACCCATTCTATCCCTGTCATTTTACTTGTGTTGAAGGAACACCT
CTGGAAAATATAACTATTGACTCCATTAAATGCTTAAATATGCCATTGCGTTGTTTCTTCAAGGAATTAAGGATTAAGCGC

GGACGAGAGGTCCATTGAGAATTGAATCATTAGTCACCTTACTTGTTGACTCAACTTTGGAAATTACCTAACAGAGGGCGTCGAAT
CAACATACCGATATTGAATTCTGGAAAATTACAACAACTAAACTAAAGGAATTAAATT
SEQ ID 174
MLLISLKEAIMSFQTNYIHLADEILSGKTSISYEQALEIILNSDENWWWEIYAAALYLKNQVSRRNIRNLVLLSAKQGLCAENCGYCSQSKESTADI
DKFGLLPQNVILKQAIVAHQNGASVFCIAMSGTKPSKREIEQLCQVIPEIKKSLPLEICLTAGFLDREQLHQLQAGIDRINHNLTPEENYPNIA
TTHSKFKDRCDTLERIHNEIDVCSGFICGMGESDEGLITLAFLRKELDPYSPIVPNFLAVEGTPLCKYNYLTPIKCLKIMAMLRVFFPKELRLSA
GREVFHFENFESLVTLVLDSTFLGNLYTEGGRNQHTDIEFLEKLQLNHTKKELI
SEQ ID 175
ATGATATACTGGTCTTATTTGACGGGAGATAAGATGAAAAACTATTAAAAAGCGATAGCTATGTGCCGAGATTGCCGTTAATTTGTA
ATTGTTGAACCTTAGTTGATCAAAGAGAGGATGGCTCATCTGATAATTAAATGGATTCTAAGAGAAATTCTGAGGTAACGTAACGTGATCAG
CAATGGATTACCATTTGAGGATGCTTAACTAACGAACTTAAAGCCAATGTCACTAGCCAGTGCAGTGTCTGCAAGGGAAAGAGAAGGGCTAGT
CTTATTCTAACATAGAAGAATGTCAAAATTCACTAGCTTAGTGCAGATAAAACCTTTCACCAAGGGGAAGCAGCTATTGCTCTGCGGCTCTA
TTATTGAAAATAATGGAAGTTAGAAAAGAAAATAAGGAGATTCAATTGACTTTTATCTCCAGTAAGGGTAATCAAGAAATTCTCAGTG
CAAGTAGTGGATAACACAGTGAATTCTCAGCATCAAATTATGG
SEQ ID 176
MIWWSYI LTGDKMKKLFKKAIAMCRDLPLNFVIVELSLYQREDGSSDNIKWISKRILEVTVDQQWIYHLRMLNLPKLPMSLASSDCPAREEKAS
LISIEECQKFTSLVRDKNPFHQGEAAIVPAALLKEKIMEVRKGKIKEIHLTFLSPVRVNQEFSQVVDNTVIIFQHQILW
SEQ ID 177
TTGTTTAATGCACGATGCTGCTGCATTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTCACATTGAGAAGTAGCAGGAGATCCCAA
GCT
SEQ ID 178
MFNARCCCISNASESENRI PDCSHCRSSRRSQA
SEQ ID 179
ATGAAAGAATAGAGATGTTTATATTGGTTTGGGCTACGAACACCTATCGTATAAAAGGGAAAGCAATTAAACATTACCGTCCAGAACCTTGTAGGA
GCACACCTTTAAATCAAATAAAAGAATCAGAATCTAACATTGATAGTATTATTGTGGAACACAGTTGACTGGGCAATATTGGT
CGTTGATGACTCTTTCTGATTATGAATCCTATATTCCAGTACAAACGATTGATATGCAGTGTGCTCATCAAGTCTGCCTTGTGTTGGT
TATCTAAAATCAGTACCGTATTAAATGAAAAGGTTGTTGTTGGGGGATTGAAAGTAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGAT
AATCGTAACGGAGAATACAGTTGCTAGTTCTCTGACTCTTATGCTGAAACTGTAATGTTAGAAGGGGCCAGAGAGTCTGTCAAAATAT
GGTTTAAAGGAGAAAATGTTAGATAAAATTGGCATTCTGAGCATAAACGCCCTTAAACAGCTAAACAGGTTGCTATTAGAAGGAGTAATCTTA
CCAATGGAAAGGGATGGCAGATAAGGGCTTAGAAAACACTTTTCAAAATTACCAAGGTTGATGGAAATTCCGTTGCTCACATTGAGAAGTAGCA
ATTGGAATGTTGTTAATGCACGATGCTGCTGCATTCTAACGCTTCAGACTCAGAAAACAGAATTCCGGATTGTCACATTGAGAAGTAGCA
GGAGATCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTACAGAAACTCATACTAAATATGAGGATTGATGCAATTGAA
TGGAAATGAACCATTGAGCGATTGATGCTCTATTAAATCCTGAGAGAGAGAAAATTCAATATTGGAGGGACATTAGCTTAC
GGACACCTTATGCTGCTCAGGAATTATAATACCTTATGCAGGCAATTAAACCTATGGGTCTAACGCCATTGCA
GGGGCAGGAGGAGTGGCATATCAATAGAGTACTTAGGAGTTAAGAATGCT
SEQ ID 180
MKNRDVYI1GFGLRTPIG1KGQFKHYRPELLGAHLLNQIKKIESSENIDS1ICGNTVGTGGNIGRLMTLFSDYESY1PVQQTIDMQCASSSSALFFG
YLKISTGNEKVLVGGIESSSLQPMMRYYAKEDNRNGEYTVAFQSPDSYAETVMLEGAQRVCQKYGFRREMLDKLAFLHKRALTAKQGGYLEEVIL
PMEGMRDQGVRLKETFFQKLPRLMENSPLLTIGNVCLMHAAFLTLQSQKTEFRIVHIVEVAGDPKLSPELVHTATEKLLTEHTKISDYDAIE
WNEPFAAIDALFNHYYPEEREKFNIFFGTLAYGHPYACSGIINILHLMQALKYKNKPMGLTATAGAGVGMAISIEYLGVKNA
SEQ ID 181
ATGACGGATGTTATTCGCTGCAGGCCTAGAACCCCTATCGGTTAGTAGGGAAACAATTGCTAAAGAACAAACAGAAATCTGGAGCAAAG
CTCATCACGCTTACAAAATAAGTATCCAGTCCATTGACCAAGTGTATTGTCATTGCACTAGCTGCTGCACTCAGCTGGTCACTCTCCGCGTTATGCTAAA
ACCCCTGATTCTCATTTAGGAGAATCTGCTCTGCTTACGGTTGATATGCAGTGTGCTCAGCTGGTCACTCAGCTGGTCACTCTCCGCGCCAA
ATCAAGGAGGAGTGGCAAGAACCTTTAGTGGGAGGGATTGAAAGCAGCTCCTTACACCTGAATCGTATATGCTCAGCTGATTGGCGCCAA
GGAGCCTACAAGGAGTGGCTAGTTCTCCAGATAGTATGCCCTTTCGCGTATTGAAAGGGCAGAACGAGTGGCAAGAGAGCATGGCTTACA
AAGGAGTATTGAAATCACTGGACATTGAGAAGTCATCAAAGGCTAGTTATTGCCAGGAGCAAGCCCTGTTAGCTGATCTTATCTAGACCTGTC
GGAGCCAGTGTGATCAAGGTTACGACCGCCTGTCAGAAGGTGTTGTCAGGTTACCCCTATCTAGGAGAAGGTACGTCAGTGTGAGG
AATGCCCTACAACCATGATGCTGCTGCTTACAGCTAAGTACTGTCAGCTTAAACTGATTGATGTTGAGAAGTAGCAGGAGAC
CCACAGCGTAGGCCCTTATGGTATTAAAGGCTAGTCAGTCACTCCTTGGAAAACATGGTCTAGGGATGGCAGATATGACAGCAGTGAATGGAAC
GAAGCCTTGGCGTTATGATGGTCTATTGAAACCCATTATCCAGATTATGGACCGCTATAATATATTGGTGGTGCATTAGCTTATGGTCT
CCCTATGGTGCCTCAGCAGCATTATAATATGCACTTAATGGGGCTTGTAGAGATAAAATGGACGCTATGGAATAGCTGCTATAGCAGCAGCT
GGTGGCCAAGGGTTGCTTTACTAAATATCATAGGAGTTAGTCATGTCAGCAAAAGCTAGAAATTGGGCAAGCAATGCCAAAA
SEQ ID 182
MTDVYIAAGLRTPIGLVGKQFAKEQPEIILGAKLINALQNKPVPIDQVICGNTVGTGGNIGRLMTLHSILGEVSALTVDMQCASAGAALSVGYAK
IKAGMASNLLVGGIESSSLQPESVYASADWRQGAYKVAQFSPDSISPFAMIEGAERVAREHGTKEYLNHWLRSHKQASYQEQALLADLILDLS
GASDQGIRPRLSSKVLSKVPPILGEGHVISAANACLTHAAFLQLSSQPSAKLIDVVEVAGDPQRSPLMVIKASQVLLKHGLADMFTAIEWN
EAFAVIDGLFETHYPDLDRYNIFGGALAYGHPYAGASAIIILHLMRALEIKNGRYGIAAAIAAGQGFAQVLLKYHKEFSHADKARILGKAMPK
SEQ ID 183
ATGCTTGAATCATTGAAAACGATAGTTAAACCAATAGCGATAAAAAGTTATTGATGGTATTACAGGTCAGTTATGGAGAATTCTAACTTA
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CAAAAGCTCTTCTTATTATTGTAACCTTACTCATATAATGAAATACTGCAATTAGAAGGAGTGTGAGTATGCTCTCAACTAGCTGAT
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AAGTTAGTGGAAACAATAGCAAGGAGACTGCGTTAGACAATAAAACTATTACCTCTGCAATATGCTCTGACTCATTACTGGAGGTTA
TATAGAAAGCATCTTAAAGTGTCAAGTAAATTCTCTATGCTGCTGTTAGCTGACCTCAATTATGCTCATGGTACGATGGTCGTGATATCCGAGAAG
CCACAGTATGGAGAAAATCTGTCCTAAAGTGTAGCTGTTAGGATAAAAGAGGAAAGAATTGGTAAACACCGTATAGTATCTGTCCTTCA
AGTGAATATTGTCGCTGGTATTGGTGAACCTGATAGTGGCAATTATGCTTATCTGCTCTGACTCATTACTGGAGGTTAAGCAT
CTCTATTACCTAGATAATGAAAAATAAAACATGCCCTTATATCAAGGATGCACTAGCATTACAAAGAGAGTCAAAGTCAGGACAAGAG
TCACATTGCTGATTGTTTAATTGAAAATCAGATGCAACAGAGTGTGTTGAGTGGTTATGGGAAACATTGAGTGGTTAAGCAT
TATCATATTGATCTAAATTCTTGTGATGCCATCTGGAAAATTGATTATCAACAACTCAAAGACAGTTAGCA
SEQ ID 184
MLESLKTIVKTNSDKLFDGDLQVSYGEFYNLVRQDMAQDNRKHVISTHSLLNQLVRFVSKLCQKALPIICKPNLTHNEISRLEKEVQYAPQLAD
FGVLSGGTADAKLLWRSFTSWSDFFSIQNAYFSVTSNSKLFIQGDFSFCTGMLNLSLLGGTLVVTQKNSVKYWQTLWEKTGVTHLYLLPSYL

KLVEQYSKETALDNKTIITSSQYVSDSLLEGGLYRKHPKVSVKIFYGASELNYWSYDGRDIRDKPQYVGEIVPNAVRIKEGRIFVKTPYSICGLS
SEYCAGDYGELIDGKLYLFGRGGDWNCNSGKLYLPRLIEKIKTCPIKDAVFTKESQSHQESHCCIVILIEQMQQECLKWLSEHFEKKYGFHK
YHIVSKIPIMPSGKIDYQQLKROLA

SEQ ID 185

ATGCTGACAAAGCTAGAATATTGGCAAAGCAATGCCAAATAAAAAGCTATCGTAGCCGATCAGATAAGCTTGACTTATCAAGAGCTATGGCAA
GCGGTTTAAATAAAGGATCAGACAATAAAAGACAGTGTACCATAATCATCAGTCATAGTCGCTATCTTAATCAGTTACTCTCTTTACGAGGA
TTAAAAGAAGGCAGTTGCTCATCATTTCACCCCTAATATCTCAGGTACATTTCAGCAGCAAATAAACACGTCGATGGTAGCCTCTTAAAGA
GCTGATTTGCTGTTAGTGTGAACTGGTAATAGTTGCTATTCTACATGGTAGTTAGTTACTGCAATCTTAACTTAGCATTAGCTCAACTATGGCC
GGGGGATGCTGGTTAAGCAAAGCTGTCTTAAAGCTGGTTAAGCTTATGCAAGCAAAGGAGACTTTGAGCTACCTTACCTTACCGACC
TACCTAAATCGCTTGCTACCTTATTGACTAAGAACACATGACTGCACTCACTTATTGACCTCTTCGCAAATGATATCACAGAAATTACTAAGA
CATTATTACAAAAATTCCTCAGCTGAAATGTCATTCTACGGGCTATGAAATTATCTTATAACGTCGTTAATGGCAGAGCTGCTGTC
AAAATTAGTGGTTGGTAGACAGCCCCTTCTGTGCTATCAGTTCAAGAAAGGAAATTGGTAGAGACTCTTATAGTGTAGAGA
ATGTCACAAACATACAGTGTGCACTAGCAGGGTTAATTAGAGGGCAGACAGATGACTGGGTTAATCACAGGAGA
GTGAAATGCCACCTGCTAGCCTAGTGAACCTGCTCACAAAGGCCAACGTCAAAGAAGGCAACGCTTAAAGATAGGAAAAGGAGAACAGAA
ACCCTAATATTAGTATTAGTGGACTAAGAAGGATTGCTTAGCACCTATTAAAGACTTTAGCTCTTATTTAAACTCTGACAACCTCCAAAG
TACTATCTGTGATTGATTGTTGCTTAAAGATAATGGTAAATTAGTCAGAGTCTTTAAATAAAACACAGTGGCTTAAAGATAATGGAAAAGGAGAACAGAA
SEQ ID 186

MLTKLEYWAKQCPNKKAIADQISLTQELWQAVLKDQTIKDSVPYIISHSRYLNLQLLSLFLRGLKEGSCPIILHPNISGTFQQQJKHVDGELLKK
ADFAVLSSGTGAKLFWRRLSTWTRLDYQNKVFQMTGNNSCLFLHGSFSFTGNNLNLAQWLWAGGCLVLSQKLSLKTWSLWQAKKVSHLYLLPT
YLNRLLPYLTKNNMATHTHLLTSSQMSIQELLRHYYKKFPQLEIVIFYGASELSPITWCNGRAAVKINGLVGQPFDPVSISFKDKEIFVETPVSVEG
MSQPQSVSDLGKMSPALILEGRQDDVNQRGVKCHLPSLVELAHQAPNVKEAHALKIGKGENETLILVVLVLTKKDCLAPIKDFLALYLNSQLPK
YYLVIDCLPLKDNGKINREVLLNKIPKQWLS

SEQ ID 187

ATGTTATCAAAGCAAATCACGATATATTACCGTGAGATTATTAAGTTATTCCAGATGCTAACCTAGCTTAGACTTTACTAATGCTTTGAG
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TTGGCACAAGCTGATCCAAAGAGATTGAAACCTATTTCTAAATTGGGCTTACCGTAATAAGCTGCTTAAATCAATGCGCTAAACAA
TTGATAGAGCATTGATGGAAAAGTCCCCGAACTCGTCAGAGAGCTGAAAGATTGGCTGGCTGGAGGAAACCGCTAACGTCATGAGT
GTTGGATTGGTATTCCGGTTTGCCTAGTACATGTCATCGGATTGTTAAACACACCAGATTGCAAACAGTCGGCTTCTCCACTGGAA
ATTGAGAAAAGAGCTGGAGCTTACCCAGAGAGTGGCTAGCTGCACATCATTGATTTGGCTGCAATTTCATGATTATTGGCTGCAATTGTCATCCTAA
AATCCAAATGCGACCAGTACCCACAACCTTATCATTCTGATAATTAAAG

SEQ ID 188

MLSKAKSRYIIREIIKLFPAKPSLDFTNVFELLVAVMLSAQTTDAVNKVTALFERFPNPLVLAQADPKEIEPYISKIGLYRNKARFLNQCAKQ
LIEHFDFGVKPRTRQELESAGVGRKTANVVMSVGFIPAFADVTHVTRICKHHQICKQSASPLEIEKRVMEVLPPEEWLAHQSMIYFGRAICHPK
NPKCDQYQPLYHFPDNLK

SEQ ID 189

ATGAGAATTGGAAAAGCAAGATTAGCAAAAGCTCTGACCATCATTGGCTAAATGTTCTGAGGCTAAGGGAGAGTTAGACTGGGAAACACCTTT
CAATTGTTGATGCGGTGATTTATCAGCTCAAACGACAGATAAGGCCGTCATAAGGTAACCTCTGGACTATGGCAGTCTTATCCAGAAAATAGAA
GACTTAGCTTCTGCTGAACCTCTGATGTTGAAATGCTCTGAGAACGATTGACTCTATAAAAATAAGGCCAAAATATCATTAAACTGCTCAG
GCTATTGCTGATGATTTAAAGGTCAGTGCACAAACCCACAAAGAGCTGAAAGTTACCGGGTTGGCCGAAAACAGCCAATGCGCTG
GCAGAGGTTATGGTCTCAGCTATTGCGGTTGACTCATGTCAGTGGCTAGGCTCAAAGAGGCTCAATATTCATGCCAGATGCCGATGTCAG
CAGATTGAGCAGATTGATGGCTAAATTCCAAGAAAGATTGGATTATTACTCACCACATGATTGATTGGACGCTACCTGGCC

SEQ ID 190

MRIGKARLAKVLTIIGQMFPEAKGELDWETPFQLLIAVILSAQTTDKAVNKVTPLWQSYPEIEDLAFALSDVENALRTIGLYKNKAKNIKTAQ
AIRDDFKGQVKTHKELESPLPGVGRKTANVVAEVYGVPAIAVDTHVARVSKRLNISSPDADVKQIEADLMAKIPKKDWIITHHRLIFGFRYHCL
KKPKCEICPVQSYCKYYQDTYGKS

SEQ ID 191

ATGAAAGTTTATTGATGTGAGAACTCTTGTGAAAAAATTGGTATTTATGGTAAACGCTTTATGATATCGAAGTTAGGAGACTAAGGAAAGAGCAGACTAGAATTGGAG
GAATTGCAACGCTCTACGATAATGGTCTGATAAGTAGAGATGATTATTAAAAGCAGAACTGATTAAAGAAGAGAGCACAGACTAGAATTGGAG
AAGGAAAATAAAAAA

SEQ ID 192

MKVLFDVQNLKKFGIYVYIGKRLYDIEVMKIELQRLYDNGLISRDDYLKAELILRREHRLELEKENKK

SEQ ID 193

TTGCTAAATCTACTTATGAAAACACTATATGATGTGCAACAATTGCTAAAAACTTGGCATTGGTTACCTGGCAAACGCTTTATGATGTTGAGCTCTATGGCTTATGAG
ATTGAGATTGATGAAGATTGAACTTCAGCGTCTCTATGATAGCGCTTATTGGATAAGAGGATTACTTAAATGCGGAGTTAATTGGCTGACGTGAG
CATAGATTGAAATTGGAAAAAGAAGGA

SEQ ID 194

LLKSTYMKTLVDVQQLLKNFGIFVYLGKRLYDIEMMKIELQRLYDGLLDKRDYLNAELILRREHRLELEKEG

SEQ ID 195

ATGAGTAAGAAATTATGGGATTGACCTCGGAGGAACGACCATAAATTGGTATCTGACGCTTGAGGGAGAGTACAAGAAAATGGCAATT
GAGACCAACTTTAGAAAACCGAAGACATATCGTTCTGATATCGTAACTCTCAAACATCGTTGAGCCTCTATGGATTAACAAAGATGAC
TTTCCTGGTATCGGTGGTTCTCAGGAGCTGTGATAGAAACTAGTAAACAGTAACAGGGCTTTAATCTAAATTGGGCTGATACTCAAGAA
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GCCAATAACCGACGTTGTTCTGTAACCCCTCGAACAGGAGTAGGTGGAGGTATCGCAGATGGTAACCTCATGGTGTGGAGC
GGTGGAGAAAATTGGGATATTGTTGATTCAGGAAATGGATTACGTGACATGGTAAACAGGCTGCCCTGGAGACAGTTGCTCAGCGACA
GGTGGTTAGAGTAGCAGTCACCTCGCAGAACAAATGAGGGCTGCTGCCATTAAAGCAGCGATTGACAACGGTGTACTGTTACAAGTAA
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AATATTGTTAACCTGATTGTTGTTATTGGTGGCGGTCTCAGCAGCAGGTAAATTACGTTAGTCAGCAGCTGGAGAAATACTTGTACATT
GCTTCCCAAGTTAAAGCTCAACTAAATTAGATTGCTGAACTAGGTAATGATGCTGGTATTATTGGTGGAGCAGCTTAGCAACAA
GCAAGT

SEQ ID 196

MSKKLLGIDLGGTTIKFGILTLEGEVQEKWAIEINTLENRHIHSVDESILKHLRLSLYGLTKDDFLGIGMGSQPGAVDRTSKTVTGAFNLNWADTQE
VGSVIEKEVGIFFIDNDANVAALGERWVGAGANNPDVVFVTLGTVGGGVIADGNLIHGVAAGGEIGHMIVDPENGFTCTCGNKGLETVASAT

GVVRVARQLAEQYEGSSAIKAAIDNGDTVTSKDFIAAEDGDKFANSVVERVSRYLGLAAANISNILNPDSVIVGGVSAAGEFLRSRVEKYFVTFAFPQVKKSTKIKIAELGNDAGIIGAASLANQQAS
SEQ ID 197

ATGAGTCAAAAATTACTGGGGATTGATTAGGTGTTACGCCATTAAATTGGAATTTCACAGCAGCAGGAGAACGAGCTCAAGAAAAATGGGCAATTGAGATAATTAGGAGGAGCAACATATTGCTCCATCATCGCTCCATCAAACATCGCTTAGACTTGTATGGTCTAAGCAGTGCTGAC
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GAAAATAACCCAGATGTGCTTCATGACACTTGGAACAGGTGCGGTGGAGGCATTATTGCTGATGGTAATTGCTATGGTCTACACGGCTGTTGGAAACAGTAGCTCAGCAACA
GGGGTGAATCGGCCACATGATTGGTGGAGCAGAAATGGCTTGCTGACTTGTGCTCACACGGCTGTTGGAAACAGTAGCTCAGCAACA
GGAGTTGCTAAAGTGGCACCTTACTGGCAGAACGCTACAGGGATTCAAGCCATCAAAGCAGTATTGACAATGGTGAAGGTGTTACAGTAA
GACATTTCTATGGCGGCTGAAGCAGGGATTCCCTTGCTGATTCTGTGTTGAAAAGGGTTGTTACTACCTTGGCTTGCTCACGAAATATTCC
AATATCTGAATCCAGACTCAGTGGTTATCGTGGGGGTGTCAGCAGCAGGAGAAATTCTACGCTCACGTTGAAATTGCAACTTGGCAATGATGCTGGAATTATCGTGCAGTAGCCTGCTGACAATT
ATCACAAA

SEQ ID 198

MSQKLLGIDLGGTTIKFGILTAAGEVQEKAIEETNILEGGKHIVPDIIASIHKRLDLYGLSSADFVGIGMGS PGAVDRDTNTVGAFLNWKETQE
VGSVVEKELGIPFAIDNDANVAALGERWVGAGENNPDVFMILTGVGGGIADGNLIHGAGGEEIGHMIVEPENGFACTCGSHGCLETVASAT
GVVKVARLLAEAYEGDSAIAKAAIDNGEVTSDIFMAAEAGDSFADSVVEKVGYGLASANISNILNPDSVIVGGVSAAGEFLRSRIEKYFVTFTFPQVRYSTKIKIAELGNDAGIIGAASLARQFITK

SEQ ID 199

ATGGATATGCTGTTATTTCATTGTTATTCTCTGGCTTGTGCTGGCATTGGAAATTATGGAGGGTTCTGTAGGGCAGCTAAATT
TTAGATAACGAGTCTTTCAAAAAGAAATGTCAGGAGACGTTAATTGATATCGAGAACGCTGGTCTTTCATAGAAAGCATATTCTGGAGCA
CGTAACATTCCAGCAACTCAATTAAAGTGCCTTATCGGCTTGCGCAAAGATAACCTGCTCTTATATGACGCAAGCCGTGCAATCTATT
CCAAGGATTGTTGTTACTCAGAAAAGAGGTTTAACTCAACTTACGTGTTAAGGACGGTTCAATTACTGGACGGTAGAGTTAAG

SEQ ID 200

MDMSVILIIVILLAFVAWASWNWYWRVRAAKFLDNEFSQKEMSRGQLIDIREAGAFHRKHILGARNIPASQFKVALSALRKDKPVLLYDASRGQSI
PRIVLLLRKEGFNQLYVVLKDGFNYWTGRVK

SEQ ID 201

ATGTCCTAACATCACACTTCTTATGGTACTCTTGTGGCATTGGTGGTTATTATACATGGAACTATTCTCTTTGAAAATGGCAAAGCAG
GTTGATAACGAGACTTTAAAGACGTGATCGCTCAAGGTCAATTGATTACGAGAGCCAGCGGCTTTAGAACTAAGCATATTAGGAGCT
CGAAATTTCAGCGCAACAATTGATGCTGCTATTAAAGGACTACGCAAGGACAACCTGTTCTTATACGAAAATATGCGTCCCAGTACCGT
GTGCGCTGGTCAAAAACCTTAAAGGCTGTTATGTTAAGGACGTTCAATTACTGGACGGTAGAGTTAAGGAGGTTAATGGTCAAAGTAAACAAACA
ACC

SEQ ID 202

MSPITLILWLLVGIVGYYTWNYFSFRKMAKQVDNETFKDMRQQLIDLREPAAFRTKHILGARNFPAQFDAAIKGLRKDKPVLIYENMRPQYR
VPAVKKLKKAGFEDVYVVLKDGFNYWTGRVK

SEQ ID 203

ATGACAAATTAAAGAACAGATATCGTAACGTTGCGATCATTGCCACGTTGACCACGGTAAACAACTCTCGTTGATGAATTATTAACATCA
CATACTCTGATGAGCTAAAGAGCTTGAAGAACGTCATGGATTCAATTGATATCGAAAAGAACGTTGATTCACCAATTCTGCAAAAATACA
GCCGTAGCATACAACGATGTTGATCAATTATTGACACACTGGTACCGGGACTTTGGTGGTGAAGTGTGGTATTATGAAAATGGTGT
GGTGTGTTAGTCGTTGATGCCAGAGGAACAATGCCACAAACAGTTGTTGAAGAAAGCTTGAACAAAATTCTCAATTGTT
GTTGTAATAAAATTGATAAGCGTCAGCTGTCATCAGAGGTTGTTGATGAAGTCTTGAACATTATTGAGCTCGGTGCTGATGATGATCAA
CTAGATTCCCTGTTATGCTTCAGTATCAATGAAACATCTCAATTGTCAGATGATCCTCAGATCAAGAAAAACATGGCACCGATT
GATACTTACATTGATCACCTTCCAGCCCCAGTTGACAACCTCGGAAGAACCCACTTCAATTCAAGTTCTCTTGTGATTACAATGATTGTTAGGA
CGTATTGGTATTGGACGCTTCCCGGGACTGTCAGGAACTGTTGAGATCAAGTTGAGATCAAGTTACTCTTCAAAAACCTGATGGTACAAC
ACAAACATTGGTTGGACTGTAAGGCTAAAGGAAATCCAAGAGGCTAAAGCGGGTATTGCTTCTGGTATGGAAGATATTCTC
GTTGCTGAGACAGTAACCCGACAGTGCTATTGAAACACTACAGTTTACGTTGATTGACGCCAACACTCAAACGCGTTGATTCTTGT
TCACCAATTGCAAGGTCGCGAAGGTAATGGATTACGTCAGCTAAGGTTGAGAACGCTTTAGCAGAATTACAACAGACGGTTCTTGT
GACCCAACAGATTGCCAGATAATGGACGGTTCAGGGCGTGAGAATTACATTATCTATGAAACATGCCGCGTGAGGGATATGAA
CTTCAAGTATCAGCTCAGAACGTTATCATCAAAGAAATTGATGGTGTCAATGCGAGCCGTTGAGCGTGTCAATTGATACTCCAGAAGAATAT
CAGGGTGTATTCTCAAAGTGTGAGAGCTAAAGGCTAAAGGCTATTGCTGAGATGCTGAGGTTGATCTGAGTACACTTGGACCA
CCTGACGTTGTTGATTCAACAGAGTTCTTCAATTGACAGTGGTGTGAGTATGCTGAGTACACTTGGACCA
GTTCAAGGAAATTGGTGTGCTCATGTTGCTGTTCTGGTTCTATTGAAATTGTAAGGCAACTACATATTGCAATTGCTGAGGTT
GGGACTACTTGTAAATCCAGGTATAAGGTTATGAGGAAATGATTGTTGTTGAGAATTCTGCTGAGTAAATGACCTCGGAGTCAATT
GCTAAACAAATGACAATGTCGTTCAGCAACTAAAGATCAAACCTGCACTCATCAAGGCCCTGTTACTTGTAGAGGTCACTTGAATT
TTAGCAGATGATGAGTACATGGAAGTAACCTCTGAGTCTATTGCTCTCGTAAACAAATTAAAGCAGCAGTGACAAGCTAAT
AAAAAAATCAGCTAA

SEQ ID 204

MTNLRTDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELEERAMDSNDIEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKVD
GVVLVVDAYEGTMPQTRFVLKKALEQNLIPVVVNKIDKPSARPSEVDEVLELFIELGADDQDFPVVYASAINGTSSMSDDPSDQEKTMAPIF
DTIHDHIPAPVDNSEPPLQFQVSLLDYNDFVGRIGIGRVRGTVKVDQVTLSKLDGTTKNFRVTKLFGFLGERIKEIQA
KAGDLIAVSGMEDIF VGETVPTDAIEPLPVLRIDEPTLQMFVLVNNSPFAGREGKWITSRKVERLIAELQTDVSLRVDPDSDPKWTVSGRGLHLSIL
IETMRREGYE LQVSRPEVIKEIDGVQCEPFERVQIDTPEEYQGAIQOSLSERKGMDLMQMVGNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQGEIGGRHRGALVSIENGKATTYSIMRIEERGTIFVNPGIEVYEGMIVGENSRNDLGVNITTAKQMTNVRSATKDQTA
VICKPRILTEESLEF
LADDEYMEVTPESTRILRKQILNKAARDKANKKKKSAE

SEQ ID 205

AIGACTAACCTAACGATATCGTAACGTTAGGGATTATTGCCACGTTGACCACGGAAAACAACACTTGTAGATGAATTATTAACATCC
CATACTCTGATGAGCTAAAGAGCTTCAAGAGCGCTGGCATGGATTCCAATGACCTTGAAGAAACGCTGGATTACAATCCTTGC
GCACTGAGCTATAACGATGTTGCTATTACATCATGGATACCCAGGACAGCGGGACTTCGGTGGTGAAGTGTGAGTCA
GGGGTTGTTCTGTTGCTGAGCTAACGAGGAACAATGCCAGGCCAGCGCTTGTGTTGAAGTGTGAGTCA
GTGTTGAACAAGATTGACAACACCTTCAGCTGTCAGCAGAAGTTGAGATGAAGTGTGAGTCA
TTGGAATTCTCCAGTTGTTACGCTATTGGAACATCATCATTACAGATGACCTCTGCTGAGCAGAGCATA
TTGGCACCGATCTT
GATACGATTATTGATCATATTCCAGGCCAGTTGATAATTGAGATGAGCCTTGCAATTCAAGTGTGTC
CGTATCGGTATCGCTGTTCTCGGTTACTGTTAAAGTGGTGAACAGTA
CTTCAAAACTGATGGTACCACTAAAACCTCCGTT
ACAAAACCTGTTGTTCTCGGTTGGAAACGTCGTTGAAATTCAAGAAGCTA
AAAGCAGCTGACTTGCTGTTCAAGTGTGAGTGAAGATATCTT

GTTGGGAAACCATTACACCAACTGACTGTGAGCTCTGCCAATTCTCGTATTGATGAGCCAACACTTCAGATGACTTCTGGTCAATAAC
TCTCCTTTGCAGGTCGTAAGGTAATGGATCACGTACGTAAGGTTGAAGAACGTCCTTCTAGCAGAACAGACGTCGTCACCTCGTGT
GACCCAAACAGATTCGCCAGATAAAATGGACGGTTCAAGGGCGTGAGAACATTGCAATTATCCTCATGAAACCAGCGCTGAAGGCTATGAA
CTTCAAGTATCACGTCAGAAGTTATCATCAAAGAACATTGATGGTGTCAAATGTGAACCGTTGAGCGTGTCAAATTGATACACCAAGAACATT
CAGGGTGCAATCCTCAGTCTTCAAGACGTAAGGGGATATGCTTGATATGCCAGATGGTTGTAATGTCAAACGCCCTTGATTTCTGATT
CCTGCAGCTGGTTGATGGTTATTCAACAGAGTTCTTCATGACACGTCGATATGGTATCATGAAATCATCTTTGATCAGTATCACCCTGGTT
GTTCAAGGAGAACATGGTGGCCGTCATCGTGGTCTGGTTCTATTGAAATGGGAAACGACATATTCAATCATGCGTATTGAGAACAGCT
GAAACTATCTTGTCAATCCAGGTACAGAAGTTAACAGGGATGATTGTTGGTGAACACTCAGTGATAACGACCTGGTGTAAACATTACAACAA
GCTAAGCAAATGACAAATGTCCGTTACCGCACTAAAGATCAAACACTGCGATTATCAAGACGCCCTGATCTTCAACGCTTGAAGAACATTAGATT
TTGAATGACGACGAAATACATGGAAGTAAACGCCAGAATCTATCCGCTTGCCTAAACAAATCTGAAATAAGCTGCGCTGATAAAGCTAATAAAAG
AAAAAATCAGCGAA

SEQ ID 206

MTNLNRNDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELQERAMDSNDLEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKMDV
GVVLVVVDAYEGTMPQTRFVLKKALEQNLIPIVVVNKIDKPSARPAEVVDEVLELFIELGADDEQLEFPVVYASAINGTSSLSDDPADQEHTMAPIF
DTIIDHIPAPVNDNSEPLOFQVSSLIDYDFVGRIGIGRVRFRGTVKVGQVTLSKLDGTTKNFRVTKLFGFFGLERREIQAAGDLIAVSGMEDIF
VGETITPTDCVEALPILRIDEPTLQMTFLVNNNSPFLAGREWKSRTKVEERLAAEQLTDVSLRVDPDSDPKWTVSGRGELHLSILITEMRREGYE
LQVSREPIVIIKEIDGVKCEPFERVOJTDPEEYQAGAIQSLSERKGDMQDLMQMVNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQEIGGGRHRLGALVSIENGKATTYSIMRIEERGTIVFVNPGTEVYEGMIVGENSRDNDLGVNITTAKQMTNVRSATKDQTAVIKTPRILTLLESLEF
LNDDEYMEVTPESTRLRKOILNKAARDKANKKKKSAE

SEQ ID 207

ATGGGACGAGTAATGAAAACAATAAACACATTGAAAATAAAAAGTTTAGCTTGGTTAGCAGCTGGAGAAGCTGCTGCACGTTGTT
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TTAGAAAACAATCCCTGTTGACTGAAGTGAAATTAGCATCTTAGTTCTAGAATCTCAGCTAATAGGTATTACAGGCTCTAACCGGAAACG
ACAAACGACAACAGTGTGGAGCTTAAATGCTGGAGGTCAAGAGGTTTGTAGCTGGAAATTACGGCTTCTAGTGAAGTGTTCAG
GCTCGCAATGATAAAGATACTCTAGTTATGGAATTCAAGTCTTCTAGCTAATGGGAGTTAAGGAATTCTGCTCTCATATGCTCTAGTGAAGTGTGCT
TTAATGCCAACTCATTAGATTATCATGGGTCTTTGAAGATTATGTTGCTGCAAATGGAAATTACGGCTTCTACTACCGAAAAAGTTGATGGTGCT
GTACTTAATTTCATCAAGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAACTGTTCTTCTACTACCGAAAAAGTTGATGGTGCT
TACGTACAAGACAAGCAACTTTCTATAAAGGGGAGAATTATGTCAGTAGATGACATTGGTGTCCCAGGAAGCCATAACGTAGAGAATGCTCTA
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CTCGGTAAGGTTCTATGGTTATGTTCTATAACGACAGCAAGTCACAACTAATATTGGCAACTCAAAAGCATTATCTGGCTTGTAAATACCTAA
GTTATCCTAATTGTCAGGAGGTTCTGATCGCGGTAACTGAGTTGATGAACGATACCTACTGGACTTAAACATATGGTGTGTTAGGGAA
TCGGCATCTCGAGTAAAACGTGCTGCACAAAAGCAGGAGTAACTTATAGCGATGCTTGTAGAGATGCGGTACATAAGCTTATGAGGTG
GCACAAACAGGGCGATGTTATCTTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTGCAAGTCCGTGGTGTGATTCAATTGATAC
TTGCAAGTCTTAGAGGAGAG

SEQ ID 208

MGVRVMKTITTFENKKVLVGLARSGEAAARLLAALKGAIVTVDNGKPFDENPTAQSLLEEGIKVVCGSHPLELLDEDFCYCMIKNPGIPYNNPVMVKA
LEKQIPVLTVEVELAYLVSSESQSLIGITGSNGKTTTTMIAEVLNAGGQRGLLAGNIGHFPAEEVVAQAAANDKDTLVMELSSFQLMGVKEFRPHTIAVITN
LMPTFLHDYHGSFEDYVAAKWNIQNMQNSSDFLVLFNQGISKELAKTTKATIVPFSSTTEKVGDAYVQDKQLFYKGEMIMSVDDIGVPGSHNVENAL
ATIAVAKLAGISNQVIRETLSNSFGGVKXHRLQSLGKVGHSIFYNDKSSTNLATQKALSGFDNTKVILIAQGLDGRNEFDLIPDITGLKHMVVLGE
SASRVKRAAQKAGVTYSDALDVRDAVKAYEVAQQGDVILLSPANASWDMYKNFEVRGDEFIDTFSLRGE

SEQ ID 209

ATGAAAGTGTAAAGTAATTTCAAAACAAAAAATATTAATATTGGGTTAGCCAAATGGCGAAGCAGCAGCAAAATATTGACCAAATCTGGT
GCTTAGTGAATGACTGTAATGATAGTAAACCATTTGACCAAAATCAGCGCACAGCCTGTTGGAAGAGGGGATAAGTCATTGTTGAGGCCAC
CCAGTAGAATTATAGATGAGAACCTTGAGTACATGGTTAAAACCCTGGATTCTTATGATAATCTATGTTAAACGCGCCCTTGCAAAAGGA
ATTCCCCTATCTGACTGAGTAGAATTGGCTTATTCTGATCTGAAGGCCCTATTATCGGGATTACAGGATCAAACGGGAAGACAACCACAGCA
ATATGGTCCGATTTGAATGCTGGGGCAATCTGCACACTCTATCTGGAAACATTGGTTATCTGCTCTAAAGGTGTCCTAAAGGCAATTGCT
GGTAGTACTTTGGTAGGGATTGTCCTCTTTCATTAAGTGGAGTGAATGCTTTGCCTCATATTGCTGTCACTAAATTATTAATGCCACT
CACCTGGACTATCATGGCAGTTTGAGGATTATGTTGCTGCTAAATGGATGATTCAAGCTCAGATGACAGAACTCAGACTACCTTATTAAATGCT
AATCAAGAGATTCAGCAACTCTAGCTAAGACCACAAAGCAACAGTGAATTCTTTCAACTCAAAGTGGTTGATGGACCTTATCTGAAGGAG
GGAATACTCTATTAAAGAACAGGGATTATAGCTGCAACTGACTTAGGTGCCCAGGTAGCCACAACATTGAAAATGCCCTAGCAACTATTGCA
GTTGCCAAGTTATCTGTTAGTGTATTATGCCCCAGTGCCTTTCACATTGGAGGCCTAAACATGTTGCAACGGGTTGGTCAAATC
AAAGATATACCTCTACAATGACAGTAAGTCACCAAACTATTATGAGCTCCTTACAAAAGCTTATCAGGTGTTGATAACAGTCGCTGATTGATT
GCTGGCGGTCTAGATGCGCAATGAATTGACGATTGGTGCAGACCTTCTAGGACTTAAGCAGATGATTATTTGGAGAATCCGCAAGCGT
ATGAAGCAGCTCTAACAAAGCAGAGGCTCTTATCTTGAAGCTAGAAATGTCAGGCAAAACAGGCTGCTTTAAGCTGCCAAACAGGCG
GATACTATCTGCTTAGCCCAGCCAATGCTAGCTGGATATGATCTTAATTGGAGGTCTGGGATGAAATTGGCAACCTTGGTATTGTTA
AGAGGGAGATGCC

SEQ ID 210

MKVISNFQNKKILILGLAKSGEAAKLLTALKALVTVNDSKPFDQNPAAQALLEEGIKVICGSHPVELLDENFEYMVKNPGIPYDNPVMVKRALAKEIPIFTEVELAYFVSSEAPIIGITGSNGKTTTTMIAVLNAGGQSALLSCNIGYPASKVVKQKAIGDTLWMELOSSFQLVGVNAFRPHIAVITNLMPHTLDYHGSFEDYVAAKWM1QAOATGKESDYLILNANQEIATSLAKTTKATV1PFSTQKVGVDYLGKDILYFKEQAI1AATDLGVPGVSHNTENALATIAVAKLSGIADD1TAQCLSHFGGGVKHLR1QRVGQ1KIDTFYNDKSNTN1LATQKALSGFDNSRL1I1AGGLDGRNEFDDLPVDDLLGLKQMI1LGEASERMKRAANKAEVSYLEARNVAEATELAFKLAQTGDTILLSPANASWDMPNFEVRGDEFLATFDCLRGDA

SEQ ID 211

ATGGGGAAAAAAATTGTTTACAGGGGGTAGGTCACTAACACTAAACCTAATTAAATCCCCAATTATCAAAGATGGTGGGA
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CGTCGCTATTTCATGGCAAAATATTGGTAGATGTCCTTAAGTAGGGGGTTGGCCTTCATCAATCGATTGCTATTATTGCTAAACTAGACCCAA
GCCCTTATTCTAAAAGGGGGATTGGTTCAGTACCTCCTGAGTAGCTGCAGCCTATTAAAGTCTCTTTTGTTCATGAATCGATTATCA
ATGGGGTAGCAAAATAGATTGCTTATAAATTGGCAGTATTATGTTAGCTTAAAGATTAAATCAAAACTAACGATATTGCT
GCTGTAACAAAAGTCATGGATTGTAAGGACTCGTTGAAAATACTGACTTAACTAGTATAAAAAGAGCCTTCGATCCAACCTAAAGACCTTACTA
TTTATTGGAGGATCAGCAGGTGCAAAAGTATTCAATGATTTATTACTCAACACCTGAGCTGGAGAAAAATATAATGTTATCAATTTCAGGC
GATTCTCTCAATCGATTGAAGAAGAACCTTATCGCGTGGATTATGTTACAGACCTTATCAGCCTTAATGAATTAGCAGATGTGGTGT
ACACGAGGGCTTAATACTATTGGATTAGTAGCTATGAAAAACTTCATCTTATTACCCCTTCTGGACGCTGAAGCGAGCCGAGGTGACCAA
TTAGAGAAATGCTCTTATTGAGAAAAGGGCTACGCATTGCGAGTTACCAAGATCTGAATTAAACATAAAATACACTTGAGAAACAGATAAATT
TTAATTCCTAACACTGAGGTTACGAAAAAAACATGTCACAATCATCTGAAATTAAACATCTCAAGATGAATTTCATCAATTATTGATGATATG
GCAAAAGTAACAAAAGGA

SEQ ID 212

MGKKIVFTGGGTGVTNLNLLIPKFIKGWEVHYIGDKNGIEHEQINQSGLDITFHSIATGKLRRYFSWQNMLDVFKVGVLQSIIAIACKLRPQ
ALFSKGGFVSVPPVVAARLLKVPVFVHESDLSMGLANKIAKYFATIMYTTFEQSVDLKIYTKHIGAVTVMDCKSFENIDLTSIKEAFDPNLKTL
FIGGSAGAKVFNDFITQTPELEEKYNVINISGDSSLNRKKNLYRVDYVTDLYQPLMNLADEVTRGGSNTLFELVAMKHLIIPLGREASRGDQ
LENAAYFEKGYALQLPESLNINTLEKQINLLISNSEYENMSQSSEIKSDEFYQLLIIDDMAKVTKG

SEQ ID 213

TTTATCAAGGACGGTTGGAAGTACATTATATTGGTATAAAAATGGCATTGAAACATACAGAAAATTGAAAAGTCAGGCCCTGACGTGACCTTCTAT
GCTATCGGCACAGGCAAGCTTAGACGCTATTTCATGGCAAATCTAGCTGATGTTTAAGGTTGCACTTGGCCCTCACAGTCCTCTTATT
GTTGCCAACGCTTCGCCCTAAGGCCCTTTTCCAAAGGTTGCTCAGTACCGCCAGTTGCTGCTGTAATTGCTGTTAAACAGTCCTT
ATTCAATGAAATCAGATCGGCTAATGGGACTAGCAAAACAAGATTGCTCACAAATTGCAACTTACCATGTATACTTGTAGCAGGAAGACCAGTTG
TCTAAAGTTAACACCTTGAGGGCTGACAAAGTTCTCAAGATGCCAACAAATGCTGAAACTCAGTTAGAGGCCGTTGAAAGAGTATT
AGTAGAGACTAAAACCCCTTGTATTGCTGGTCCGGCAGGGCGCATGTTTAATCAGTTTATTAGTGTATCAGAATTGAAAGCAACGT
TATAATATCATCAATATTACAGGAGACCCCTCACCTTAATGAAATTGAGTTCTCATCTGTATCGAGTAGATTATGTTACCGATCTACCAACCTTTG
ATGGCGATGGCTGACCTGTAGTGACAAGAGGGGCTCTAATACACTTTTGAGCTACTGGCAATGGCTAAGCTACACCTCATCGTCTCTGGT
AAAGAAGCTAGCCGTGGCGATCAGTTAGAAAATGCCACTTATTGAGAAGAGGGGCTACGCTAAACAATTACAGGAACCTGATTAACTTGCAT
AATTGATCAGGCAATGGCTGATTGTTGAAACATCAGGCTGATTAGGAGCTACTATGTTGCAACTAAGGAGATTCAAGGACTCAGGACTCTT
TATGACCTTTGAGAGCTGATATTAGCTCCGATTAGGAGAAG

SEQ ID 214

LFKRRCLMPKKILFTGGGTGVTNLNLLIPKFIKGWEVHYIGDKNGIEHTEIEKSGLDVTFHAIATGKLRRYFSWQNMLDVFKVALGLLQSLF
VIKLRPQALFSKGGFVSVPPVVAARLLKVPVFVHESDLSMGLANKIAKYFATTMYTTFEQQEDQLSKVKHLGAVTVFKDANQMPESTQLEAVKEYF
SRDLKTLIFIGGSAGAHVNQFISDHPELKQRYNIINITGDPHNLSSHLYRVDYVTDLYQPLMAMADLUVTRGGSNTLFELLAMAKLHLIVPLG
KEASRGDQLENATYFEKRGYAKLQEPDLTLHNFDQAMADLFEHQADYEATMLATKEIQSPDFFYDLLRADISSAIKEK

SEQ ID 215

ATGCCATAAGAAGAAATCAGATACCCCAGAAAAAGAAGTTGCTTAACGGAATGGCAAAGCGTAACCTTGAATTTTAAAAACGCAAAGAA
GATGAGAAGAACAAAACCTTAAACGAAAGTTACGCTTAGATAAAAGAAGTAAATTAAATTTCTCTGAAGAACCTCAAATACTACT
AAAATTAAGAAGCTTCATTTCAAAGGTTCAAGACCTAAGATTGAAAGGAAACAGAAAAAAAGAAAAAAAGTACAGCTTACGCTTACCTTAA
CGCATTAGAACCTGACCTATATTGAGTACGCTTCTAGTTAGTCTCTACTAATCTTTAGTAAGCAGGAAACAAATACA
GTTAGTGGAAATCAGCATACACCTGATGATATTGAGATAAGAAACGAATATTCAAAACAGGATTATTCTTTCTTAATTAAACATAAA
GCTATTGAAACAACGTTAGCTGAGAAGATGTTGGTAAAAACAGCTCAGATGACTTATCAATTCCAAATAAGTTCTATATTCAAGTCAAGAA
AATAAGATTATTGATATGCACATACAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAGGCTGATCCTGAAATAGTTAGCAGAGCTACCA
AAGCACTTCAACAATTAAACCTTGATAAGGAAGATAGTATTAAAGCTTAAAGGCTTACGCTGATTTAAAGTGGATT
CAGGTGATAAGTTAGCTGATTCTAAACGACACCTGACCTCTGCTGTTAGATATGCACTGAAAGTATTAGAATACCAATTACTAA
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ATTGAATCAACCCCTGTTAAGCAGAAGATACAAAAAAATCAACTGATAAACACAAACAAACAGTCAAGGCTGAGGTTGCGGAAATAGTCAAGGA
CAAACAAATAACTCAAATCAACAAAGCACAGATAGCAACAGGACACCTAACCTCAAAATGTTAAT

SEQ ID 216

MPKKKSDTPEKEEVVLTEWQKRNLLEFLKKRKEDEEEQKRINEKLRLDKRSKLMNISSPEEPQNTTKIKKLHFPKISRPKIEKKQKEKIVNSLAKTN
RIRTAPIFVVAFLVILVSFVLLTPFSKQKTITVSGNQHPTDDILIEKTNIQKNDYFFSLIFKHATEQRLLAEDVVWVKAQMTYQFPNKFHQVQE
NKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLIKDLKALDPDLISEIQLVSLADSKTPDLLLLDMHDGNSIRIPLSKF
KERLPFYQIKKNLKEPSIVDMEVGVYTTNTTESTPVKAEDTKNSTDKTQTQNGQVAENSQGQNNNTNQQGQOIAEQAPNPQNVN

SEQ ID 217

ATGGCAAAAGATAAAGAGAAACAAAGTGTGACAAGCTCGTTGACAGAGTGGAAAAGCGTAACATTGAAATTAAAGAAAAGCAGCAA
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CAAATCGCTTCAAAATCCTGCTGTTCTTTGGGGCGCTCTACTCATGGCGGTGCTATTGTTATGATCACTCTTATAGCAA
GAGTTTCTGTAAGAGGAAACATCAAACGAACCTGACGAAATTATCAAAGCTAGCAAAGCATCTGACTATTGTTAACGCTGTTA
TCGCCCTGCTAGTGTGACGACCGATTCTGACTATTCCATGGGTGAAATGTCATCTCTTACCAATTCTTATACACTTTCTATTAA
GTTATTGAAATTGAAATCATCGTTATGCAAGGTGAAAACGGTTTACGCTTATTTGGAGATGGAAAACGTTGAGCACAAGGTGAGGGCATCA
GAACATCGGAAATCTTCTGATTCTTAATTAAAGATGAGAAGCGATCACACAGTGTAGTAAAGCATAACGACATACCTTAAAGTACT
AAGAATACGTCAGTGTCTGTCAGGAAATTGCAAAACGAGCAGCGGATTACTTACTTGTGAAATGTCAGGTTAGAGTACCGCAG
TCACAACTCAGATTGAACTTCTTATTGAAAGGAACTTGTGAAATTGAGTATGTTAGGATATGGAAGTGGGAAATTACTACA
ACACAGGAGATTGAAACCTGAAAGTTCTCTTACGCTGAAACAAACGAGCTGATAAAAGAAGGAGATAAGCCTGGTAACATCAGGAACAG
ACAGACAATGATTGAGAAACGCCAGCAAATCAGAGTAGTCCTCAGCAAACACCCAGAAACCGTCCTGAAACAGGCCATGGC

SEQ ID 218

MAKDKEKOSDDKLVLTEWQKRNLIEFLKKKKQQAEKKLKEKLLSDKKAQQQAQNASEAVELKTDEKTDQSBEIESETTSKPKKTKVRQPKESAT
QIAFQKSLPVLLGALLMAVSIFMITYPSKKKEFVSRGNHQTMLDELIKASKVKASDYWLTTSPQYERPLRITIPWVKSVLHSYQFPNHFDFN
VIEFEIAYAQVENGQFILENGKRVDKVRASELPKSFLILNLKDEKAIQQLVQLTLPKLKVKNIKSVLANSKTTADLLIIEMHGDGVVRVPQ
SQLTLKLPYQKLKNLENDSIVDMEVGIVYTTQEIEQPEVPLTPEQNAADKEGDKPGEHQEQTDNDSETPANQSSPQQTTPSPETVLEQAHG

SEQ ID 219

ATGGCTAGAAATGGCTTTTTACTGGTTGGATATAGGAACAAGCTCGATTAAAGTTAGTTAGTGTGAGAATTATTGCAAATGAAATGAAATGTAATT
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GAGGAGAAAGCAGGCATCACCATTGACAAAATCAATGTTGGATTACAGCAATCTCTCAAATTGAAACCAACTCAAGGAATGATTCTGTTCCCT
AATGAATCAAAGAAATTAGGATGAAGATGTCGAAAGTGTGTTAAATCAGCATTGACTAAAAGCATTACTCTCTGAAAGAGAAGTTATTCTATTG
ATTCCGCTTGAATTCTGAGATGGTTCCAAGGGATTAGAGACCCCTAGAGGGATGATGGGATTCGCTTGTGAGATGCGTGGTTCTATCTTACT
GGACCAACAACTATCCTTCTATAATTCTCGTAAACGTTGAGCAGGTTGAGGAGCTGAGGTTGAGGTTGCTAACAAATTGGAAACTAGAGTTAA
TCAGTTCTAACGAGGTGAGCTGGTCAACTGTCATTGATATTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGTTGCTAACAAATTGGAA
CAATATACTAATTATTCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTT
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AGCTATTTGCAAAATTATTGAGGAGCTGCAAAATTGAGAACATGTCAAACAAAGACTGGGTTAGAGGCGTTACTTGTTAGGTTAATTCGAGCGTTA
GGTATTATTCTGAGGAGCTGCAAAATTGAGGAGCTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCT
CAAGTAGGTTACGCAATCCTAACTGTTGCTAATGTTAGTGTAGGAAATGTCAGGAGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCTGAGGTTGAGGAGCT
GTAACTGGCAGCAAATGCTAAGACATAACAGTCGACTTGTGATTATAAGGAAAACAAATACAATGTCGACAATGCTTATTCTGAGCGTTA
ACCTCTTCTATGGAAGATTCTAATTGAGAACATCCGAGCAAGAGAAAACGCTCAAGGCTACTGAGGCTAAAGCTAATATTGAGCGCATH
AGAGGAATTGGAGAGTATGTTGAC

SEQ ID 220

MARNGFFTGLDIGTSSIKVLVAEFTIANEMNVIGVSVPSSGVKDGIIDIEAAATAIKEAVQAEKAGITIDKINVGLPANLQIPTQGMIPVPM
NESKEIKDEDEVSVKSALTKSITPEREVISLIPLEFIVDGFQGIRDPRGMMGIRLEMRLIYTGPTTILHNLRKTVERAGIKVEHVVIAPLALAK
SVLNEGEREFGATVIDMGGGQTTVASMRNQELQYTNIYSEGSVDTKDISKVLRTTVEIAEALKFNFGQANVVEEASTSDTVQVNVVGNEEPVITE
SYLSQIISGRIRQILEHVVKQDLGRGRLLDLPGGIILVGGGAIMPVVEVAQQIFGTRVKLVHPNQVGIRNPMSNFANVISIVDYVGMMSEVDIIAQHA
VTGDEMRLRKPVDFYKEKTNTMSTMPYSEPLTSMEDSNLEPIRARENAQEPTPEPKANIGERIRGIFGSMFD

SEQ ID 221

TTGGACATTGGAACAGCTCGATAAAAGTTTAGTAGCAGAATTATTCGGTGAGATGAACGTCAITGGTGTAGTAATGTCAGTACCCGC
GTAAAAGATGGCATAATAATCGATATAGAGGCAGCTGCCACTCAAACACTGCCGTTAGACAAGCAGAAGAAAAGCAGGGATGACAATTGAA
AAGGTTAATGTTGGGCTACCGCAAACCTTCTCAAATTGAACCAACACAAGGAATGATTCTGTCCAGTGTAGCTAAAGAGATAAAAGATGAG
GATTTGATAGCGTTGTTAAATCGGCTTAAACAAAAGTATCACACCAAGCAGAGGGTTATCTCTTAGTTCAGAAGAGTTCAAGCAGTCACTGGGATGCC
TTTCAGGGCATTCTGAGATCCACGTGATGAGGGATTAGAGATGCGCGGGCTTATTTACTGACCAAGCAGCATTTCATACTCG
CGTAAAAGCTAGGAGCAGGCTTAAAGTGAACACATCATTATTCCTCGTAGTGTGCTTAAACAGGATTTAAACGAAGGTTAGCGCAG
TTTGGAGCTACTGTAATTGATATGGAGGTGGACAGACAATGTCGCTTCTATGCGAGCACAAGAATTGCAAGTATACCAATAATATGCGCAGGC
GGCGAACATACATTAAAGATATAAAAGTATTAAAACGCTTTGCTTATTGCAAGAACACTTAAGTTAATTTGGTCAAGCGAGATACTCA
GAAGCTAGTATAACTGAAACAGTAAAGTGTGAGGGTAGTGTAGGAGCTGAGAGGCTGTTGAGGTAACTGAACGTTATTTATCTGAAATTATTCAGCG
CGTATTGTCATATTTAGATCGTGTGAAGCAAGATTGGAAAGAGGTGTTACTAGACTTACCAAGGAGGCTTGTGTTGATGGGGCGGTGCA
ATCATGCGCTGGAGTGTAGAAATTGCAAGAAATCTTGGAGTAGTAACTGTCAGGCTTACAGTCAAGCTGGTATTAGAAATCCAATGTT
TCAAACGTTATCAGTTGGTAGAATATGTTGATGATGTCAGGTTAGCAGCTTCAAGGAGAAGAAACTTTGCGACGC
AAGCCTATCGATTGAGGCAAGAATCTTATTACAGGATTATGATGATTCAAGAACGACCAATGGCTATGAAACAAAGCAGTCA
CAAACAGCATATGATTCAAGCTTCAAGTGTGATCTAACAAAAAATTTCAGAACGTTCTGGCATATTGGAGTAGTTGAT
SEQ ID 222

LDIGTSSIKVLVAEFIGEMNVIGVSVPSTGVKDGIIDIEAAATAIKTAVEQAEEKAGMTIEKVNVGLPANLQIPTQGMIPVPSSESKEIKDE
DVDSVVKSLTKSITPEREVISLVEEFIVDGFQGIRDPRGMMGIRLEMRLIYTGPTTILHNLRKTVERAGIKVENIIISPLAMAKTILNEGERE
FGATVIDMGGGQTTVASMRNQELQYTNIYEGGEYITKDISKVLKTSIAIAEALKFNFGQAEISEASITETVKVDVVGSEEPVETERYLSEIISA
RIRHILDRVVKQDLERGRLLDLPGGIILVGGGAIMPVVEIAQEIFFGTVKLHVPNQVGIRNPMSFSNVISLVEYVGMMSEVDLAQTAVSGEELLRR
KPIDFSGQESYLPDYDDSSRPESTIGYEQQASQTAYDSQVPSDPKQKISERVRGIFGSMFD

SEQ ID 223

ATGGTATTTCTATTGATACAGCATCAGTACAAGGTGCAAGTTAAAGTTGGTGTGGAGGGCGGTGAAACGCTATTAAACCGCATGATT
GACAAAGGTGTCGCTGGCGTTGAGTTATTGCAAGCAAATACTGATATTCAAGCCTTAAGTAGCTCAAAGCTGAAACTGTCACTTGGTCA
AAATTAACTCGCGGACTTGGTGCAGGAGACAACCTGAAGTTGGTGTAAAGCAGCTGAAGAAAGTGAAGAAGTTTAAAGCAGACTTACTGGC
GCTGATATGGTATTTATCACAGCAGGTATGGGGCGGTCTGGTACAGGTGCGGCTCCAGTTATTGCAAGTGTATTGCAAGAGTTAGGAGCACTT
ACAGTAGCGGTCACTCACACGCTCTTGGCTTGGAGGTAATAAACGTTCTAAGTTCGCTATCGAAGGTTATTCAAGAATTAAGAGAACAGTTGAT
ACAGTGTCTATCATTCAAATAATACTTCTTGAATTTGAGATAAGAAGACACCATTGCTGAGCTTGTGAAAGCAGATAATGTTTACGT
CAAGGTGTCATAGCTTACGGATTGTTACTACCCAGGTTAATAACCTTGTACTTGAAGTAAACAGGTTATTGCAAGTGTGAAACAGTTGAT
GCACTGATGGGATTTGGTATCGGTTCTGGTGGAGAACGACTTACTGAGCTGTCGAAAAGCAACTTATTGCAACACAGGTT
GGACCGAGAACGCTTATTGTCATGTTACCGGGCGGTATGGTATGACACTTACTGAGCAGGAGAACGATGTTGCAACAGGCTACGAGCAGGTT
AAAGGTGTCATATTGGTAGGTACTCTAATTGACATGGATATGAAAGACGAAATCCGCTAACAGGTTGCAACAGGTTACGTAAGAGATAAA
ACTAATCAAGTATCTGGTTTACAACATCAGCTCCAACATCAAGCACCTTCAGAACGCTCAAAGTACTTCAAACTTTGATCGTGTGGC
AACTTGTATGACAGAGTCTCGCGAAATGCCACTAACAAACATCAGCTCATGCAACAAACAGTTCTGCTTTGGTAAATTGGAC
CTTCGCTGTGATAATTTCACGTCGACAGAAGGTGAACTTGTGATAGCAAGTTGTCTATGTCACGTTTCAAGAAATGATGATATGGATGAA
CTTGAAACACCTTCAATTCTTAAACCGT

SEQ ID 224

MVFSFDTASVQGAVIKVIGVGGGGNAINRMIDEVGAVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAESEEVLTALTG
ADMVFITAGMGGGSGTGAAPVIARIASKLGLALTVAITRPFGEFGNKRNSFAIEGIQELRQVDTLLIISNNNLLEIVDKKTPLEALSEADNVLR
QGVQGITDLITNPGLINLDFADVKTVMANKGNALMGIGIGSGGERITEAARKAIYSPLETTIDGAEDVIVNVVTGGLDMTLEAEAEASEIIVGQAAG
KGVNIWLGTSIDDMKDIEIRTVVATGVRKDKNQVSGFTTSAPTNQAPSERQSTSNSNFDRGNFDMTESREMPQQNQPHAQNQQQSSAFGNWD
LRRDNISRTEGELDSKLSMSTFSENDDMDELETPPFKNR

SEQ ID 225

ATGGCATTTCATTTGATACTGCATCAATTCAAGGTGCAATTATAAAAGTAATTGGAGTCGGCGGAGGGCGGAAATGCCATTAAATCGTATGATT
GATGAAGGGTGTGCTGGTGTGAGTTCATCGCAGCAAACACAGACATTCAAGGCTTAAGCTCATCAAAGCTGAAACGTTATTCAACTAGGCCCT
AAATTAACTCGGGACTTGGTGTGGAGGACAACCTGAAGTAGGAGCTAAAGCTGCTGAAGAAGCGAAGAAAGTAAACAGAAGCTTACAGGA
GCGGACATGGTATTTTACTGCGGTATGGGTGGCTCTGGGACAGGGGCTGCACCGGTTATTGCTGTATCGCTAAAGTTGGAGCTTGC
ACAGTAGCTGTTACTCGCCGTTGGTTGAAGGTAACAAACGTTGAATTGGTGTATTGAAGGTTATCGAAGAACACTGTAATGTTTACGC
ACTTTGTTAATTCTAAATAACCTTCTTGAAGGTTGAAGGTTGAAGGTTATTGAAGGTTATAGAACGACTTACTGAGCTGATAATGTTTACGC
CAGGGAGTCAAGGATAACCGACTTAAATTACTAGTCTGGCTTATCATCTGATTTGCCACGTTGAAAGAACAGTTATGGCAAAATAAGGGAAT
GCCTTGATGGGATTGGTCTGGAGAAGAGGCCATTGTTGAGGCCGGCGTAAGGCAATCTATTACCCCTATTGAAACAGACTATTGAT
GGTGCACAGGTTATTGTCAGGAGCTCTGCACACTGACACTTACAGAAGGCTCTGAAAGAACGCTCTGAAATTGGGCAAGCTGCTGGT
CAAGGCTTAACATTGGTAGGAAACATTTGATGACTATGAAAGATGACATCTGGTGTACTGGTAGCAGCTGGCAAGAACGAA
GCCAACAAAGTTTCACTGGTAGGACTTACCCAAACACAGCGCAGAACAGGCTGGTGCACATGATCAGATCAAGGAA
CAGTCGGTCAACACAGGGTTGATCGTCGCTCAAATTGTTGACATGGGGAGTCGGCAGAGATAACCAAGTGCACAAAGGTTATTCTAAT
CATATCAAACATCAAGGTTCTGCTTTGGAAATTGGGATTGAGACGTTGATAATATTCTCGTCAAACAGAACAGGTTGAAATTGATAACCATCTTAAAT
ATGTCACGTTCTCAGCTAACAGTGCAGTGTGATGAAATTAGAAACGCCATTCTTTAAACCGT

SEQ ID 226

MAFSFDTASIQGAIKIVIGVGGGGNAINRMIDEVGAVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAESEEVLTALTG
ADMVFITAGMGGGSGTGAAPVIARIASKLGLALTVAITRPFGEFGNKRNSFAIEGIQELRQVDTLLIISNNNLLEIVDKKTPLEALSEADNVLR
QGVQGITDLITNPGLINLDFADVKTVMANKGNALMGIGIGSGGERIVEAARKAIYSPLETTIDGAEDVIVNVVTGGLDMTLEAEAEASEIIVGQAAG
KGVNIWLGTSIDDMKDIEIRTVVATGVRQEKAEQVSGFRQRTFTQTNQVAGAQYASDQAKQSVPQPGFDRRSNFDFDMGESREIPSAQKVISN
HNQNQGSAGFWLRRDNISRTEGELDHNLNMSTFSANDDSDELETPPFKNR

SEQ ID 227

ATGATGAATTCAAAGAAAATAAAACAGCGATTGGACAATGTTAGTAATAGCACTAAAAGCAGGTGCGCTCATGAATCAGTCATATCGTA
GCTGTAACAAATATGTTACTGTCACAAACAGAAGCGCTTATTAGAACAGGTGTTAATCATATCGGTAAGGTTGAAATTCTGAA
AAATATCAAGCATTAAAGATGAAAGCTTACATGGCATCTCATTGGTAGTTACACGTCGAAAGTAAAGATGTCATTAATTATGTTGATT
TTTCATGCTTGTGTTAGATTCTGTTAGTTAGCAGCTGAGGATTCAAAACATGCTCAAAACTAATTAAAGTTCTACAGTTAATATCACCGAGAA
GACAGTAAGCATGGTTTACTATTGAGCAAATAGATGATGCACTGAACCTTAATTCTCGGTACGATAAAATTGAACTTATCGGCATCATGACTATG

GCTCCCTTAAAGCAACTAAAGAGGAAATATCATCAATTGGAGAGACTGAGAGTCTTAGGAAAAGGCTTCAAGCTAGGAACATAGAACGAATG
CCGTTTACAGAATTAAGCATGGCATGAGTAGAGATTATGCTATTCAAATGGATCACATTGTAGGATAGGAACATTCATTCTTAA
SEQ ID 228
MMNLQENKTAIFDNVSKLALKGRAHESVHIVAVTKYVNCQTTEALIRTGVNHIGENRVDKFLEKYQALKDEKLWHLIGSLQRKVKDVINYVDY
FHALDSVKAEEIQKHAQKLIKCFLVNISREDSKHGFTIEQIDDALNLISRYDKIELIGIMTMPLKATKEEISSIFEETESLRKRLQARNIERM
PFTELSMGMSRDYDIAIQNGSTFVRIGTSFFK
SEQ ID 229
ATGGATTACTGACAAATAAAAAGAAAATTTTGAGACTATCCGTTATCTACAGAGGCAGCAAATAGGACTAATGATAGTGTTCAGTTATTGCT
GTAACAAAATATGTGGATAGTACAATTGCAAGGTAGCTTATCGAACAGCAGGAATTGAGCACATTGCCAAAACCGTGTGATAAATTCTTGAAG
TATGATGCTTAAAGTATATGCCAGTAAAGTGGCATTAAATTGCTACCTTACAACGCTGTAAGGAAAGTTATCAATTATGTGATTATT
CACGCTCTAGATTCTGTGAGATTAGCTTGGAAATCAACAAGAGCTGACCACCTGTGAAGTGTCTTACAAGTAAATATTCTAAGAAGAG
AGTAAACATGGTTAACATTCTGAGATTGATGAAGCAGTGGAGAAATAGGTAAGATGGAGAAAGATACTAGTTAGTGTGTTAACAGTATGGC
CCAGCAAATGCCAGTAAAGAAAGTATTATAACTATTTCGACAAGCAAATCAATTAGAAAAACTGCAAGTTAAAAAAAGAAAGAATATGGC
TTTACAGAATTGAGCATGGCATGAGTAACGATTCCAATTGCTATTCAAGAAGGCTCAACTTTATTGGATTGGTAGAGCTTCTTCAC
SEQ ID 230
MDLLTNKKKIFETIRLSTEANRTNDSVIAVTKYVDDSTIAGQLIEAGIEHIAENRVDKFLEKYDALKYMPVKWHILGTLQRKVKEVINYVDY
HALDSVRLAEINKRADHPVKCFLQVNISKEESKHGFNISEIDEAIGEIGKMEKIQLVGLMTMAPANASKESIITIFRQANQLRKNLQLKKRNMP
PTELSMGMSNDYPIAIQEGSTFIRIGRAFFH
SEQ ID 231
ATGGAGGGAATATGGCATTAAAAGATAGATTTGACAAACTGACGATGTAAGTGAAGAATGAGTACACGAAGTACAA
GAGAGAACTTCAGTGAAAGAGATTCCAGAGCAGTACAGCACAGGAAGCTTCTAGCGTAGTCATATGACTAACCTCGCAGAGGAAGAGATGATT
GGTAGTCGAGAGAACTTACCTATGATCCTAATCGTCAGAGAGACAAAGGGTACAGAGAGACATGCTTATCAGCAAGCTACTCTAGGGTT
CAAATAAAAGACTCAGTCAGAACAGAGAACAGTAACAATTGCTCTGAAGTATCCCGTAAGTATGAGGATGACAAAGAAATTGTTGATT
CTTATCGTTATGAATGTGCTTGATTGATTTCAATATATGCTGATGCGCAAGCACGACGTTGCTGGATTATATTGATGGTCAAGTAGAGTA
TTATATGGTCATTACAAAAGGTTGGAGTTCAATGTTCTATTAAACACCAGCCAATGTTATGGTGTGATATTGAGGAGATGAATATTCCAAGACT
GGTCAAGAGACGAGTTTGATTTGATATGAAGAGACGA
SEQ ID 232
MEGNMALRKDFDKIISYFDTDDVSENEVHEVQERTSVQRDSRAATAQEASQRSHMTNSAEEEMIGSRPRTYTDPNRQERQRVQRDNAYQQATPRV
QNQDSVRQREQVTIALKYPRKYEDAQEIVDLLIVNECVLIDFQYMLDAQARRCLDYIDGASRVLYGSLQKGSSMFLTPANVMVDIEEMNIPKT
QQETSFDPMKRR
SEQ ID 233
ATGGAGAATAAGATGGCTTTAAAGATACATTTAACAGATGATTCTTATTTGACACGGATGAGGTTAACGAAGTTGAAGAAGATGTTGAGCA
TCAACTGATAACGTTATTCAGATCACAACAATCAGTCAGAGCAAGTAGTCTAGCATCCAAAACAAGAACCTAGAAACAATCAGTACAACAAGATCAT
CAAGCGAGATCCAAGAACAGAACAGGTACAATGCATCCAAAACATGGCACTTCTGAACGCTTATTATCAGCAGTCTAGCCAAAAGAACGGCCAT
GAAATGGTGCAGAGAACAAAACGGATGAGCACTCTAGTATTGCAAAATGCCGTGAGCAGTACAAACATCAACTTGTAGCATCAAACAAACTATT
GCCCTAAAGTATCTCGTAAATATGAGGATGCTCAAGAAATTGTTGATCTTAAATAGTTAATGAATGCGTTGATTGATTTCTAGTTATGCTA
GATGCTCAGGCTAGACGGTGTAGATTGATGGTCTAGTAAAGTGTCTATGGTAGCTTACAAAAGGTCGGCTTCAATGACTTACTG
GCTCCGTCAAATGTTACCGTCAATATAGAACAGATGACTATCCCACATACTACACAGATATTGGCTTGTGATATTGAGGAGATGAATATTCCAAGCG
SEQ ID 234
MENKMAFKDTFNKMISYFDTDEVNEVEEDVAASTDNVIPSQQSVRASSHPKQEQPRNNHVQOQDHQARSQEQTRSQMHPKHTSERYYQQSQPKEGH
EMVDRRKRMSSTSSIANRREQYQQSTCSDQTTIALKYPRKYEDAQEIVDLLIVNECVLIDFQFMLDAQARRCLDFIDGASKVLYGSLQKGSSMYLL
APSNVSVNIEEMTIPHTTQD1GFDPMKRR
SEQ ID 235
ATGACGTTAGATGATAATTATCAGCATTTGACACAGAACAGACTGCGTTATCCATAAAAATGACCAATTAGCTCAATATGTCAAAACACCTAT
TCGTTTATTACCACTGAATTCTAAATCCTAGGAAATTAAAATACTCGAAAGTGTCTAGAGAGGGCGAGGTAGTCATTACCTTCTGGTCAG
TATTTCAGAAATATGTTAAAGTAAATAGCAGGAAATCTAGTTAGTATGGCTTAACTTCTAGCTTAACTTCTAGCTTAACTTCTAGCTTAACTTCTAGCT
AATGCTAAATTAAATCACCTTACCCATGCTAAATTATGGAACTTTACTGTAATTACTTAGGGTAAACGATCAATTAGGGATATCTAGTT
GAAGAAGGCTGTGCTCAGGTTGGTGTAGTCAATGACAATCACCTTGTTCATTCAAGTTACAAAATTGGAACTGCTAGTGTACAATTAGCT
GAAGTTCCTGTCAAACCTCTAACAGAACAGTCAAAACTAACTGTTATTGCTTCAAGTCTGTTAGTAAACGGTAAATTGCAACCGTCATCGAGTTCTGAACAAATT
GTAGAGGGGGATTGATTAGTGTAGAGGATATGGTCATTACGTTGAACCTAACCTAGGGTTAACTAAAATATAATTAGAAGTAA
GACAAAATGATACATAAC
SEQ ID 236
MTLDDIYQHFREPEYAFIHKIDHLAQYVENTYSFITTEFLNPREFKILESVLERRGSHYYTSGQYFQTEYVKVIIAPPEYQQLDMADFNLSLIEIKY
NAKFNLTHAKIMGTLLNYLGVKRSILGDLIVEEGCAQVLVDSQMTNHLVHSVTKIGTASVQLAEVPLSKLLTPQD1QKLTIVIASSRLDKILAT
ILKISRTQSTKLIADKVKVNYATVNRVSEQLVEGDLISVRGYGRFTLNHNGLTKNQKYKLEVDKMIH
SEQ ID 237
ATGGTTAGTCAGTAAAGATTTATCAGCATTTACCAAGAACAGATATCCTTTATTGATAGAATGTCAGTATGATTAATAGAGTTGAAGGATTAC
TATCCTTTAGAAGTACTGAGTTTAAATCCTAGGAAAGTCAGTGTGATTAAAAGTTGATGCTTAAACAGATCTAAAATGTTCTATCAACA
GATTACTACCAAGCGAATATGGTCGTGCTATTGCACTCTGGTACTATGACTTAGAACAAAGTCAATTAGCTTAACTGTTAGAGATAAGT
TATCAGGCAAAGTTAACTGAGTGTGACACATAGTCATAATTAGGAACTTTAGGAACTTAATTAATGAAATTAGGAGTAAAGCGAATTATTGAGGATGTT
GTTGAAATGGGATATGCCAGCTCATGATTAAGCAGGAGATTGGATTATTTAGGAAACATTAACTAAAGTCAACTTCTAGTTCTAGTTCTAGTT
AGAGAAGTAACTTGTAGTTAACTAGGCTATTGATAACAGCCAGACCCCTGGATATTCTAGTTCTAGTTCTAGTTCTAGTT
ACTATCTAAAAAAATCTGAACGCAAGTTAGCATTAAATTGAAGCAAATAAGATTAAGGTTAACTATCGAGTTCTAATAAGCTCAGATAAT
CTAGTCATAGGGGATATGGTGTAGTACAGAGGTACGGCGTTACTCTTCTAGCAGATAATGGAGTGACCAAATGGCAACATGGCAAACAAAAATAACA
CTAAGTAAATGATACATAAC
SEQ ID 238
MVSHSKIIYQHFQEEYPFIDRMSDMINRVEDYVLLLEVTEFLNPREFMILKSLIALTDLKMFVSTDYYPSEYGRVIIAPGYYDLEQSDFQIALVEIS
YQAKFNQLTHSQQILGTLINELGVKRNLFGDVFVEMGYAQLMIKRELLDYFLGTITKIAKTSVLRREVNFQDQLIRSIDNSQTLIDLVSSFRLDGVVA
TILKKSRTQSTKLIADKVKVNYATVNRVSEQLVEGDLISVRGYGRFTLNHNGLTKNQKYKLEVDKMIH
SEQ ID 239
ATGCCACTTACAGCACTTGAAGATAAAGATAAAACATTTCATCAAATTCGCGGTTATAGCGAAGAAGAGTTAATGAATTAGAGATTGTT
GTTGACGATTACGAGGACTTGTAGAGCTGAGTCAATCGTAGAGAGCAATACATTAAGGATTAGAGAGAAAATCGCTACTTCACAGCAAATGAAG
GAATCGTTAAGTCAATCAGTTATTAGCTCAAGAAACTGCTGAGCGTGTGAAATTTCAGCACAGGATGAAGCATCTAACCTAATGGGAAAGCT
ACATTGATGCTCAACATTAAATTGATGAGGCTAATTAAAGCAAATCAAATCTTCGAGATGCGACAGATGATGCTAAGCGTGTGCTATAGAGA

ACAGAACATTGAAACGTCAATCACGTGTTCCACCAACGTTGCTTCTGAGTTAGAAGGGCAGCTAAAATTAGCTAACTCATCTGCTTGGGAAGAATTTAGTGTGAAACCAACAGCTATTCTCAAATTCGTATGCTCTTCTGAGTTAGTGTGAAAAAGTCTTGTGATGAAGATGTGCTTACCGTGGTGGATGACACTGAGTCATTGATGCTACTCGTCAATTCTCACCAGATGAAATTGGAAGAAATTACAGCGTCGTGTTAGAAGAAGTACAACAAACAACTTGAAGAGTCAGGTTATTAGATACTAATAATTCCAATGGAAAGAACCGATCAATTAGGTGAAACTCAAACTTAAATTAAATTGAAGAT

SEQ. 20

SEQ ID 241

ATGGCACTTACAACGCTAGAAATTAAAGATAAAAATTCTTAAAGCAAAATTCCGAGGATACTGTGAAGAAGAAGTCAGAACGATTTCTTAAATGTT
GTTGATGATTACGAAGCTCTTGACCTTAAACGCTGATAACGAAAGCAAGAATTAAAGATCTTGAAGAAAATTATCTTACTTTGTAAATGAAAGAAAA
GAGTCACTTAGCCAGTCTGAACTCTAGCTCAAGAACAGCTGAAAGCAGCCTAAATCGCGAGCAACAAATTGGTTAGTAAAGCG
ACTTATGATGCTGCAAGCATTATTAGATGAATCTAAAGGCAATTCAAATGTTGCCTGATGCAACTGATGAGGCTAACGAGTTGGCATTGAA
ACAGAAGAACAAAGCTCAACACGGTGTGTCACCAACGTTAATCTCATCTATTGAGTCACAATTAAAGCTTATCAAATTCACCTGAATGGGAT
GAACGTCTACAACCGACTGCAATCTTCAAAATTCTGACGATGCTTTAAGGAAGTCGTGAAGACCGTCTTAATGAAGACATTCTGAATCT
GATGATAGTGCCTTTGATGCAACACGTCAGTTACTCCAGAAGAGTTAGAAGAAATTGCAACGTCGTGATGAAAGCAATAAGGAGTTAGAG
GCTTACCAACTTGACTCTCAATCTGATTCTACGACTGAGCCAGAGGTAATCTCAGTGAACACAAACGTTAAATTAAATATC

SEO ID 242

MLQ ID 212
MALLTLEIKDKTFKTKFRGYCEEVEVNEFLDIVVDDYEALVRKNRDNEARIKDLEEKLSYFDEMKESSLQSIVILAQETAEKVKATANAEATNLVSKA
TYDAQHLLDESKAKANQMLRDAYDEAKRVIAETEELKRQTRVFHQRLISSIESQLSLSNSPEWDELLQPTAIYLQNSDDAFKEVVKTVLNEDIPES
DDSAFEDATROFTPSEELELORRVDESNKELEAYQLDSQSDSTTEPEVNLSETQTFKLNI

SEQ ID 243

SEQ ID 243
ATGAAATTAAAAGAAACCTTGAATTAGGACAAACAGCTTTCCAATGCGTCAGGGCTTCAAATAAGGAACCTCAATGGCAAGAACATGGGAT
CAACGTGACATTATAAAAACGTCAAGCATTGAATGAGGAAACAGCCTTCACCTCATGACGGACCTCCATGCTAATGGGAATATTGAT
GTAAGGACATGCACTAAATAAATTTCGAAAGACATTATGTCAGCTTCAAATCAATGTCAGGTTTCGAGCTCCTTATGTCCTGGTGGGATACT
CATGGACTCCATTGAGCAAGTATTAGCTAAAAAAGGGGTTAACGCTAAAGGAATGGACTTGGCTGAATACCTGAAATGTCGTGATTATGCT
CTCAGCCAAGTGTGACAACAAACGTGATGATTAACTCTGGCGTTCTGCCGATGGGAAATCCTTATATTACACTAACACAGATTATGAA
GCAGATCAAGTACGTGTTCTGGTGTATGGCAGATAAAGGATATATCTCGTGTGCTAACACCAGTGTATTGGTCATGGTCATCAGAGTCTGCC
CTTGTGAGGCTGAAATGCAATTATGCAATTGATTGACTACCTACTATGCCAATAAGTTAAAGATGGTAAGGGAAATTCTTGATACAGAT
ACCTATATCGCTTGGCACGACAACACCAATTACTGTAACAGCTTACGCCGTTAACAGTAGGACCAGATATGGAGTATGTTGATGTTGACCA
GTAGGTAGTGTGAGCGTAAATACCTCTTCAGAGGGTCTTGTAGATGTCGCTGCTAAGTTGGCTGGAAAATTTGAAATTGTGACTCATCAC
ACTGGTAAAGAACCTTAATCACATTGTCAGAACATCCATGGGATACAGAAGTAGAAGAGTGTGGTTATCTTGGAGACATGTTACACAGATTCT
GGTACAGTATTGTCACACGGCTCTGGTTTGTGAGATGACTAACCTGGTGTATTGCTAATGGACTTGTGTTAGTTACCGTAGATAGT
CGTGGTTGATGATGGAAAATGCTGGCTGTTGATTTGAAGGTCAATTCTATGCCAACACCCACTTGGTAAAGAAAATGGGAGATCTTCTT
TAGGCCGAGGTTATCAACACTCATATCATTGACTGGCTGACGAAAAGCCAATCATTTGGCTGCGTTCCACATGGTTGCCTCTGTT
TTAGGAAATTCTCGTCAAGAACATTCTCGTGAATTGAAAAGCAATTCCAAACCTGAGTGGGTTAAAAAACGCTTTATAACATGATCCGTGACCGT
GGCAGCTGGTAATCTACGTCACCGTCTGGGGTGTCCACTTCAATTGTCAGAACAGATGGTACAGTATCATGACAAAAGAAGTGA
GATCACGGTCAAGGTTATTGCTGAATACGGCTCAATCGTGGTGGCAACGTGATGCTAAGGACCTTCTACCCAGCAGGTTAACTCATCCAGGT
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CTTCCATCCAGCAGATCTTATCTTGAAGGTTCTGATCAATACCGTGGTGGTCAACTCATCACTAATACATCAGTGTGTTAATGGTCA
GCTCCATACAAAGCAGCTTATCTCAAGGTTCTGACTCTGAGTGGAAAGGATGCTAAATCTCAATGGGTTACATTCTCCAGTGT
GTTGAAAACAAATTCTGGTGGCAGAAATCTTGGCTCTGTGGTAACCTCTGGTACTCAAGTAATGATGTTGCTATTCAATGGATATCTTAAACAA
ACATCAGAAACATTCTGGTCAAGGATCAGGAATACATTGCGTTCTGATTGCAAAACTTCCGATTAACTCTAAACAAAGATGCACTGAGTGCCTATGAA
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TATAAGGTGCTTAACCTGTAACAGTTGATCTACGATTTACCTGATTGGTCAAGGATGTGGTTACATTGAGCGCTAACAGTCC
GAACGACCTGCTATGCAAACCTGTTCTATGATATTAGTAAACTTACAAACCTTGTACTCCGATTCTACACATACTGCTGAAGAACATTG
TCATACCTCGAACATGAGGGAGGAGGAGTGTGTCATTAGCAGAAATGCCCTGTCACAGACATTCTGGTCAAGAAGAAATTCTTGAAGATGG
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ATTATGCTAGTCAAGAAGTGGAAACAGTGTATTAAACAGCTTAAAGCGTATTCGACTCTGATGTTGCTCACAATTAAACATTGCTGATGAA
CGAGCACAAACAGCTGACTCAGTACATTGAGGTGTTGCACTTACTGTTGAAACACGCTGAAGGTGAAGTCTGCGAACGCTCACGCCGTTATTGAT
CCAACCACAAAGATGCGCTGATGGTGTAGCTGTTGTGATGCTAGTGCAGCAATTATTGAGCAATATTATCTGAAAGCAGTAGCTCAAGGTTT
GAAGCT

SEQ ID 244

MKLKETNLGQTAFFPMRAGLPNKEPWQEAWDQADIYKKRQALNEGKPAFHLDGPPYANGNIHVGHALNKISKDIIVRSKSMSGFRAPYVPGWDT
HGLPIEQVLAKKGVKRKEMDLAEYLEMCRDYALSQVDKQRDFKRLGVSADWENPYITLTLPDYEADQVRVFGAMADKGYIYRGAKVYVWSSES
LAABAEIYEYHDIDSTSILYANKVKDGKGILDDTDYIVVVTTTPFTVTASRGLTVGPDMEEVVVVVPGSERKYLLAEVLVDSLAAKFGWENFEIVTHH
TGKELNHIVTEHPWDTEVEELVILGDHVTTDSTGTIVHTAPGFGEEDYNGVIANGLDGVVTVDSRGLMMENAGPDFEGQFYDKVTPLVKEKLGDL
LASEVINHSYPFDWRTRKKPJIWRAFPWFASVSKFRQEELDIEKTNQFWGKKRLLYNMIRDRGDWVSIQRANGVLPPIFYAEDGTAIMTKETV
DHVADLFAAEYGSIVWWQRDAKDLLPAGYTHPGSPNGLFKEKTDIMDVWFDGSNSWGNVMNARENLISYPADLYLEGSQDQRGWFVNSSLITSVAVN
GHPYAKVLSQGFVLDGKEMCSKSLGNTLPSDVEKQFGAEIIRLWVTSVDSNDVRISMIDILKQTSETYRKIRNTRFLIANTSDFNPKPQDAV
AYEYLGAVIDRYMTIKFNQVVDTINKAYAAAYDFMAIYKA VVNFTVWLDSAFLDFAKDVVYIEAANSPERRMQTVFYDILVVLTKLLTIPILPHTAE
EWSYLEHEEEFVQALEMPVAQTFSGQEEILEEWSAFMLTRTQAQKALEEARNAKIGKSLEAHLTIYASQEVKTLLTALNSDIALLIVSQLTIADE
ADKPADSVSFEGVAFTVHAEGEVCERSRRIDPTTKMRSGVAVCDASAAIIHQYYPEAVAQGFEA

SEO ID 245

ATGAAATTAAAAGAGACACTTAATCTAGGAAAAACAGGCCCTTCCAATGCCGCAGGTCTCTAATAAGAGGCCAATGGCAAGCAGCTGGGAA
CAAGCAGAGCTTACAAAAAACGTCAGAATTGAATGCAAGGTTAGCCCTTCATCTCATGATGGACCTCCATCGCTAACGCAATATTCAC
GTTGGGCATGCCCTTAATAAAATTCAAAGATATCATTGCGCTTAAGTCATGTCGGCTTCAAGCGCCTTATGTACCTGGTGGGACACA
CACGGCCCTTCAATCGAACAAAGTCTGGCTAACAGGAAGAACGTAAGGGATGGATTAGCAGAATACCTTGAGATGTCGCTAACATACGCT
TTAAGTCAGGTTGATAAACAGCGAGATGATTCAAACGGTTAGGTGTTCCGAGACTGGGAAATCCTTATGTCATTTGGACCCACAGTTGAA
GCTGATCAAATTGCTGTTTGGAGCGATGCGTAAAAAGTTACATCTACGTTAGGTGCTAAACCTGTTATTGGTCATGGTCTTCAGAACATGGCC
TTGGCAGAGGCTGAAATTGAATACCATGACATCGATTCAACCTCTTATACTACGCCAATAAGTTAAAGTGGATAAGGTTACCTTGATTA
ACGTTATCGTTGTTGGACACACACCATTACCGTTACAGCATCAGCGGTTGACTGTTGGCTCTGATATTGGATTATCTGTGTTGAAACCT
GCTGGTCTAGACGGCTCATATGTTGCGCAGAGGTCTTTGGTAGCCCTTGCTGGAAAATTGGCTGGAAATCTTGTGAAACTTTAGCTAGGCCAT
AAAGGAGCTGATTAGAGTACATTGTCACAGAACACCCATGGGAACTGACCGTAGAGAATTGGTTACCTGGTGCACATGTTACCCCTGAGTCA
GGGACAGGAGTGTCCACACAGCACCAGGTTGGTGAGGATGACTACAATGTTGGGACAAAATACAAACTGGAAAGTGTGACTGTTGATGAA
CGTGGCTTAATGATGAAAAATGCAAGGTCCAGATTCCACGGACAATTATAACAAGGTAACGCCGATTGTCATTGATAAAACTTGTTGATCTTAA

TTGGCACAAGAAGTGATCAATCACTCTTACCCATTGACTGGCGGACGAAAAACCAATCATGGCGTGTGACCGCAATGGTTGCTCTGTTCTGCTGTTCTGCTGAAAGTGAATTTGGATGAAATTGAAAAAAACACCTTCTCATGGGTGAAACACGCCCTTACAATATGATTGATGTCGACTGGCGACTGGGTTATTTCTCGTCAACGTCTTGGGAGTTCCGCTTCTCATCTCTCATGGCGAAGATGGCACAGCTATTATGACTAAAGAAGTGACA GATCATGTGGGTTGATTGTCAGAAAATGGATCAATCATGGTGGCAAAAGAAGCTAAAGACCTATTACAGAGGGCTTCACTCATCCAGGG TCACCAATGGCGAGTTAACAAAGAAACTGATATCATGGACGTTGGTGTGACTCTGGITCTCTGGGAATGGAGGTGATGAAATACTAAAGAAAAT CTTTCTATCCAGCGGATCTATACTTAGAAGGCTGACCAGTATCGTGGTGGTCAATTCACTCTTAATTACATCTGTGGCTTTAATGGGCAT GCTCCATATAAGGCTATTTATCGCAAGGCTTGTCTTGATGGTAAGGGAAAAATGTCATAATCAAAGGAATATCATTTCTCTAATGAT GTGGCTAACAAATATGGCAGATATTCTGACTTTGGTAGCTCTGTGGATACCGATAATGATGTCGGTGTCTATGGAGATCCTGGTCAA GTCTCTGAAACTTACCGTAAACCGTAAACCCCTCGCTTCTTGATTGCTAAATACATCTGATTCAACCCCTGCTACGGATAACAGTACTGTTATGCA GATTAGTAGGAACTGTTGATAAGTACATGACAATTGCTTTAACTCAGTTGGTACACGATTACTGACGCTTATGAGCGTTATGACTTTATGGCTT TACAAAGCAGTGGTGAACCTTGTGTTACGGTGTGATTATCAGCCTTCTATCTGATTGTTGCTAAAGACGTTGCTATATTGAAGCTGCAATAGCTTA GAACGCTCTGCATGCAAGCAGTCTCTCATGATATCTGGTAAAGATTCAACAGTATTGACGCAATCTGGCTTCAACACTACTGAAGAAAATCTGG TCTTATCTAGAGCATGACTCAGAACAGTCAATTGCTTCAATTGGCAGAAATGCCCTGGCAGAAACCTCTCGGCTCAAGAGGATAATTAGAAGCTGG TCAGCTTCTCATGACTTGCCTACTCAAGCTAAAAGCTTGGAGAAGCGCGAAATGCTAAAGATTATCGGTAATCATGGAAGCCCATTGACC ATCTACGCTAGTGAAGAAGTGAACACCTTATTGACTGCTTACAGCGATATTGCTTGTGATCGTCTCAATTAAACCATTGCTGACTTG GCAGATGCCCTGCGATGCACTGGCATTGAGGTGTTGCTTATAGTAGAACATGCCATAGGTGAAGTTGTGAGCGTTACGTGCAATGAC CCAACTACTCGCATGCCCTCTTACAATGCACTTGCTGATCACAGCGCTAAATCATTGAAAGAAAATTCCAGAAGCTGTGGCTGAAGGGTT GAAGAGAGTGGCAA

SEQ ID 246

MKLKETLNGLKTAFFPMRAGLPNKEPQWQAAWEQAELEYKKRQELNAGKPAFLHDGPPYANGNIHVGHALNKISKDIIIVRSKSMSGFQAPYVPGWDT HGLPIEVLAKOGIKRKEMDLAEYLEMCRQYALSOVDKQRDFKRLGVSAWDENPYVTLDPEQFEADQIRVFGAMAEGYIYRGAKPVYWSWSESA LAEAEIEYHDIDSTSILYYANKVKDGKGLDTNTYIVVWTTPTFTVTSRGLTVGPMDYLVVKPAGSDRQYVVAEGLLDSLAKFGWESFETFLASH KGADLEYIVTEHPWDTDVVEELVILGDHVTLESHTGIVHTAPGFGEEDDYNGVTKYKLEVAVTVDERGLMMENAGPDFHGQFYNKVTPIVIDKLGDLL LAQEVINHSYPFDWRTPKPIIWRAVPOWASFDRQDILDEIEKTTFHPSWGETRLYNMIRDGDWVISRQRAWGVPLPIFYAEDGTAIMTKEV DHVADLFQENGSIWWQKEAKDLLPEGFTHPGSPNGEFTKETDIMDVWFDGSWSWNGVMNTKENLSYPADLYLEGSDQYRGWFNSSLITSVAVNHF APYKAILSQGFVLGDKGKBEKMSKSGNIIISPNVAKQYGADILRLWVASVTDNDVRVSDFNPLIYQVSETYRKRNTLRFIANTSDFNPATDTVAYA DLGTVDKYMTIVFNQLVATITDAYERYDFMAIYKAVVNFTVTDLSAFYLDFAKVVYIEAANSLERRRMQTFVYDILVKITKLLPILPHTTEEIW SYLEHSEAFVQLAEMPAETFSQAQEDILEAWSAFMTLRTQAKALEEARNAKIGKSLEAHNTIYASEEVKTLLTALDSDIALLLIVSQLTIADL ADAPADAVAFEGVAFIVEHAIGEVCRSRRIDPTTRMRSYNAFVCDHSAKIIEENFPEAEGAEEFESGK

SEQ ID 247

ATGAGACTAATTAATACAACCACTAGTCAGTCACCCAGAACTCATCAAAACAGCTAAACAGATGCAAAATTAGTGAAGTCTATTAGCTGAGTATACTCAGCTGGC AACACCCGATGTCGTTTACAAAGCACCTAACATTAGAATTATTAACTTCAACAAATATCGTCTATCAAAGATGAAGAATTAGAAGCTATT CGTAGTCTCTTAAAGCTAAAATAGATCAATCTATTATTCAAGAGCAGATGAAACACTCCATACTGCCAAGTAAATTGAAATTTCATAT CCAACACAGCA

SEQ ID 248

MRLINTTSSHPELVRNQLQNTDAKLVEVYSAGNTDVVFKAQKHYELLISNKYRAIKDEELEAIREFFLKRKIDQSIQEQMKSLSHTAKLIEISY PTTA

SEQ ID 249

ATGAGACTCATCAATACCACTAGCAGTCACCCAGAACTCATCAAAACAGCTAAACAGATGCAAAACCCGATGCCTATTAGTCAGTATACTCAGCAGGA AATACAGATGTCATTTTACCCAAGCACAAACATTAGAACTACTTATTCAAATAACCGTGCATCAAGGAGGATGAACTGATATCATT CGCGAATTTTTAAACGTTAAATTGATCCTAAATTGTTATTCCCTGGACATCAAACACTTCACACGAATAACCTTATTGAAATTTCATTT CAAACTCTGTA

SEQ ID 250

MRLINTTSSHPELIKNLKNTDAYLVEVYSAGNTDVIFTQAPKHYELLISNKYRAIKEDELDIIREFFLKRKIDPKIVIPGQSKTLHTNNLIEISF QTSV

SEQ ID 251

ATGACTAATCCTACTTCCGGTAAAAATAGATAATGTAACATAGGTCAAGGATTTGGTGTCTATGCTATTATCCAAATCCAACCTCATGATAAA ATTATTTAGTACAGGCACCTAATGGCTTGGTTCTCCAGGTGGGGAAATTGAAGAAAATCACCTAGAAGCTTAACTCGTGTAGTTA ATTGAAGAAATTAGGTTATTCCGCAACAATTGGCCTACTATGGTCAAGCTGATGAATATTCTACTCTAGACACCGTGATACTACTATAAT CCCGCTTATTTATGAAGTTACTGCCATCATAAGGATCAAGCGCCACTAGAAGATTCAACCATCTAGCTGGTTCTATCCAAGAAGCTAAA GAAAAGCTAAAACGAGGAAGCCATAGATGGGTGTCAGCTGGGAAAAATCACCATTCTAGGAAA

SEQ ID 252

MTNPTFGEKIDNVYRSRGVYAIIPNPTHDKIILVQAPNGAWFLPGGEIEENENHLEALTRELIEELGYSATIGHYYGQADEFYFSRHRDTHYYN PAYIYEVITAYHKDQAPLEDFNHLAWFPPIQEAKELKRGSHRGVQAWEKNHHSRK

SEQ ID 253

ATGATGATTCCAACATTTGGACATAAAAGCACATAAAGACTATGTCACAGCTTACGGTGTCTATGCTATCATTCCAAATCACGAACAAACAAAA ATTATTCTTGTCAAGCTCTAATGGTCTGGTTTACCTGGTGGTAAATTGAAGCAGGTGAGCTTCAGGCCCTAGAGCGTGAACTG ATTGAAGAACTTGGTTTCTGCTACTATTGGTTCATATTACGGTCAAGCGAGATGAATATTCTACTCTGCCATCGTGTACCCACTCTACCAT CCTGCCCTATCTTATGAAGTAACGCACTTCAAGCGTTCTAGAAGATTAAACTTAGGTTGGTTCTCTATCGAGGAATT GCTAAATTAAAAGCAGAGAGGCCATATGGGGAGTCAAGGAATGCCAAAAAGCATCATTCTACTAAC

SEQ ID 254

MMIPTFGHKNAHKDYVTRYGVYAIIPNHEQTKIILVQAPNGSWFLPGGEIEAGEGQLQALERELIEELGSATIGSYYGQADEFYFSRHRDTHFYH PAYLYEVITAFQAVSKPLEDFNNLGWFSPIEAIKLRKRESHQWGVEWKHHSTN

SEQ ID 255

ATGCTCTGTCAAAACCTGCAAACCTAAACGAATCAACTATTCACTTGTATACAAATGTAATGAAAACAAAGCAAGTTGATCTTGTCAAAATTGCTACCAAAATTATTAACTGACCCCTAATAATCCACTTTTCAGGTTAAATCATGTTCACTGCGCTGGCATCAATCCTTCTTGTGATGAT TTCTTITGGAGATTTAAATATTCAAGAGCCTTAAATGGCAAGGATTACAAACACTCCTCTCATACAACTCAGGAGGAACCGAGGTGGAGGAACCGTAATGGACGAAATAATACGCAACCAAACACTGCAACTCCCTCTCAAGCCTAAAGGAGATTCTAGAAGAATTCTGTATCAATGTCACTGAAATAGCC CGCCATGGTATATTGACCTGTTATTGGACGCTGACTCAGAAATTATTCTGTGTTATCGAAATCTTAACTCGTGTCAAAACAAATAATCTGTACTT ATTGGCAACCCGGCGTTGGAAAACCTGCGCTGTTGAGGACTTGTGCTCAAGAAAATTGTTGATGTTGATGCTCATAAACTTCAAGGCAAACAA GTTATTCTGTTGGATGTTGAGTCAAGGAACGGGATTCTGTTGAGTCAAGGAACCGCATGCAAAAGTTGATGAAAGAATTCTGTCAA CGTCAAGATGTTATTCTATAGATGAAATTCAAGGAACGGGATTCTGTTGAGTCAAGGAACCGCATGCAAAAGTTGATGAAAGAATTCTGTCAA CCTGCCCTTGACGTGGAGAATTACAACCTAGTAGGTGCTACTACTCTCAATGAATATCGTATTATCGAAAGGACGCTGCCCTAGAACGCCGTATG CAACCTGTAAGAGTCGATGAGCCTTCTGTTGAGAAGAAACCATTACTATTGAAAGGTATCCAAAAAAATAGAAGATTATCATCATGTAACATATAAATAATGATGCCATAGAAGCAGCTGCACTATCTAATGCTTATATCCAGGACCGCTTTTACCTGATAAAAGCAATAGACTTATTAGATGAGCT

GGTTCTAAATGAACCTAACACTAATTGTTGATCCAAAAGAAATTGATCAACGTCCTATTGAGCAGAAAATTAAAGCGCAAGCGACTCGTGAAGAAGATTACGAAACGTGCAGCTTACCTCCGTGACCAGATTGCAAATATAAGAAATGCAACAAACAAAAGGTCGACGATCAAGATAACCTATTATTACCGAAAAAAACATATTGAGCACATCATTGAAAGAAAAACGAAATATCCTGTTGGTATTAAAGAAAAGAACAATCTCAATTAAATTACCTCGAGCATGACTGTGAAACAAACATGTGATCGCCAGGTAGCAGCTGCTGTTAAAGATTGCAAAGGACTATTGCTGTAATCGAGTTGGTCTGGTAGCCAAACCGTCTATTGGTCTCTTTTATTGTTAGGACCAACCGCGTTGGTAAACTGTAATTCTAAACATGCAATTGAGCTCTTGGTCACTGATAGTATGATTGCTTTGATATGTCAGAGTACATGGAAAAGCATGCTGTTGCTAAATTAGTCGGAGGCCCTCAGGATACTGGGATACGAGGAACTGGACAACTGAAAAGGTTGCTGAAATCCTTACTCGCTCATCCTCTAGATGAAAATTGAAAAGCTCATCCTGATGTATGCATATGTTCTTGCAAGGTTCTTGATGACGGTCGATTAAACAGATGGACAAGGAAGAACTGTTAGTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTCTGGTAAACTGAAACCGCTTGGCTTGGTCTCAGGAGAAGGTTAGAAGCATTCCGTACTAGGTCAACTAGGTAACTCTTCAGCCCTGAATTATGAAACCCCTTGACGGTATTATGATTCAAGGCTTAAAGGATAATCCTCCATATTGCTGATATTGTTAGTATCTGACGTTAATGCACTCTGCATCATGTTAGTCAACTGAGTCAACGAAATTTGGGAGAAGGAAATTTGGTTGATTAGGTATTAGGTACAGATCCAAAAGGAGACGTCATTGAGAATCCTGCTGTTAGGTTACGATCCAAAATGGGAGCACGTCATTACGTCGTTACATTGAGAATCCTGAGGAAATATGAAACCTGCTGCTATTATGACTAGCAATTGAAATATCATAAAAAACTGAAGAAAAGTACAAAAGGT

SEQ ID 256

MLCQNCKLNESTIHLTYTNVNGKQKVQLDCQNCYQIIKTDPPNPLFSGLNHVSAPGGINPFDDFGDLMNFRAFNGQDLPNTPTQSGGNRGGGGN
GNGRNNNRNQTTATPSQAKGILEEFGINVTEIARHGDIDPVGDRDSEIIIRVIEIILNRRTKNNPVLIGEPGVKTAVVEGLAQKIVDGNVPHKLQKGQ
VIRLDVVSLSVQGTCIRGQFEERMQKLMBEIRQRQDVLFIDEIHEIVGAGTAGEGSMSDAGNILKPALARGLQLVGATTLINEYRIIEKDALEERRM
QPVKVDPESVETITILKGIQKKYEDYHHVVKYNNDAEAAAVLSNRYIQRDFLPDKAIDLLEDEAGSKMNLTLNVFDVPKEIDQRLLAEENLKAQATR
EEDYTERAAYFRDQJIAKYKEMQQQVDDQDTPLIITEKTIIEKTNIPVGDLKEKEQSOLNINLADDLKHQHVIGQDDAVVKIAIRRNVRVGLGSP
NRPFGSFLFVGPTVGKTELSKQIALELFGSADSMIRFDMSYEKMHAVAKLVGAPPGVYGVYEEAGQLTEKVRNPNPSLILDEIEKAHPDVHMFM
LQLVLDGRLTDQGQRTVSFKDTIIIMTSNAGSGKTEASVGFGASREGRNTSVLGQLGNFFSPEFMNRFDGIIIEFKALDKENLLNIVDMLSDVNAR
LAINGIHLVDVTDKVKEKLVDLGYDPKMARGPLRRTIQEHIEDAITDYYLENPSEKELRAIMTSNGNIIIKSSKKTEESTKG

SEQ ID 257

ATGCTGTGCAAAATTGTAATTAAACGAATCTACTATTCTATCTTATAACAGTGTAAAGAAAACAAGACAGGGTGTCTCTGTCAAAATTGT
TATCAAATCATGAAATCCGATCTGCCAATTCTATTAAATGCCCTAACCCAGGATATAGGCACAAGATAGATCCACAAGTCCTTCTTGAT
GACTTTTTGGTATTGTAATTTAGAGCTTTGGTAACTCTTAAATACCCCACCTACTCAGGCAGGGCAAATGGAAATGGCGGAGGACGC
TATGGTGGTAACTACACAGGACACGGACCTGCTCACGCCAACACACCCAAATCAGCAAGCAAGAACAGGGCTTGTAGAAGAGTTGGGATTAAATGTCACAA
ATAGTGCACAGAAATGTAATTGACCTGTTAGGCTGTGAGGAAGAGATTACACGGCTTACAGATCTCAACCCCGTACTAAAAATAAT
CCTGTGCTAATTGGTAGCGCTGGAGTTGGTAAACTCTGTGTAGAAGGTTGGCTCAAAAATTATTGATGGTACTGTCTCCTCAAACACTCAA
GGCAAGCAAGTGTCTGTGATTCTCAGGGAAACAGGTATCCGTGGTCAGTTGAAGAGCGCATGCAAAATTAAATGGAAGAA
ATTGCAATCGCAAGGATGTGATTCTTTATTGATGAAATTCTAGAGATTGTCGGTGTGGTCTGCAGGGACGGCAATATGGATGCTGGTAAT
ATTTAAACACAGCCTGGCCCGTGGTGAGTTGCAACTCGTTGGTCTACTACATTAAATGAAACCGTATTGAAAAGACGCTGCCCTAGAA
CGACGTATGCAACCGTAAAGTGTGAAACCTCTGTTAGGAAACCATCAGATTAAAGGTATCCAACCGAAATACGAAGACTATCATCAT
GTCAAATAAGCCAGCGCTATTGAAAGCTGCCGCTATTCTAACCGTATATTCAAGGCGTTCTCTGTATAAGGCTATTGACCTCTG
GACGAAGCTGGTTCAAATGAACTTAACCCCTAACCTTGTGATCTAAAGGAAATGACAACCGCTTATTGAGCTGAGAATCTCAAGGCCAA
GCTACTCGAGACAGAAGACTATGAAACCGCAGCTTATTCCGCGTAAACATTACAAAAGAAATGCGAGCTCAAAAGTCGATGAGCAAGAT
ATTCCCATCATTACTGAAAACACATTGAGCTATTGAGGAAACAAATATTACATTGAGCTTGGGGACTTAAAGAAAAGGAACAGTCACCT
GTAACCTTAGCAATGATCTGAAAGCACACGTGATCGGCAAGACGATGCTGTTGATAAAATCGCTAAGGCTATTGCTCTAACCGTGTGGGATTAA
GGAACCTCAAATGCCCTATTGGTTCTTCTTATTGCTGGACCGACTGGGGTTGGTAAACTGAATTGCTAAACAACTAGCCATTGAACTCTT
GGTCGACAACAAATATGATTGCTTGTGACATGTCGAATACATGGAAAAACACGCTGCGCAAATTAGTCGGGCTCTCAGGTATATGGC
TATGAAGAAGCTGGACAGCTAACCGAACAAAGTTCGTCGAATCCATATTCACTTATTCTTAGATGAGGTGGAAAAGCCCATCTGACGTGATG
CACATGTTCTAACAGTCTGATGATGGCCGTTAACAGATGTCAGGACGAAACGTCAGCTTCAAGGACACCATTATTATCATGACCTCTAAT
GCCGAAACAGGTAACAGGCAAGCTTCTGTCGGATTGGTGTGCTGAGAAGAGCGACAAGGTTCTGCTCTGGTGAATTAGCAACTTCTCAGC
CCAGAGTTATGAACTGCTTCGATGGTATTATTGAAATTCTAACAGCTTATCTAAAGAGCATTGTCGATGTTAATGTCGGAAAGATGTT
AATGAGCGCTTAGGCTATAATGGGATTCTATGTCGATGTCGACACAAAGGTCAGGAAAGAAAATTAGTAGATTAGGCTATGCTCAAATGGCGT
CGGCCGCTCCGCTGACTATTCAAGATTATCGAAGAGTGCCTACAGACTATTATTGAGAACACCCAACTGAAAACAGTTACGTGCACTGATG
ACAAACAGTGGAAAATATCAGGATTAAAGCTGTTAACAGGGAGATTCTTCTAACGAAGAGTCTCTCGAT

SEQ ID 258

MLCQNCLNNESTIHLYTSVNGKQRQVDLCQNCYQIMKSDPANSILNGLTPGYRAQDRSTSFPFFDDFFGDLNNFRAFGNLNPNTPTQAGQNGGGGR
YGGNYNGQRPAPQQTNPQQAKGLLEEGFINVTIDARNGNIDPVIGRDEEITRVIEI1NRRTKNNPVLIGEPVGKTAVVEGLAQK1IDGTVPKLQ
GKQVIRLDVVSLVQGTGIRGQFEERMQKLMEERINRKDVLIFIDEIHEIVGAGSAGDGNMDAGN1KPALARGELQLVGATTLENEYRIIEKDAALE
RRMOPVKVDEPSVEETITILKG1QPKYEDYHVKYSPAAIEAAAHLSNRYIQDRFLPDKA1DLLDEAGSKMLNTLFNDFPKEIDKR1EAENLKAQ
ADTREDEYERAAYFRDQITKTYKEMQAKVQDQPI1ITEKTEIAVEQKTNIPVGDLBKEQSQLVNLANDLKAVHIGQDDAVDKIAK1RRRNVRG
GTPNPRIGSFLFLVGTGVGKTELBSKOLAI1ELFGSTNNK1RFDMSYEHMKHAVAKLGVAPPYIGYEAEAGLTLTEQVRNRPYSL1DDEVEKAHPDV
HMFLQVLDDGRLTDGQRTVSFKDT11IMTSNAGTKSEASVGFGAAREGRTSSVGLRSNFSPEFMNRFDGIIEFKALSKIEHLLH1VDTLMLEDV
NERLGYNTHLDVTQVKKEKLVDLGYDPKMGARPLRRTI1QDYIEDA1TDYYLEHPTEKQLRALMTNSE1TIKAVKEGDSFLNEESLD

SEQ ID 259

ATGTCATGAACTTTTACCTTACACAATTGGTCTATTAAATTATGGTGTATGGTAACCATTGATTCAACATGTTGTTTTTT
GGAACATTAGGTGTTAATTGCTTAGTAAGCGTACTAATTACATTCTCACAAATTAGCTAATTCTATGTTGTTGGTATTCGTTG
ACACCGATGGTAGTTCAATTATGATTGCTTCGCATGGATGCATTAAACAATTACCAACGATTAGCTTGGTGTAGTTAGATTAGATTAA
CGACTTTTACCTGGTACTATTACCTTAAATAGTGGTGCCTATATTCCGAAATTGTACGTGCAAGGGATTGAGGCTGTACCATCTGGACAA
ATAGAACGCCCTTACTCTGGGATTCGACCTAAAATACATTCCGCTATGTTACCTTACCCCCAGCTTTAAATATTACCTGCTTAGGG
AATGAATTATTAAACATTAAAGATAGTGCCTCCTCAAACATTGGTGTATGGAATTATGGAACGGAGCACAATCAGTTGTAACGGTACT
TACTCACCAGTTGCACCGTTATTTCAGCATTACTATTAAATGTTGACAACGATTCTCTCAGCTTGTAAAACAAATGGAGAAATATTCTT
GGGAAAGGGTAAAAATAGATGGT

SEQ ID 260

MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTILANFYVWWFRGTPMVQYQIMIAFAWMHFNNLPTISFGVLDLDFTRRLPGIIISLNSGAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITIIKDSALLQTIGVMELWNGAQSVVTATYSVPAPLLFAAFYYLMLETTILSALLKQMEKYLGKGVKIDG

SEQ ID 261

ATGGATTGTCATTTGCCAAACTGGCTACTTAACTACGGTGTACTTGTACCCATTATGATTCAGTCAGCGTGTCTTTTGAAAC
CTTATTGGTGTCTGGTAAACCTGATTAAGCGTAGTCATGTGAAGCGCTTGACCTGGTGTAAATCTTACGTTGGATCTTCGGGAACACCT
ATGGTGGTCAAAATCATGATTGCCCTTGGATCCTTAAACATATGCCTACTATTGGTTGGGTTAGACTTGGACTTTCAAGACTA
CTTCTGGAAATTATATTATCATTTCTTGAATAGCGGTGCTTATATTCTGAAAGATTGTTAGAGCAGGTTAGGGCTGTACCAAAGGGCAATTAGAA
GAGCTTATTCACTAGGTATTGCTCTAAAATGGCATCGGTATGTGATTTCGCTCACGGCTTAAATAATTTCGCAAGCTTAGGAAATGAA
TTTATTACCATTTAACCGATAGTGGCTTTACAAACCTTGGACTGATGGAACTTTGGAATGGTGCCTACGGCTAATTATCT

CCAATTCCCTTACTGGTGGCTGTTTACTACTTAATGGTCACAACAGTGATGGCACAGTTATTGCCAGTCTTAGAACGTACATGGCGCAA
GGAGGTAATCAT

SEQ ID 262
MDLSFLPKYWAYFNYGVLVTIMISVSVFFGTLIGVLVTLIKRSHVKPLTWVNLYWVIFRGTPMVQIMIAFAWMHFNNMPTIGFGVLDLFSRL
LPGIIISLNSGAYISEIVRAGIEAVPKGQLEAAYSLGIRPQNAMRYVILPQAFKNILPAIGNEFITUOIKDSALLQOTIGVMELWNGAQSVVTATYS
PISPLLVAFAFYLMVTTVMAQLLAVLERHMAQGGNH

SEQ ID 263
ATGTCTCATATGAATTATAAAGAGATTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAGAGATATTAAGTCAGATTAGAAGCTATTAAAGGC
GATGAATCTGAAATTCAGGATCGTTTACAAAACATTAGAATTGGAACCGGGGATTGAGAGGTAACCTGGAGCAGGAACCAATCGTATGAAT
ACTTATATGGTGGGAAGCAGCACAAAGCATTAGCTAATACGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAATTGAGTTAGTATGAT
GTCGTTATCAATCTAAGGAATTTCAGAATTAACTTGTCCATTATGCCAGAAATGGTATTAAGTCCTTATATTATAAAGGGATTGCCAAC
CCAATGTCTCATATGCTATTCTGCTCTAGGATCTGTTGGGTGATGATTACTCTAGTCATAATCTCAAGCTTATAATGGTATAAAGGC
TATTGGAAAGAAGGATCTCAGATTAGTATGATCATGCTAATGCCAACTCATATGGATGCTATAACCGATTATCAGCAAATTAAAGC
CCCCTTGAAGAGGCTCTGGCAAGTGGTCCGGCAAGTATTATCGATGAGAGTATTGAAGAACATATAAAAAGAAGTGTGTTTAAC
GATACTAATATTGATAAGTCAGTCGGTAGTTTAACTCTTAAATGCCAGGAAATTCTGTGCGGAAGGTTAAAGACGCCGTGTT
GAAAATGTTATGTTGACCTGAGCAGGAAATGCCGATCTGATTAAACGGTTGGCTATCAAACCCCTGAAGTCTCTAACGATTGCTT
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GTATTGGAAAATCCATGTAACTGGTGTATCTAAAGATTGAGATAAAATATTAATATTGAAACTGTTGAAAGACTTAAACAGGATTAAA
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CGTGTGATAAAAGATCTGTGAGTCTCAATGATGGTAGAGAAATGACTGCTTATATAAAGAACGGGGAAACACTTTAGACGTTTGCAAACC
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TTAGACAGGACCAATTACAGTAGGTGAGATGACATTGGAGAATTCTATTGATTTCAAGGATGGTTAAGGATTTCAAAGCAAATTG
TTAAAATATTATTTAATGAGGGTTCATGGTATGCTTAAGGCCGTAGGGACGGAACTAAGATAAAATGTTACCTTACGATTGGTT
GAAGCAGATAGTTATGAAACTTAATGCAATTGAGTCGGCTTGTGCTAAAGAATAGTACTAA

SEQ ID 264
MSHMNYKEIYQEWELENDLSLGKDIKSDEAIKGDESEIQDRFYKTLERFTAGLRLKGLAGTNRMNTYMGKAAQALANTIIDHGPEAIARGIAVSYD
VRYQSKEFAELTCSIMAANGIKSYIYKGIRPTPMCSYAIRALGCVGVMITASHNPQAYNGYKAWKEGSQILDDIADQIANHMDAITDYQQIKQI
PFEEALASGSASYIDESIEBEAYKKEVGLTINDTDNIDKSVRVVYTPNGVGNLPREVLRRRGFENVYVVPQEEMPDPDFTVGPNEPVPKAFAY
SESLGKSVDAILLATDPDCRVALEVKDSKGEYIFLNGNKIGALLSYYIFSRQCALGNLPHHPVLPVKSIVTGDLSKVIADKYNIETVETLTGFKN
ICGKANEYDISKDKTLYFGYEESIGFCYGTFRDKDAVSASMMVEMTAYYKERGQTLVDLQTYIDKFGYYNERQFSLLEGAEQGRERISIMED
FRQDPILQVGEMTLENSIDFKDGYKDFPKQNCLKYFNEGWSYALRPSGTEPKIKCYLYTIGCTEADSLSKLNIAESACRAKMNSTK

SEQ ID 265
ATGAGTAATATGACTTACAACGAGGTATATCAAGAATGGTTGACAATAATGATCTTAGTGATGATATTAAAGCAGATTAGCAGCCATAAAAGAC
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ACCTATATGGTGGTAAGGAGCACAAGCTTAGCTAATACTATTATTGATCATGGACCTGAAAGCCTTAAAGGGCATGGCTTAAAGGGATTGCCAAC
GTTCGCTATCATCTAGAACATTCTGCAAGATTAAACATGCTCTATTATGCCAGCTAACGGTATTAAAGGGTACCTTATAAAGGGATTGCCAAC
CCAATGTGTCGTACGCTATTGTCGTTGGATGTTCTGTTGTTGATGATTACGGCTAGTCACAATCCTAACAGGTTACAATGGTTAACAGCT
TATTGGCAAGAAGGTTCTCAAATTGGATGACATTGCGGATCAAATTGACAACACATGGCTGACTAACCTAGTATCAGGAAATCAAACAAATG
CCTTTGAAAAGGCTCTGGACAGTGGACTTACTTATATTGATGAGAGTATTGAGAAGCATATAAAAAGAAGTGTGGTTAACGATTAAAT
GATACTGACATTGATAAGTCAGTCGAGTAGCTATACCCCTTAAATGGTGGTGGAACTTACCACTGCGTAGGTTAAAGACGCCGGTTT
GAAAATGTTATGTTGACCTGAGCAGGAAATGCCGATCTGATTAAACAGTGGCTATCTAAATCCGAACTGCTTAAACTTTCATAT
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GACTATGTTTCTCAATGCAATAACATGGCAGCCTTTTATCTACTATATCTTCAACAGGTTGACTTAGGCAATTACCGGCTTAACTCCT
GTTTAGTGAATCCATTGTAACAGGAGACTCTCACGGGCTATTGCTAGGCCATTATGGTATTGAAACCGGTTGAAACATTGACTGGTT
ATTGTGCAAGGAAACGAATATGATGTGAGAAACAAAAAAACTACCTGTTGGTTATGAAAGAAAGTATTGGTTTGCTATGGCACTTTGTT
CGTGACAAAGACGCTGTAGCGCTCTATGATGTTGAGAAATGGCAGCTTACTACAAGAAAAAGGGCAGAATTACTAGATGTTGAGACT
ATTATGCGACATTGGTATTATAATGAAACGCTAAATTGCTTGGAGCTTGGAGGGATAGAAGGACAAAACGCAATTGCGAGGATAATGGAAGAT
TTCAGACAGACACCAATTGCTAGTGTGAGAGATGGCTTAGACAAGACAATTGATTTATTGATGGCTATCAAGATTCCAAAGCAAACACTGT
CTCAAATTTTATGGATGATGGTTCTGGTATGCACTTAGACCATCAGGAACAGGCCAAATAAAATAAATTGATTTATGACATTGGC
CAAGAAAATGCAACAAAATTAGATGCTATTGAGAAGCAGCGTGTGCAACAAAATAAATCAGGTTAAT

SEQ ID 266
MSNMTYNEVYQEWLHNNDLSDDIKADLAAIKDNEAETQDRFYKTLERFTAGLRLKGLAGTNRMNTYMGKAAQALANTIIDHGPEAVKKGIAVSYD
VRYQSRTFAELTCSIMAANGIKAYLYKGIRPTPMCSYAIRALGCVGVMITASHNPQAYNGYKAWKEGSQILDDIADQIAQHMAALTQYQEI
PFEKALDSLVTYIDESIEBEAYKKEVGLTINDTDKSVRVVYTPNGVGNLPREVLRRRGFENVYVVPQEEMPDPDFTVGPNEPVPKAFAY
SEKLGKAVADILIATDPDCRVALEVKNAVGDFYVFLNGNKIGALLSYYIFSRQFDLGNLPANPVLVKSIVTGDLSRAIASHYGIE
ICGKANEYDVTQKNYLFGYEESIGFCYGTFRDKDAVSASMMVEMTAYYKERGQTLVDLQTYIDKFGYYNERQFSLLEGAEQGRERISIMED
FRQTPIASVAEMALDKTIDFIDGYQDFPKQNCLKFYLDGWSYALRPSGTEPKIKCYLYTIGQTQENSATKLDIAEACRTKINQVN

SEQ ID 267
ATGACTGAATTAATAGATGGTAAAGCCTTACACAAAATGCAGGCTGAGTTAGGGCGAAAAGGTTAAAGGAACAGCATGGTATCATA
CCTGGTTACGTGTAATCCTGTTGGGATAATCCAGCTAGCCAATGTCAGTTGCGAAATAAGAACGCTCTGCATTAGAACGCTGGTTTAAAGT
GAGACTCTACGATTATCTGAATCCATTCTCAAGAAGAACTGATTGATATTATCCATCAATACTGAAGATAAAAGTATCCATGGTATTAGT
CAACTCCGTTACACACATATTAACGATAAAAAATTATTTAGCAATAGATCCTAACAGAAAGATGTTGATGGTTCCACCCAATGAATAACGGGT
CATCTTGGTCAGGACGACCGATGATGGTACCTGTCAGGCCAGCTGTTAGGAGATGTTAGAGAGTACCATGTTGACACATTCAAGAAC
GCTGTTATCATGGAAAGGCTCAATATGTTGTAAGCCAATGCCACAACCTCTCTTGTATAAAACGCCAACAGTTACTTGACACATTCAAGAAC
CGAAACCTTCTGAGGTAACAAAGGAGGCTGATATCTTATTGTCGATTGGCAGGGACTTGTGTTACAAAAGACTTCGTTAAAGAACGGTGC
GTGGTGATTGTTGATGTTGATGTTGAGTAAATTGTTGAGAGCTTGTGTTAGGAGAAGCTTGTGTTAGGAGTGGCTAGTATGATAACA
CCTGTTCTGGGGCGTAGGACCTATGACGATTACAATGCTTTGAAACAAACTTATCAAGCAGCTTACAAGTGTGAGTCTA

SEQ ID 268
MTELIDKGKALSQKMQAELGRKVERLKEQHGIIPGLAVILVGDNPASQVYVRNERSALEAGFKSETLRLSESISQEELEIDI
IHQYNEDKSINGILV
QLPLPQHINDKKIILAIDPKDVGFPNMTGHLWSGRPMVPCPTAGIMEMFREYHVDFLEGKHAVIIGRSNIVGKPMALLLDNATVTLHSRT
RNLSEVTKEADILIVAIGQGHFVTKDFVKEGAVVIDVGMNRDENGLIGDVVFQVAEVASMITPVGPGVGPMTIMLLEQTYQAALRSVSL

SEQ ID 269
ATGTCATGACAGAACACTAATTGATGGTAAAGCCTTAGCTCAAAAGATGCAACAAGAGTTAGCAGCTAAAGTCACAACTAAA
AAAAAGGA
ATTGTACCGGCTTAGCCGTTATTCTGTAGGTGATGATCCTGCTAGTCAGGTGTTAGTCCGTAATAAGAACGCGTCAGCTTACTG
AAAAAGTGAAGACGCTTAGATTCTGCAAGAACGCTTATTGCAAGAACGTTACAATGCAACCTTACAATGCAAGATAACACTATTG
GGTATT

TTAGTGCAGCTACCCCTGCCAAATCATATTAAATGATAAAAAAAATTATTCTGCCATTGATCCAAAAAAGATGTGGATGTTTCACCGATGAAT
ACAGGTCACCTTGGCAGGACGTCCTTGATGGTCCTTGACTCCTCAGGGATTATGGAATTGCTTCGAGAAATATAATGTTAACCTGAGGT
AAACATGCCGTATTATGGCAGATCGAATATCGTGGAAAACCAATGGCACAGCTCTACTGGACAAAATGCAACAGTCACGTTGACACATTCA
AGAACACGTCATTAGAAGAAGTAGTCGCTGTGAGATGTGTTGATGGCAATCGGACAAGGTCTTCAAAACAAATATAAAGAT
GGTGCAGATGTGATTGATGAGGAATGACCAGTGTGATAATGCAAGGCTAATTGGAGATGTGGCCTTGATGAGGTGGCAGAAGTGGCAGCAGA
ATCACCCCTGTACCAAGGAGGTGTCGGCTTATGACGATTGCTATGTTGCTAGAGCAAACCTATCAATCTGCTCTCGTAGTACTCATAAA

SEQ ID 270

MSMTELIDKGKALAQKMQELAAKVNNLQKQKGIVPGLAVILVGDDPASQVYVRNKERALTIVGFKSETVRLSEFICQEELIAVIERYNADNTIHG
LVQLPLPNHINDKKIILADPKDVFDFHPMTGHLWSGRPLMVPCPSGMIMELLREYNVNLEGKHAVIIGRSNIVGKPMQQLLDKNATVTLHS
RTRQLEEVRCRADVLIVAIQGQHFITKQYIKDGAIVIDVGMNRDNGKLIGDVAEVAAKITPVPGVGPMTIAMMLEQTYQSALRSTHK

SEQ ID 271

ATGATTGTTGGTGAACAAGAACAGCAGGGCGTTAATTAAAGCCACCCCTAAATCAAGGCATAAAAGGTGATTATGGTAGTGTCTCTGATAGGAGGT
TTTATCCCTATGGAGGTGCTTATATAATGGCAGCTTGGCCTGTGTCAAAACCTGGCAGGATTAGTTACTGTAGCAACCCAAAGTGCATATC
CCCTCTTGCATAGTCACCTACAGAGGTAACTGGCCTTGATAGTCATGATTAAATGGTGGAAAATCAATTGTCAAAGTGTGATTGTTATTGTA
ATTGGTCCTGGATTAGGAGTATCAGAATCATCTGAAAATTTGAAACCAGACCATGGAGAAGATTCAATCACATCAAAGTGTATCCTTGACGGA
TCAGCCTTGACTCTGTTATCAGAAGGTGCGTTCCGAAACAAAGGCTAAAATTTAGTGTGACACCTCATCAAAGAATGGGAGCATTGTC
GGTATCGCTGATCGAACAGACAAAAGAAAATACCCAAACCGCTTAAATCTTCCCAGGGACGATTTAGTCAGAGTTCAGCTACAGGTTATTGCA
CGTATTTTCAGATTAGCAGAAAAGAAAATTATAGTAGGAGGTCTTACAGGAGCAGTGGAGGGATGGGGATACTTGTGTTGATTGCA
GGTATGTTAGCAGCAATTAAAGAAGCCTCTCTAGATAAGGTATCAGTGGAGTTATCTACATTCCGGAATTGCTCAAGGATTATCTAAAGA
GCCTATGTTCTACCGACAACGATTAGTGTGAGATTCAAAGAATGGCTAGACTATCTAA

SEQ ID 272

MIVGEQEARALIKPRPKSSHKGDYGSVLLIGGFYPPYGGAIIMAALACVKTGAGLVTVATQSCNIPSLHSQLPPEVMAFDSDDYKWLEKSIVQSDVIV
IGPGLGVSESSRKILNQTMKEIQSHQSVILDGSALTLSEGAFPQTAKANLVLTPHQKEWERLSGIAVSQQTENTQALKSFPKGTILVAKSSHT
RIFQDLDEKEIIVGGPYQATGGMDTLCGMIAGMIAQFEASPLDKVSVGVYLHSAIAQGLSKEAYVVLPTTISDEIPKEMARLSK

SEQ ID 273

ATGTCAGACTATTTATCGTGTGACACTGACTAAGTATTTAAATTAAAGACCTTATTAGAGAGGGTTATTAACTGGGCAA
GTGTCATAATTTCGTCGCCCCAACCATCAATATTTCTCTTAAAGATGATAAATCAGTCATTTCAGGGCAGGTCAGGTAACCTTC
AAATTGGGTTGAATTAGAGGAAGGGATGAGGTTAATGAGTGTGGCTGTCACCTTATGAACCAAGCAGGCTCTACTCTATTATGTTGAA
AAAGCAGAACCGGATGGTATAGGAGCTTGTCTATCAATTGAAACAACTAAAGAAGAAACTCTCTCAAGCAGGTTATTGATGATGTCATAAG
CAATTAACTCTCAATTGTTAGAAAAATAGGAGTGTGACTAGTCCAAGTGGAGCGTTATTGGGATATTAAACAGTATCTCGTCAAG
CCAGGAGTGGAAATATTACTTTCCCACAAAAGTCAAGGAGAGGGCGCAGCTCAGGAAATAGCACAAACTATTGCTTAGCTAAC
GAGTTGGATCTATTAAATTGTTGGCCGTGGGGAGGGTCTATTGAGGACTTATGGGCTTTAATGAGAATGTGTTGAGAGCTATTGTA
CGTCCTCCGTTATTCAGTGTGGACATGAAACTGATACAACCTTAGCAGATTGAGCTGAGCAGCAGCAACTCCACTGAGCAGCT
GAGCTGCTACACCGGTTACTAAATGATATCTGTCTGGATTACTGAACGTGAAAATAGAATGATCTAGTCTAGCCTCGTCTATCAGGACA
AAAGAGGAGGAGGTTGCAAAATCAAAGAACATCAGTTAGGCAACAGAGCGCTATATGATGGTTCTTCAAAATTAGATAACCTAAAT
CAGCAGTTAACATATTCTAGCTGATAACTAACAAAGCTAGAACAGGTTGCTTATCAAAACACTGCAAGGAGTACAGTAA
CGTATTCTATTTACCAAGAGCGTTGTGCAAAGTAGACGACTATTACAGTACATGACTAGTCAGTATGACAGCAGCTAGAAC
AAGGCTCAAGATGCGTTATATCATTGGAGTAGTTCTAGAATTGTAGCGCTGGTTACGCTATTATCGAAAAAAACCATACTTGTACTACT
AATGGAATAATGAAGGAGATCATTGCAAGATGCAAGATGGTTAGAAGTGTGAGGTGAAGGATGTCAGACAAGAAAACATT

SEQ ID 274

MSDYLSSVLTLYKLKFDKDPYLERVYLTGQVSNFRRRNHQYFSLKDDKSVIQATMWSGHFKKLGFELEEGMKVNVRVQLYEPGSYSIIVE
KAEPDGIGALQFEQLKKKLSQAGYFDDRHKQLIPQFVRKIGVUTSPSGAVIRDIIITVSRFPGEVILLFPTKVQGEAAQEIATIALANEKK
DLDLLIVGRGGGSIEDLWAFNEECVVEAIFESRLPVISSVGHEDTTLADFVADRAAATPTAAEELATPTKIDLISWIITERENRMYQSSLRLIRT
KEERLQSKSOSVIFRQPERLYDGFQLKLDNLNQQLTYSMRDKLQTVRQKQGLHQKLQGIDLQKRHIYQERVVQSRILSSTMTSQYDSKLARFE
KAQDALISLDSSRIVARGYAIIEKNHTLVSSTTNGINEGDHLQVKMQDGLLEVEVKDVRQENI

SEQ ID 275

GTGAAAGGGCTTGATGGCAGATTATTAACCGTCACTCATTGACGAAATTTAAATTAAAGACCTTATTGGAACGGGTT
TATCTGACTGGTCAAGTGTCAATTTCGAAACAGACCAACTCATCAATATTTCTTAAAGATGAAAGTGTGCTGTGATTCAAGCACCAGTGTG
GCAGGACTCTATAAAACTAGGATTGACCTAGAAGAAGGCATGAAAATTAGTAATTGGGAGGTCAACTTATGAACCTAGTGGCTCTTAC
TCTATCGTATTGAAAAGGCAGAGCCAGGGTATAGGTGCTTGGCTTGCAGTTGAACTTAAAGAAAATTAAAGCAGGTTATT
GAGAAAACACAAGCAGCCCTGCCACAGTTGATCAAATGGGGTCTTACAGTCTAGTGGCTGTGATTGAGATATTACAAACC
GTTTACGGCGTTTCCAGGGTTGAGATTTTATTATCCTTCAACTAAAGTACAAGGTGATGGCGCCCAAGAAGTAGTGGCTAATATTGCAAGA
GCCAATCAAAGAGAGGATTGGACTTGCTCATGTCGGCCGTGGAGGTGGCTGATAGAAGACCTTGGGCTTCAACGAGGAAATAGTGGTTCAG
GCTATCTTGAATCGCACTCCAGTGTGGGTCTGAAACAGACAGACTTACGGGATTGGCTGGCAGATCGCAGAGCAGCCACA
CCAACAGCAGCAGAGTTAGCAACGCCTATTACAAAACAGATCTTATGTCCTGGATAGTAGAGCGGCAAATCGTCTTATCAGGCTGCTTG
AGGGGATTAAAGCAGCGCAAGAGTGGGTGATAACTCTCGCAATCTGTTATTAGGCAACAGAACGATTATATGATGCCATCTGCCAAT
ATTGATGCCCTAGCATGACCCCTGATGAAATCAGTGAAGAGTCGCTGAGTTGGCCAAAGAAAACAAGGTTAGTGGACCATGCCCTGGCCAAAT
AGTCATTACAGACAAAATCGAGCATAACCAAGAGCGTGTGCTACCGCTAACGGTTACTGATGGCTAATATGCTAGTCAG
CTGGCTCGCTGAAAAGCACAGGATGCTTGTCTACTGGATGCCAGCGAAATTACGCCGTGGTTATGCAATATGATAGTCAG
CTGGTAGCCTCTGTAAGTCAAGATAACAAAGGGTGTAGCTTAAGATGCCGTAGGACAATTAGATGTAGAGGTTAAAGATGCAAAAC
AAAAACATT

SEQ ID 276

VKGGLMADYLTVTHLTKYLKLKFDKDPYLERVYLTGQVSNFRRRNHQYFSLKDESAVIQAQMAGVYKKLGFDLEEGMKINVGRVQLYEPGSYS
SIVIEKAEPDGIGALQFEQLKKKLTAEYQFEQKHKQPLPQFVSKIGVITSPSGAVIRDIIITVSRFPGEVILLFPTKVQGDGAAQEVVANIR
ANQREDLDDLLIVGRGGGSIEDLWAFNEECVVEAIFESRLPVISSVGHEDTTLADFVADRAAATPTAAEELATPTKIDLMSWI
ERQNRSYQACL
RRIKQRQEWVDKLSQSVIFRQPERLYDAYLQKIDRLSMTLMNTMKDRLSSAKENKVQLDHALANSQLOTKIERYQDRVATAKRL
LARFEKAQDALISLDSSRIVARGYAIIEKNHTLVSSTTNGINEGDHLQVKMQDGLLEVEVKDVRQENI

SEQ ID 277

ATGTCAGACAAGAAAACATTGAAAGAAAATTACAGGAATTAGAGACAATTGTCACGTTAGAAACAGGTGATGTTGCTTAGAAGATGCCATT
GCTGAATTTCAAAAGGAATGCTTATTCTAAAGAGTTACAAAGAACCTTAAAGAAGCTGAGAGAGACGCTGTGAAAGTGTGCAAGCTGACGGA
ACGGAAGTAGAAATGGGATACT

SEQ ID 278

MSDKKTFEEQLELETIVSRLETGDALEDATAEFQKGMLISKELQRTLKEAEETLVKVMQADGTEVEMDT

SEQ ID 279

ATGTCAAAACGAAAATTTGAAGAAAATTACAAGAGTTAGAGACTATTGTGAACAAACTGAAAATGGGATGTCCTTGGAAAGAAGCTATT
TCAGAATTCTAAAAGGAATGCTCTCTCAAAGAACCTTACAAGCGGCAGAAAAAACACTCGTCAAAGTGTGCAAGCTGTGATGGC
ACAGAAAGTAGATATGGATGAT

SEQ ID 280

MSKTKTFEENLQDLETIVNKLENGDVPLEEAISEFQKGMLLSKELQKTLQAAEKTIVKVMQADGTEVDMDD

SEQ ID 281

TTGATCGTTACTATTGAAAAATTGTGAAGCTATTGATCGTTATTACAAACAGACACATAGTGTGTTCTCCTGATTGATTAAGGCTATCCTC
TACTCGATTGATGGAGTGGAAACGTTACCGTCACGCCATCCTTTAGAAATTAGGGATTGGAGTTGAGTTGAACATAAGATGGTCATTATGAT
GTGGCTGCTGTTGGAGATGATTCAACCGGCTATTAAATCCATGATGATTACCGGCATGGATAATGATGATTTGCTGTCGGCGCTTAA
AACCATAAAAAGTTGATGAAGCTACAGCGTTTAGCTGGAGATTCCCTTTAGACCCATTGATTAGTGTAAAGCTGGTTAAAGCT
GATGTTACTGTTAGGTTAATAGAGTTATTGCTATGTCGCGGTAGTTGGCATGGTGGACAAATGTTAGATATGAAGGGAGAAA
GTTTATCTATTGACGATTAACTGATGATTCAATTAATAAAACGGGACCCCTGTTAGCTTATCCCTTGTCAGCAGGTATTAGCTGAGAAG
TCGGAAGAAGTAAAAGGAAACTGCAAGCTGGCTTTAATCGGTATGCTTCAAGTACGTGATGATATTAGTGTACTGCTAGTT
GAAGAATTGGGAGACACCAAATAAGACATTGTTAGCAGAAAAGACAATTATCCAAATTATTGGGTTGGATAAGTCACAGGAATACTTGAT
GATACTTGAAGAAAAGCTCAGGCAATTTCAAAATCTAGAGAAAAGCTAATTGCTAGAGAAAATAATGATAATAGGGATTACGG
TTGAATGGC

SEQ ID 282

MMVTIEKIDEAIHRYYKQTHSVVSPDLIKAILYSDGGKRIRPRILLEILEFGFVELIDGHYDVAAALEMIHTGSLIHDDLPAMDNNDFRRRLT
NHKKFDEATAVLAGDSLFLDPFDLVVKAGFKADVTVRLLSMSAGSGFMVGQMLDMKGENKVLSIDDSLIHINKTGRLLAYPFVAAGILAEK
SEEVKGKLHQAGLLIGHAFQVRDDILDVTASFEELGKTPNKKDIVAEKTTYPNLLGLDKSQEILDSTLKKQAIFQNLEKKANFNARKIIDIEGLR
LNG

SEQ ID 283

ATGGACAAAATTAGCTAGAATTGACGAAGCCATTGTCGCTACTATAAGACGACTAGTAACGGTGTATCTGAAGAGTTGATTGATGCTATCTGTAT
TCTGTTGACAGTGGTGCAGCGCATTGCCCACCTTATCTTATTAGAGATGATTGAGGGATTGGGATCTGTTACAGAATGCTCATTGATTG
GCTGCAGCTCTGAAATGATTCAACAGGAAGTCTGATTCAAGCATGGTACGATGATTGCGCAGCCATGGATAATGATGATTACCGACGTGGCAGACTGACCAAT
CACAAACAATTGGAGAAGCCACGCCATTGGGGAGACAGCTTATTAGACCCCTTGGGTTAATAGCTCAAGCTGAATTAAATAGTGAG
GTTAAAGTAGCCTTAATCCAAGAACTTCCCTAGCTTCAAGGAACTTTGGCATGGTTGGTTCAGATGTTAGATATGAAAGGGAAAATCAAGCA
TTAGTCTCCCTAGTTGCACTGATTCACTTAAACCCGAAAATTATTAGCTTCTTTAAACGAGCAGCTTATAACAGAAACAGGCT
ATGACTGTCGTCACAAACTAGAGCAAGCGGAATGCTCATGGCACGCCATTGCAAGATTAGGGATGATATTAGCTGACAGCTAGCTTGTGAA
GATTTGGAAAAGCCTAAAAGGACTTATTGCAAGAAAAGCTACTTATCAAGTTACTGGGTTAGAAGCCTTACCAACTGCTGACAGAG
AGTTAGATCAGGCTTACGATTTCAGACACTAGAAAGCAGATGTTAGGCTTAAAGCCTCAAATAATTACAAAAGCTGATAGAAGGGTTACGACTT
AATGCC

SEQ ID 284

MDKLRIDEAIRYYKTTNSGVSEELIDAILYSDGGKRIRPLILLEMIEFGFVSLQNAHFDLAAALEMIHTGSLIHDDLPAMDNDYRRRLTN
HKQFGEATAILAGDSLFLDPFGLIAQAELNSEVKVALIQELSLASGTFGMVGQMLDMKGENQALSLPQLSLIHLNKTGKLLAFPKAAALITEQA
MTVRQQLEQAGMLIGHAFQTRDDILDVTASFEDLGKTPKDKLFAEKATYPSLGLEASYQLTESLDQALTIFQTESDVGFKPQIITKIEGLRN
NA

SEQ ID 285

ATGGCTAAAGAGAGGGTAGATGTTCTGCTATAAACAGGGACTTTTGATACACGAGAGCAAGCAGGAAACGGTGTATGGCAGGAATGGTATT
AACGTTTATCAATGGAGAACGTTTATGATAAACCAGGTGAAAGGGTTCAGACGATACTGAATTAAACTAAAGGTGAAAACACTAAATATGTTAGT
AGAGGTGGATTGAAATTAGAAAAGCTTACAAGTTTGGAAATTTCAGTTGAGATAAGCTAACTATAGATATTGGCCCTCTACGGGTGTTT
ACTGATGTTATGCTACAATCAGGAGCGCTTACTGAGTAGATGTTAGGAACAAATCAATTAGTTGGAGTTACGTTCAGGATCATGCTGTT
CGTTCTATGGAACAAATATAATTAGGTATGCCAAAAGAAGATTTCAGGAGGGACTGCTGAATTGCACTGATAGATGTCATTTATCTCT
CTTAATTGATTTCAGCTTAAAGAAATTGTTAGGATGGTGGACAAGTAGTTGGCATTAATTAAACACAATTGAGCAGGTGCTGAGCAA
ATTGGTAAAAGGGATTGTCAAAGACAAGTGGGTTCATGAAAAGGTTGCAACACGTGACCAATTTCAGGAAAGATTGGATATACGGTTAAA
CATCTGATTTCGCCATTCAAGGGGACATGGAAATTGAGTTTAAATGCTTGTGACAAAGTGTCAAGATCCACAAATCTGTGCTTGC
CAAATAACAAGATGTTAGAAAAGCACATAAGGAATTAAAGAAAATGAAGAAGAG

SEQ ID 286

MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLKYVSRGGLKLEKGLHVFGVSANQIGIDIGASTGGF
TDVMLQSGARLTVYADVGTNQLVWKLQRDHRVRSMQYNFRYAQKEDFKEGLPEFASIDVSFISLNLLIPALKEITLDGGQVVALIKPQFEAGREQ
IGKNGIVKDKLVHEKVLTVNTFTKDYGTVKHLDFSPIQGGHGNIEFLMHLQKCDPQNLVLDQIQDVIKEAHKEFKNEEE

SEQ ID 287

ATGCCCTAAAGAAAGACTAGATGTTAGCCTATAACCAAGGATTATTGAGACAGAGCAAGCTAACGGTGTGTCATGGCAGGCTTACTGGTC
TCTGTTGATTAATGGCCACGCTATGACAAGCCAGGTGACAAAAATTGACGATGGGACTGAGTTAAAACCTTAAAGGTGAAAACACTCAAATACGTCA
CGTGGTGGATTAAAAGTGGAAAGGGCTGCACGTTTGGTGTATCAGTTGCTAATCAAATTGGGATTGATATTGGCCTCAACAGGGTTT
ACCGATGTTATGTTACAAGATGGGAAACACTAGTCTATGCCGTCGACGTTGGACTAACAGTTGGTATGAAACTCAGACAAGATCCACAGAGTA
AGAAGTATGGAACAGTATAACTTCTGTTATGCTCAGGAGAACACTTTAATGAGGGACAGCTGTTATGCTGAGTGTGCTTATTCT
CTCAGCTTGTATTGCCCCCTGCATAACGTTTGTGAGATCAGGGACAGGTTATTGCTCATTAAACCGCAATTGAGCTGGCGCAGCAG
ATTGCTAAAAGGCATGTCAGGACAAACAGATTGAAAGTCAAAAGGTGATTGAAAGTGTGCTCAGGTTACGGATTACAGTTAAG
GGACTGTTATTGCTCTTCTCATTCAAGGGGTCATGGCAATATGCAATTGAGTTTAAATGCTGCTAAGTCAACAGACACCTGAAACGTTAGCCCCGCT
TTGATTGAGAAAAGTGTGCAAGGACATAAGGAATTGAGAAACATGAAAAAGAG

SEQ ID 288

MPKERVDFVLAYKQGLFETREQAKRGVMAGLTVVSVINGQRYDKPGEKIDDGTTELKLKGEKLKYVSRGGLKLEKGLHVFGVSANQIGIDIGASTGGF
TDVMLQDGAKLTVYADVGTNQLVWKLQRDPRVRSMQYNFRYAQKEDFKEGLPEFASIDVSFISLNLLIPALKEITLDGGQVVALIKPQFEAGREQ
IGKNGIVKDKLQKQIHEKVIQKVMDFASGYGFTVKGLDFSPIQGGHGNIEFLAHLAKSQTPETLAPHLIQKVVAKAHKEFKHEKE

SEQ ID 289

ATGAAGAAGAGTGAACGTTAAATTAAAGCAAATTGTTCTAACCATGCTGTTGAAACACACATGAGTTACGAGATTGAGCTTAT
GGGTAACCTCAACTCAAGCAACTATTGACGTTGATGAAATTGGCATTATAAAAGTGCCATCAACAAAGGTGCTTATATTACGGTTTG
TCAAAATGAAAAGCACCCTATCTTACAACGTCGTTGGCAAAGCTTAAACAGTATTGTTACATGAGTACTAGGTTAGAGCAA
TTTATCAATTAAATGTCATACAGGTAACAGTCAATTAAACCTTCATAATGTCACATTGTCAGAACAATATTGAGTTGAGCTGAC
GATAATGTCCTTTGATTGCAAAGGACATAAGGAATTGAGAAACATGAAAAAGAG

SEQ ID 290

MKKSERLNLLIKQIVLNHAVETQHELLRRLEAYGVTLTQATISRMNEIGIIVKPSAKGRYIYGLSNENDPIFTTAVAKPIKTSILSISDKLLGLEQ
FININVPGNSQLIKTFIMSHCQEHIFSLTADDNSLLIAKSEADADHIROSMIAMLEKKD

SEQ ID 291

TTGTTGCCAAGGCACATAAGGAGTTGAGAAAACATGAAAAAGAGTGAACGACTTGAATTAACTAAAAAATGGTTGACGCATCCAATTGAGACG
CAACATGACCTCTTAAGATTATTGGCAGAGCATGGTTAGAATTAAACCCAGGCTACTATTCAAGAGACATGAATGAAATTGGTATAGTAAAGATT
CCCTCTGGCAGTGAGCTTACATCTATGGCTTTCTCAAGATAGTGGAAAAAGATCGTCAGGACCTAGATCGATAAAGAGCACTATTTAGCT
GTATCTGACAAAACAAAAGGTTAGAACACACCTCTATTAAAAGTCGTACCTGGCAATAGTAAATTCAAAACGTATTATTAGCAGATT
TCAAAAGCTATTAGCTTATTGCTGATGATAGTTATTGTTAATTGCAAAGTCTCCTCAGAACAGCAGATATGATACGCCAAGAAATTG
CTTTGGATGAGGGTATAACC

SEQ ID 292

LLPRHRSRSLRMKKSERLELIKMLVLIPIETQHDLRLLAHEHGLELTQATISRDMNEIGIVKIPSGSRYIYGLSQDSGKKIVQGPRS1KSTILA
VSDTKGLEYHLYLKVVPNGNSKLICKYLLADFSKAIFSLIADDSSLIAKSPSEADMIRQEILLWMQGIT

SEQ ID 293

ATGGAAGATTATCTTCTTACGTGAAAAGCAGATTAACTAGCTAACATCAATCGAGATAACTCTCCTCTGAAGCCACTTTACCAATGGCTTA
AAGGCCCTCCGGGATTGTTGAAATA

SEQ ID 294

MEVLSLREKADLIANINRDNSPPEATFTNGLKPSPGFVEI

SEQ ID 295

ATGCTTAAAGGAAATTCTTCTTAAAGAATTTCGCTTATTATCGAAGGAAATTTCACCTTAAATTGAAACAGGAATGACTGTTTAACGGTGGAGACTGGT
GCAGGGAAATCTATCATTATTGATGCTATGAATATGATGTTAGGATCCCGTCTAGCGTTGAAGTGAATTGCGCATGGTCTAACAAAGCAGAAATT
GAAGGATTCTCTCTGTGAAAAAAATCAATCATTAGTCCAATTATTGGAAGGAAATGGCATTGAATTAGCAGATGAATTAAATTATTCGCGGAGAA
ATCTTCAAAATGGCGCAGCGTTAGTCGAATTATGGCAATGGTCAACACTAAAGCTGTGGGGCATTATTGGTAGACATTAT
GGTCAGCATGACCAAGAGGAACTAATGAAACCTAACATGACATTCTGATGTTAGATGAATTGGTAATACAGAATTAAATGTCATAAAAGAACGT
TATCAAAGTCTTTTGATGCTTATCGTACGGTAAACCGCTATTGATAAGCAGGAAATTGAACAAGAGAAATAATCACGTATTGAAATGCTA
GAATTTCAAATAGCAGGAAATTGAGCTCTGTAGGCCCTTAAATCAGATGAAGGACCAACCGCTACTCAAGCAGCAGTATAATTGAATCATAAGAAT
ATTGAGCAGTACTTGCAAAATGCTATCTTATGTTAGATAACGAAGAGTTCAAGGTTATTCAGTCAATGATGCTTCTGCAATGAATGACCTTATGGCT
TTAGAAGAATTGAGCAGAATATAAAAGATCTTCCACCAATCTTCAAGGCTTACTACGTTATTGAGAAGTACTAAACGTTAGGTGACGT
ATCGATGATTTAGATTTGACGCTGGTTACTACAGAAATTGAGACTAGATGTTATTACACAAATAACGCGAAAATAGCGGTGATGTTG
AATGATGTTAGACTATTTGATAACATTACTAAAGAATATAGTCTATTGACAGGTAGTGAAGAGTCCTCAGATGCTTAAAGAATTAAAG
ATTTAGAACACGATTGATGATCAGCAAATCAATTAAAGTTAGAGCGCCTAAAGCTAGCTAAACAATTGAAAATGAAATCAAACAAGAATTA
ACAGAGCTTATATGGAGAAAGCTGATTCCCAAGTTCAAAAGGAAATTAAATAAGAAGGGAACGAAATCGTTGAAATTATTTATATTCA
ACGAATCCGGAGGGCTTAAAGCATTGGTAAAGGCTTACAGGAGTTCTGCGCTGGCCAGGCTATCGCTCAAAGGTTAGGTGACTTTACG
AAGGAAGATAAAAATTCTTCAATTGATGAGGGTGGATACAGGAGTTCTGCGCTGGCCAGGCTATCGCTCAAAGGTTAGGTGACTTTACG
AGTCATGGACAAGTTGATCAATTCTCATTTAGCTCAGGTTATTGCAATAGCGGATTACCAATAATTGAAAGGTTAGGTGACTTTACG
ACAGTTCAACGGTAAGGCTTTAAGCTATGAAGAACGTTAGAAGAACGTTAGTAAAGAACGCTAAAGTGGCAGGAAACATGTAACAGACACTGC
CAAGCTAAAGAATTACTGGTAGT

SEQ ID 296

MLEISIKNFAIIIEISLNFETGMVLTGETGAGKSIIIDAMNMMLGSRASVEVIRHGANKAEIEGFFSVEKNQSLVQLLEENGIELADELIIRRE
IFQNGRSVSRRINGQMVNLSTLKVAVGHYLVDIYQHDLQELMKPNMHLMLDEFGNTEFNVIKERYQSLFDAYRQLRKRVLDKQKNEQENKSRIEML
EFQIAEIESTVALKSDEDQTLMLQDKLMNHKNIADETLTNAYMLMDNEFSSLSNVRSAMNDLMALEEFDREYKDLSTNLSEAYVIEVTKRLGDV
IDDLDFDAGLQEIENRDLVINTTRKYGVDDFLVLDYFDNITKEYSLLTGSEESSDALEKELKILEHDLIESANQLSILERHKLAKQLEIKQEL
TELYMEKADFQVQFTKGKFNKEGNEIVEFYISTNPGEFKPLVKVASGELSRLMLAIKSAFSRKEDKTSIVFDEVDTGVSGRVAQAIAQKIHIG
SHGQVLIAISHLAQVIAIADYQYFIEKISSDSSTVSTVRLLSYEERVEIATKMLAGNNVTDARTQAKELLGS

SEQ ID 297

GTGATGTTATTAGAATTCTTAAAGGAAATTCTTGTATTATTGATGAAATTCCCTAAATTGAAAGGTTATGACGGTTTGACGGGTGAAACT
GGAGCAGGAAAGTCTATTATCATTGATGCTATGAATATGATGCTTGGTGCCTGCTAGTACAGAAGTGAATTGCTCGTGGAGCTAATAAGCAGAA
ATTGAGGGTTCTTCTGGTAGATGCTACCCCGAACACTGGTTGGCTGCTGGAAATCATCAGGTATTGCTATGGAAGAAGACTGATTATTGGCGGA
GATATCTTGCCTAATGGCAGAACGGCTGAGCCGCTTAATGGTCAAGGTTAACCTGACCCCTTAAACAGGCTGGACAGTTTTGGTAGATATT
CATGGCAACATGACCAAGAAGAAATTATGCTGACCAACAGCTCCACAGGCTTGGTGAATAGGCTTGGAGCAATTGAAAG
AATTATCAGCTTATTGATGTTAAAGCTTGTGCTGCCAGGTTATTGACAAACAAAAAATGAAAGAACACAAAGATCGTATTGATG
TTGGCCTTCAGATAGCAGAAATTGAGCTGCTGCCCTGAGTCAGGAGGACGGCTTAAATCAAGAACGTTAGCTTAATGAAACACAAAA
CAAATTGCTGATACCTGACCAATGCCATCGTCTGAGATAATGACGATTTCAGTCTATCCAATTGCTCTAGCATGAATGACTTACTA
TCAATTGAGCAGTTGATCAGAGTACAAGGGATGTCGACTTCGATTCTGAAGCCTTATTATCTGAAAGAAGTGAAGCAAGCAATTATCAGAT
ACCATTGACCAACTGGATTGATGTTGGGGCTGATCAGGAAATTGAAATTCTGCTTGGATATACTCAATGCTTAACTCGTAAATACGGTGGTAAT
GTGAATGATGCTGTTGACTACGATAATATGCTGAAAGAATACCGCTTAAACAGGAGTACTGCTTCTCAGGGGATCTAGAGGCGAAATTG
AAAAGCTTGGAAAAAACATTGGTTGCTCTGGAGTTAAGGCTCTCGCATTAATGGGGAGCAATTAGAACGTTGAGATTAAAGCTGAA
CTTAAAGGAACCTTATATGGAAAAGCAGATTCAAAGTTCACTTACACATCAAATTATGCTGATGTTAATGAAAGCTTGGAAATTTCAC
TCTACTAATCCAGGGGAAGGATTCAAGCCCCTGTCAGGTTGGCTCTGGAGGAGGTTATCACGCCATTGTTAGCCATCAAGGCTGCTATT
AGAAAAGAAGATAAGACGAGTATTGTTGATGAGTAGATACAGGTTCTGCTGGCGTGCAGGCCATTGCCAAAAAATTATAAAATT
GGGCAGCATGGGCAAGTCTCGCTATTCAACTTACCTCAAGTTATTGCTATTGCTGATTACAGTATTGCTATTGCTATTGCTATT
TCCACCGTTCTAAGCTAAGGTTATTAACTCCTGAAGAACGTTGAGAAATTGCTAGCATGATTGCAAGAACAGATATGACACAAGCTGCT
ACCGAGGCTCGTGAACACTTGGCAAACAT

SEQ ID 298

VMLLEISIKNFAIIIEISLNFENGMTVLTGETGAGKSIIIDAMNMMLGARASTEVIRRANKAEIEGFFSVDATPELVACLESSGIAMEEELIIR
DIFANGRSVSRRINGQMVNLATLKQVGQFLVDIYQHDLQELMRPQLHQQTLDAGDKAFELQKENYQLIQDFYKSLRQVIDKQKNEKEHDKRJDM
LAFAQIAEIAAAALSRGEDDRNQERDRLMNHKQIADETLTNAYVMLNDNDFSSLSNIRSSMNDLSSIEQFDSEYKGMSTSISEAYVIEEVSKQLSD
TIDQLDFDGGRLQEIIFRLDILNSLTKYGGNVNDVLDYDNTVKEYQLLTGDDLSSGDLEAELKSLEKQLVAAASELSVRHQLAEQLEAEIKAE
LKELYMEKADFVKVHFTTSKFNRDGNESLEFYISTNPGEFKPLVKVASGELSRLMLAIKAISRKEDKTSIVFDEVDTGVSGRVAQAIAQKIHIG
GRHGQVLIAISHLPQVIAIADYQYFISKEESTVSKVRLTPPEERVEIASMIAGTDMTQAALTQARELLAKH

SEQ ID 299

ATGAGTAAAGGAAATTGTAACGGATTCTCCATTACATTGAAACCAGAACATTATTAAAGAGCTGACATTACAGTTGTCAGTTG
ATAGATGTTACCTTGTATTGATGACATTAAAGCACAAGGGAAATTCTGAAACCTAATGCGTGGAGTAAGGAATTGCCAAAACAAGTCAA
CCACCTGTAGGTGTTTGTGAGAAATTATGAAATGAGTAACGGTGTGGAGCATATCATTGCAATTGCAATTGCAACACTATCAGG
ACTATTGAAAGCATCACGCCAGGGAGCTAATATTGCTGGTGCAGATGTTACAGTTATTGATCTACTTTACAGACCAGTGTAAAATTCCAGGTT
GTAGAAGCTGCGAAATTAGCTAAAGAGGGAGCTGATTAGATACCATCTGGCTCGTGTGAGAAGTACGCCAGAAGTCAGAATTATTTATTGGC
GTATCGACCCCTGAAAATTAGTAAAGGTTGGCTATTGGACGTTGTAACGGTCTTCTAAGTTCTATTGCTTAATATAAAAGTAATTATGGAGCTA
ACAAACCATGAAATTAGTACCGATTGTTAAAGGTCGGCTTAAAGACCTTCAGCAATGTTAGATAATTGTTGAAAGTGCCTAACACGAAA
ATTGCTGAAATTGGCATCTCTACTGTGGTAAAGCTGATATGGCTAAACTTATGAGAAAAACTAGCTGTTCTAGGTGCTCTATATCCGTT
GAAACTGGCTCAATCATCCTAACACTCATCTGGTGAAGGATGCAATTGCTGTTATGGTTGTTATGAA

SEQ ID 300

MSKIKIVTDSSITIEPELIKELDITVVPLSVMIDGTLYSNDLKAQGEFLNLMRGSKELPKTSQPPVGFAEIYEKLNEGVEHIIAIHLTHTLSGTIFASRQGANIAGADVVIDSTFTDQCQKFQVVEAAKLAKEGADLDTILARVEEVQRQSELFFIGVSTLENLVKGGRIGRTVGLLSSLLNIKVIMELTNHELVPIVKGRGLKTFSKWLDNFVESAQTRKIAEIGISYCGKADMANNFREKLAVLGAPISVLETGSIIQTHTGEDAFAMVRYE

SEQ ID 301

ATGAAAGAAATACATCGGAACCTATAAAATTCTTACAGATTCAATAACTATTGAAACAGAATTAAAGCTTTAGATATTACTGTAGTACCT
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AAAACAGTCAGGCCACCGGGTGGTCTCTTGTCGAAACTTACGAAAATTGGTCAAAAAAGGAGTAACCTACGACATTGTTGCTATTCACTCTCACCA
GCTTTATCAGGTACTATTGAAAGCTTCCCGTCAGGGGGCTGAATTCGTCAGGGCTGTACAGTTTAGATTCAAGGATTACTGTCAAGCCATG
AAATTTCAGGTCTGGAGGCAGCAGAACATGGCAAAGCAGGGTCTAGTTGAATGAGATTTTGGCTCTGTTCAAGCTATCAAATACAAAGAG
CTCTACATTGGTGTATCTACCTTAGAAAATTAGTAAAAGGAGGTCGTATTGGCTGTGACGGGTTTGAGCTCCTACTTAATGTC
GTTATGGCAGTAAATGATGAGTTAAAACGCTTGTCAAGGTCGAGGTAAACACATTACGAAATGGTTAGATAGTTACCTCGCTAAAAT
AGTCATCGCCCGATTGCGAGAGATAGCTATTCTTATGCTGGTGAAGCTAGGCTGGCATTAACCTTAAAGAAAGAATCGCAGCTTATTACAACCAC
TCTATTTCGGTTTGTAGAACAGGCTCTATCATCCAACACATACAGGAGAAGGAGCTTGTGCGTTATGGTCTGTTAGA

SEQ ID 302

MEKYMGTIKIVTDSSITIEPELIKALDITVVPLSVMIDSNLKLYSDNDLKKEGHFLSLMKASKSLPKTSQPPVGLFAETYENLVKKGVTDIVAIHLSP
ALSGTIEASRQGAETAEAPVTVLDSGFTDQAMKFQVVEAAKMAKAGASLNEILAAVQAITSKSTELYIGVSTLENLVKGGRIGRVTGVLSLLNVKV
SAMKNDELDKLTVKGRGNKTFKWLDSYLAKNSHRPIAIAISYAGEASLTLKERIAAYNHISIVLETGSIIQHTGEGAFAVMVRYE

SEQ ID 503
CTGACCAT

GIGAGGATGATTCTGGTATGGTCTATGAAATAAGAAAAAAACTTACCGGACTTCTTTCTGGTAAGCTCTTCTTATCTTTGG
ATTTCTTCTTGTATCCAAAATCAAATCCTAAATTAAACAGGAAAGCTTCCTAACAAAAGAGTATCTTCACTTAACAAAGAAGTATCTTCTTCTGG
GATTCTCTGACCGAAGGTGTCGGCGATACAACCTCTCAAGGTGGTTTGTTCACTGCTATCAGAACTCCATAATCGATACTCTTACCAAGT
ACTTCTGTTAATTATGGTGTCTGGAAACTAGTCACAAATTAAAACGTATGACGACAGATCCTCAAATCGAAAAGATTAGAGAAAAGCT
GATTTATTGACGCTAATGTTGGTGTAAAGAGCTCAGTCATTACTAAATTCTTGTGAGAACAGCA
GAAGCATATAAGGAACGTTTGAAAGAAATCCTTGCACAAAGCAAGACAAGTATCCTAAATTGCCATTATGTTTAGGCATTATAATCCTTT
TACCTAAACTTCCACAATTAACTAAATGCAACCCGTTATTGATAATTGAAATAAAAGCTACAAAAGAAGTGTGCTCAGAAAATGTTAT
TTGTCCTCAATTATGACCGCCTTATAAGGGATAAAAGGTAAAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCCTAAATGATGCT
CTCTTACTGGAGACCAATTTCATCCAATAATTGGCTATCAAATCATGTCATAACGCCGTTATGGAGAAAATAATGAAACAGAAAAACTGG
CCG

SEQ ID 304

MRMHLLWFVMNKKKILTGLSFFLVSLLLLSFGIFSLIIPKSNPKLTKKDFLTKKVIPLNLYVALGDSLTEGVGDTSQGGFVPLLSSES LHNRYSYQV TSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKEELSHLSLNSFEKPAAEYKERLKEILAKARQDNPKLPIYVLGIYNPF YLNFPQLTKMQTVIDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDFHFPNNIGYQIMSNAVMEKINETRKNP P

SEO ID 305

TTGCGGTATGGTCGTTATGAATAATCGCATTATTTAGTGGATATTTCTTGTATTAGTTATGCTGGCTTTTATTGCTAAATATT
ATTATCCCTAAGTCAAATTCACTACGGTTGAAAAAGAGTGATTTCTGAAAAAGAACAGTAGCTATCCAATATGTTCTAGGAGATTCAATGACA
GAAGGAGTAGGTGATCTAACATCAAGTGGTTTGTCTTGTAAACGAATGATCTCAGTGAATATTTAAGGCTAATGTTAATCATCAAAT
TACGGCTATCTGGTGTACAGTCACAAATTCTTGATAGGTGATAAAAACAAAAGCAGATACTAGTATCTTAAAGGAGCAGATAATGACG
TTAACCGTTGGCTGTATGATGTTATGGCAGTTATCGGAAGAATTAGCGGATTTCGAAGTTCTAGTTTAAAGGCCAGCTCGTCAGTATCAA
AAACGATTAAGCAGATTATCGAGTTAGCAGGAAAGATAAAAGATCTTCTATTTTAGGCATCTATAATCCTGTTTATTGAAATT
CCAGAACTTAACGTATGCAAAAGTGTGACTGGAATACCAAAACTAACGGAGTTGTTGGAGATAACGATCTGTGTACTTTCTGCAAAAT
AATGACCTCTGTATAAGGGATAATGGACAAGAAGGAATTGTCATTCTCAGGAGATCAAACACTACAATTGTCATGATGCCTGTTACTGG
GACCATTTACCCAAATAACTGGCTATCAAATCATGTCAGTAATGGAGAAATTAAAAGCATGAAAAAAATCAAACCT

SEQ ID 306

LRLWFVMNRRHLFGIFFFVVISLCLAPLLLNTIIIPKSNSRLKKSDFLKKEQVAIQYVAIGDSLTEGVGDLTHQGGFVPLLTNDLSSEYFKANVNHQNYGVSGDTSQQIQLDRMIKQKQIQLSLKKADIMTLTVGGNDVMAVIRKLNADLQVSSFRKPQRYQKRLRQIIIELARKDNKDLPIFILGIYNPFYLNFPELTDMQKVIDDWNTKTKEVVGEYDRVYFVPINDLLYKGINGQEGLIVHSSGDQTTIVNDALFTGDDHFHPNNNTGYQIMSNAVMEMEKIKKHEKKIKP
SEO ID 307

ATGAAACA

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CAACTGAATAAGACAATTGCACTTTATTAAAACAATATCAAACAGAAGATGAATTATAAGATTATGCTGCTTCATCTCTATACTATTGAA
GGCTCTTATCAATTATTAGGGTTAGAAGTGCCTTATACATCTATTGGACCTTATCGCTTAAACAAATGGCGCTGTTCAACTTAAAGTGACCTCA
TTTTCAGTAGGAACCTCCCGCTTCCAGAAAAAGATGTGTTACAATATATAAAATCATCTTATAATTGCCCACCTTGTAGATATAAAACCTAAA
AAATCGGGTTATTAAATTGCAAGATTAAAAAAATAAGAAGGTATTATTGAAAGCGACTGCAATTGATTAGTAAACGATAATTAGT
TTCGATATTGAAAGAAAAAGGCC

SEQ ID 308

MKQEKTGRNLNFWKWAFLLLLAINLSFTAVIASRLLIQVREPNTGKISTGVQDKVKVGTFTTNNKSQNLNTIALYLKQYQTKKMNYKIIYAASSSLFEGSYQLLGVEVPLIYIFEPYRLTNGAVQLKVTSFSVGTLPPEKDVLQYIKSSYKLPNFVDIKPKKSVININLQDLKNKEGYLKATAIDLVNDNFSFDIFKKKP

SEQ ID 309

ATGAAACAAAAAATCAACCTTAATTGGTGGAAAGTGGAGCTCTTATGTCGTGCTTTAATACCGCCTTTTGATGGTTATTGCAAGTCGTC
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GAAACTGTAGCAAGTTATCTAAAGATTATCAGACTGAAAAATGTCTATAAAATTTATGCGACATCTCTCTATTTGTTGAAGGAACCTTAT
CAATTATTAGGGTATGAAGTCCCTTATATATCTATTTCACCTCATCGTAGAAAATGGAGCTGCCAACTACAGTGATCTTTTCAGTG
GGAACCTGCCACTCCCCAGAAAAAGATGTTTGCAAGTAAATCAAGCTACAAATTGCCAAGCTTGTAAAGTGATGCCAATCAATCAGCT
ATCCTGTTAATTACAAGATATCCAAATGATGCTAAGGTTATTAAAGCCAAGAAAATTGATTTATTAATGATGAAATCAGTTAACATC
TATAAGAAA

SEO ID 310

MKKKSNLNWWKWSFLCLLAFNTAFLMVIASRLIQVREPESELIAKKPVKNIKIGTFVTTREQLNETVASYLKDYQTEKMSYKFYATSSSILFEGTYQLLGYEVPLYIYFQPHRLENGAVQLQVISFSGVTLPLPEKDVLQYLKSSYKLPSFVKVMPNQSAIVVNLDIQNDAKVYLKAKKIDLFNDEISFNIYKK

SEQ ID 311

ATGGCTAACAAACAAGATTAAATTGCAAAAGTAGCAGAAGCTACAGAATTAACAAAAAGATTTCAGCAGCAGCAGTAGATGCAGTTTGCAAGCT
CTAGCAGATTACCTTGTCTGAACTGCAAAACTGAAATTAACTGGTTNNNNNNNTTAATTAA

SEQ ID 312

MANKQDLIAKVAEATELTKDSAAAVDAVFAAVADYLAEGEKVQLIGXXLIN

SEQ ID 313

ATGGCTAACAAACAAGATTAAATCGCAAAGGTTGCAGAAGCAACTGAATTGACTAAAAAGATTAGCAGCAGCAGTTGATGCCGTCTTCTACA
ATCGAACGCTTCCTGCTGAAGGTAAAAAGTACAATTGATCGGTTGGTAACCTCGAAGTACCGAACGTGCACTCGTAAAGGCTAACCCCA
CAAACGGTGAGAAATTGCACTTCAAAGGTTCCAGCCTCAAAGCTGGTAAAGGCTTAAAGGCTTAAAGCAGCTGTTAAA

SEQ ID 314

MANKQDLIAKVAEATELTKDSAAAVDAVFSTIEAFLAEGEKVQLIGFGNFEVRERAARKGRNPQTGAEIEIAASKVPAFKAGKALKDAVK

SEQ ID 315

TTGGCTACTAAAGTAGATGTTCAAAAGATGGCTTAACTTACAGCTACATTACGTTAAAGGCTGAGTGGTCAGATGGCAGTAAACTTACTGCA
AAGGATTGTTATTCTATGGCAACGTTAGTTGATCCTAAACAGCTTCAACATATGCTTACCTTGCTGTTGAAGGGCATGTCCTTAATGCCGAT
AAAATCAACGAAGGACAAGAGAAAAGACTGAAATAAGCTAGGTGTTAAGGCGGAAGGCGATGACAAGGTTGTTATTACTTATCTAGTCCGCTCCA
CAATTATCTACTACCTTGCATTCACTAATTCTATGCCACAAAACAAGAAGTGTGAAATGGAAAGGTTGTTAAAGGCTAACACTTCAAAAAT
ACAGTTACTCAGGACCATATACTGTGAGGTTGGAATGGTCACTGTTACAGCTGAAAGAAAACAACATTATGGGAGCCTAAACAT
GTAAAACAAAAGAAGTGTGCACTTCAAGACTGTTAAAACAGATACCCTGGCTGAAATGTATAAGCTGAGTGGTCAAGTGCAGCTAATATCTCA
AAATCTCTGCTTATTCTAACGATAAAAGAAGATGTCACAGATGTTCTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCATGCTTAAAGGCTTAA
TCTGTGAAAGGGCTTGTATAATGTTAAAGGATTCGCTCGCCCTTAAACTTAGCAACTAACCGTAAAGGAGTTGTTCAAGCAGCCGTTGATACAGGCTCA
AAACCGGCAATTGCTTGCACCTACTGGTTAGC AAAACACAGATGGAACGTGATTGGC AAAATATGTTGCCCAGGTTATGAAATATAA
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AAAAACTCTGTTGACTATATCAAGTCTACTTGGAGCTGCTCTCAGGACTACTGTTGAAGAAAATTGTAACCTTAAACACGCTTAA
GACAGTAGAAAACAAAACCTTGACATCGTAGTTCTCTTGGGGATTATCCAGAAGGATCAACTTCTACGCCCTCTTAAAGTCAGATTCA
AAAATAACGATGGAAAATTGCTAACAGGACTATGATGCTGCTTATAACAGGCAATTCTGAAGATGCGATGAAACCCAGCAGAATCAGCGAAG
GACTTAAAGAAGCAGAGAAAATTTATTGAGCAAGGTTGCTTATAACCCACTCTCCAGGACTACTGTTGAAGAAAATTGTAACCTTAAACACGCTTAA
GGTGTATTGCTAACATACAGGTTGCTAACAGCTTACACATGCTTATAAAAATAAT

SEQ ID 316

MATKVDVSKDGLTYTATLRKGLKWSDGSKLTAKDFVYSWQRLVDPKTASQYALAVEGHVLNADKINEQKEIDLNLKGVLKAEGDDKVVITLSSPSP
QFIYLYAFTNFMPQKQEVEKYGKDYATTSKNTVSGPYTVEGWNGSNGTFKLKNKNYWDAKNVKTEVRIQTVKPDATVQMYKRGELDAANIS
NTSAIYQANKNNKDVTDVLEATTAYMEYNNTGSVKGLDNVKLRALNLTNRKGVQAAVDTGSKPAAIFAPTGLAKTPDGTDLAKYVAPGYEYNK
TEAAKLFKEGLAESGLTLKLTTADADAPAAKNSVDYIKSTWEALPLTVEEKFVTFKQRLEDSRKQNFIDIVSVLWGHDYPEGSTFYGLFKSDS
QNNDGKFANKDYDAAYNAISEDAMKPAESAKDYKEAEKILFEQGAYNPLYFRSGKGLQNPKLKGVIIRNTGLSIDFTHAYKNN

SEQ ID 317

GTGACTTTATGAAGAAAAGTAAATGGTTGGCAGCTGTAAGTGTGCGATCTGTCAGTATCCGCTTGGCAGCTGTGTAATAAAATGCTTCA
GGTGGCTCAGAAGCTACAAAACCTACAAGTACGTTGTTAACGATCCAAATCATTGGATTATATTGACTATGGCCTGAAAGGTTCAAAAGACGGT
GTGATAACACAAATGGTTGATGGTCTTGGAAAACGATGAGTATGGAATTAGTACCATCACTTGCTAAAGATTGGAAGGTTCAAAAGACGGT
CTGACTTATACTTACTCTCGCAGGGTGTCTTGGTATAACGGCTGATGGTGAAGAATATGCCAGTAACAGCAGAAGATTGACTGGT
TTGAAGCACCGGGTGCAGGATAATCAGATGCTCTTACGGTCTGAGGTTAACAAACTTAAAGGCTTACCAAAATGGTAAGTAGATT
AAAGAAGTGGTGTCAAACCCCTGACGATAAAACTGGTCACTGTTGAACAAGCCTGAAAGCTACTGGAAATTCAAAACACTTATAGTGTG
CTTCTCCAGTAAATGGAAATTGGTAAAGGTTGAGTCAAACGGTCAACCTGCTCATCATCAATCTTGTAAATGGTCTTACTCTTGTG
AGCCTTACCTCAAATCATATGGAACTTCTTAAAGGAAACTGGTCAAGGACTTACGGTCTGAGGTTAACAGGCTTACCTGCTTAA
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GCTAAGAAAACATGCTGATAACATTACTACGGAAATGGTCACTGGAGATATCCGTATTAAACATGGAATTGAAACCGTACTCTTCAAAAC
ACTAAGAAAAGCCCTGCAAACAAAGATGCCGTAAGAAAGCTCTAACAAACAGGATTTCGTCAGCTTACGTTGCTTGTGACCAGCTCA
TTCAACGCAAACACTGCAAGGTCAGGATGCCAAACGGCTTACGTAACATGCTTGTCCACCAACATTGTGACCATTGGAGAAAGTGA
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GCAAAGCTGAGTTGCAAAGGAAAGCTTAAACAGCTGAGGTTGAAAGCTTCAAGCTTCAATTAGATTACCTGTTGACCAAGCAAACGCA
GCAACTGTTGAGGCCAGTCTTCAACAAACTGTTGAGGAAAGGAGATCTTGTGAAATGTCATTGTTGAAACAGAAACATCA
ACTCACGAGCCAAAGGTTCTATGCTGAGACCCAGAACAAACAGACTACGATATCATTTCATCATGGTGGGGACAGACTATCAAGATCCACGG
ACCTACCTTGACATCATGAGTCCAGTAGGGTGGATCTGTTATCCAAAACCTGGAAATCAAAGCAGGTCAAAGGATGGTGGCAGCTGCA
GCCCTTGATACCTACAAACTCTCTGATGAAGCAGCAGCAATTACAGACGACAACGATGCGCGTATAAGCTTACGCAAAGCACAAGCCTAC
CTTACAGATAATGCCGAGATTCTCAGGTTGCACTGGGACTCCACGAGTTACTAAAGCCTTCAATTAGTGGGGCTTCTTGGGCA
GGGTCTAAAGGTCCTCTAGCATATAAGGAACTTCAAGACAAACCTGTCAGTAAAACAAATACGAAAAGAAAAGGAAATGGATGAAA
GCAAAGCTAACGTTAACATGCAAATATGCTGAGAAGTTAGTGTGATCACGGTCAAAGGTT

SEQ ID 318

VTFMKSKWLAASVAILSVALAAGCGNKNASGGSEATKTYKVVFVNDPKSLDYILTNGGTTDVITQMVGLLENDEYGNLVPSLAKDWKVSKDG
LTYTYTLRDGVSWYTADGEYAYAPVTAEDFVTGLKHAVDDKSDALYVVEDSIKLNKAYQNGEVDFKENVKALDDKTVQYTLNKPEVNSKTTYSV
LFPVNAKFLSKKGDFGTTDPSSILVNGAYFLSAFTSKSSMFHKNENYWDAKNVGIESVNLKTYSDSDPGSFYKNFDKGEFSVARLPNDPTYKS
AKKNYADNTITYGMLTDIIRHLTNLNRNTSFKNKDPQAQDAGKKLNNKDFRQAIQFADFRAFSQAQTAGQDAKTKALRNMLVPPTFVTIGESDF
GSEVEKEMAKLGDEWKDVNLADAQDFYNPKEAKAFAKABALTAEGVTFPVQLDYPVDQANAATVQEAQSFQKSVESLGKENVIVNVLETETS
THEAQGFYAEPEQQDYDIISSWWGPDYQDPRTYLDIMSPVGGSVIQKLGKAGQNKDVAAAAGLDTYQTLDEAAAITDDNDARYKAYAKAQY
LTDNAVDIPVVALGGTPRVTKAVPFSGGFWAGSKGPLAYKGMLQDKPVTVKQYEKAKEWMKAKAKSNAYKAELADHVEK

SEQ ID 319

TTGCTATTAGCAATTCTAACGAAAAGGAAATGATGATTAATATATTAAAGCGTGTGCTATTGTTAGTAAACGCTATGGGTTGTCATA
ACCCCTATCGTCTTCTGATGCAGATCCCTCCAGGAACACCCCTACAATAATCCAAAACACTCACTGAAGAAATGATGCCATTGCTTAATAACAGTAT
GGTTAGACAAGCGCTGATGCCAAACATATTGACTTACCTTGGGAATGTACTTCATGGTCACTTTGGAAACGAGTTATCAATCAGTGAATGCCA
GTATCACGTGATTAGCTGAGATTAGGAGTTCTAGTACATCTAGGTGTTCTGCTAGGCTCTGTTAGGGATTCTATGCCCTCATTTATGCTATCTT
TTATTAGACTTATGGATTAAAGTGAACCTGGCTTCTGCTTACGGTTGGGGACTTTCTCTAACCCATTCTTACCTTCTTGTCTAGGACTC
CCTACATTAGCATCTGTTCTACGCTTCTCCCGTAGTGAACATGTTAAACCTTCAATTGTTGAACTAGCTGTTCAAAGGTTATGACA
ATTGCTAACGTAACCTGAAACATGCTTACCGTAAATTCTATGTTCAATTGCTTAACTCTAATTGGCCCTTGGCGGGCTGTTAACGTTCT
GCACTAATTGAGCAGATTCTCGATCCAGGAATTGGGAGCTTGTACTCTGATTCAACAAACAGACTATCTGTTATTAGTATGCTAGACCCACGTGTTGCTGAG
ATTGTTATGCTAACATGTTGATGGTGTCTCTTGTAAACAGACGTTGTTATTAGTATGCTAGACCCACGTGTTGCTGAG

SEQ ID 320

MLFLAIRKGNDMIKYILKRVAILLVLWVVITLSFFLMQILPGTPYNNPKLTEEMIALLNKQYGLDKPVWQYLTLYWNVLHGDFGTSYQSVNQP
VSRMISLRLGVSVHLGVQALVFGVLGGILVGAISARHNDKVDGILSVIATLGISMPSFIIGILLLDYFGFWNLPLSGWGTFQSITLPSLALGL

P TLASVSRFFRSEMIETLNSDYVQLARSKGMTIRQVTRKHAYRNSMIPILTLIGPLAAGLLTGSALIEQIFSIPGIGQQFVTSIPTKDYPVIMGTT
IVYAVMLMVALITDVVISIVDPVRVLQ

SEQ ID 321

ATGGCAGATAAAAACAGAACATTAACTTGTAGGTGCAGGATCTCTAGCACACAAGAAAAATTGAAAAGCCTGCTTCGTTATGCAAGAT
GCCGCGCCTGCTGAAAAAAACAAATTAGCAGTAGTTCACTCTATTAGCTCTTACTTACTTTCTTAGCCTCAAATTATTTGTA
ACTCAGAAGGATGCTAATGGTTGATTCGAAAAAGTAACATACATCGCAACTTACCCACTAAATTGAGTTCAAACCTTCTTTGGAATGGT
AGCATTAAGTACGCTGAAATACAGAACATCAGACGTTATAAGTCTAAATGCTGAGGTTAAGTAAAGTTAAGTATGCTTAGGTACAGATTCTCA
GGGAGAAGTGTGCTAACGCGCATCATCGTAGGTATCGGATTCCTACTTGTAGCTATTGAGCTACATTGATTAAATTATCGGTTACA
TACGGCTTCTTGCTGGAGGACGCCCTGATACATTAATGCAAGCTATCGTAGAGGTTAATTTCATCAATTCCAACATTAGTTATCGT
ACAATGTTAGGTTGGCTTGGTAAAGGTTACCGGCTATTATCTCTATTGCTTACCCGATGGACTTCTATGCTCAGGTAAGGAAT
TTAACCTCATATCGAGAAAGAGAGTTGTGCTGACGTTACGGTAACTTACAGGTTAAGTAAAGTCCAAATTAAAGCCTCAAACATATTAC
ATTTCGTTATTATCTATTGACAAATTATGACAACTCCAGTCTATTGATGAGGTTACCTTCAGCAATCAATTAGGTGTTAACCA
CCGACAGCTCATTAGGATCATTGATTCAGATGCAAGAAAATTACATATTCCATATCAAGTTATGCTGAGGTTAGCATTGGTAATG
ATTTCATTGGCATTATTGCTGGTATGGGTGCGAGATGCTTGTGAGGTTAGCATTAGCGATGAA

SEQ ID 322

MADKNRTFKLVGAGSSSTQEKIEKPALSFMQDAWRLKKNNKLAUVSLLYLLFLFSLASNLFVTKDANGFDSSKVTTYRNLPPLSSNLPFWNG
SIKYAGNTTESTDAYKSQNVPKEVKYALGTDLSGRSVAKRIIVGIRISLLVAIAATFIDLIIGVTYGLVSGFAGRLDTLMQRIVEVISSIPNLVIV
TMLGLVLGNGITAIISIAFTGWTMSMRQRNLTLTSYREREFLAARSLGESPIKIAFKHILPNISIIIVQIMMTIPS AIMYEAVLSAINLGVKP
PTASLGLSISDAQENLQVPPYQVILPALALVMISLAFLILLGDGLRDAFPDKSSDE

SEQ ID 323

ATGGAATGATTGATAAACTTAAATTGCTGAGGCCGATAGTGAAGCCTCCGAAGTGATTGATACCCCTGCTTATTCTTACTGAAATCA
GTGTTTCGCTCAGTTTTCTAAAAAAATCTACAGTCTTATGCTCGTAATTAGTGAAGCTTGTGATGAGCTTATTTATCCTAAATGTTGCC
AAACTACGACTTAAATGACGTTAGTAATATCAATGACTTTCAAAGCGTTATATTGGCCAATGCTGAGGACTCTGGTTGGAACCCGACAAAATGGG
CAATCTCTGGTATGGTGTGGTATGGGGCACGTAATTCTATTAACTCAGTTAGGACACTAATTAAATATCACCATTGGGTTAGTGT
GGAGCCATATGGGAGTTCTAAAGCATTGATAAAGTTATGATTGAAATTATAACATTATCTCAAATATCCTCTATGCTTATTATCATTGTT
TTGACCTATTCATTAGGTGCAAGGATTGGAATTGATTGCTTACTGGGATTTGCTGATGACTGGGATATTGGTGTGCGCTACTCCATCGTGT
TTGCGTTACCGTGTGGTAAAGAACACCTGCTAGTCAAACATTGGGAACACCAATGTAAGGTTAGTGTGTTAAGAACCTCCCTGCTCAATTGGTT
TCAGTTATCATGACTATGTTGCTAACAACTGCTACCGTTATGATCTTCTGAGGCTTCTTATCCTCTTGGGATTGGTTACCAACCAC
CCAAGTATTAGGACGTTATTGCTAATTATCAGCAACTAACAAATGCCACCTCTTGGATTCCCTTAGTAACATTGATTAGTGT
TTACCACTATACATTGCTGGACAAAATGGCTGATGCGAGTGGCCAGTCACTAGA

SEQ ID 324

MESIDSKFRFVERDSEASEVIDTPAYSYWKSVFRQFFSKKSTVFLVILVTVLMMIFIYPMFANYDFNDVSNINDFSKRYIWPNAEYWFGTDKNG
QSLFDGVWYARNISILISVIATLINIITIGVVLGAIWVSKAFDKVMIEIYNIISNIPMSLIIIVLTYSLGAGFWNLILAFCITGWIGVAYSIRVQI
LRYRDLEHYNLASQTLGTPMYKIAVKNLLPQLVSVIMTLSQLPVYVSSEAFSFFGIGLPTTDSLGRFIANYSSNLTNAYLFWIPLVTLILVS
LPLYIVGQNLDASDPRSHR

SEQ ID 325

ATGGAAAAAGAAAATATTAAAGTGTAAATAATCTCATGTTGACTTCCACACATATGCTGGAGAAGTAAAAGCAATTGATGTCACATTGAA
TTAAAAAAAGGTGAGACTTCTGCAATCGTGGTGAATCTGGTCAAGGAAATCTGTAACCTACAGAAGAGACTGACTAAGGTACGCCGGAAATGAGATT
GAGATATCAGGGATGTTCAATTAAAGGGCGTAAACCTGTTGAACTATCAGAAGAAGAGTGGACTAAGGTACGCCGGAAATGAGATT
TTCCAAGACCCATGACTAGTTGGATCACAAGTCAAAGGAAATTGGCATGCAAATAGCAGAACCAATGATGATTGATCATAAAATTTCAAAAAGGAT
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CGCAGACCTGCGGGTTAGCAGGTTAGCTGCTGATCTGAAATTGGCTGATGAACTCTCCATTGTTCTATAACTCATGACTTAGGGTCTGCGAGGAGTGGCAGAC
CAAATTGAACTTAATGAAAGAACACGAGACTCTCCATTGTTCTATAACTCATGACTTAGGGTCTGCGAGGAGTGGCAGAC
CGTGTAGCAGTTATGATGAGGAAATTGTTGAAATTGGGAACTGTTGATGAGCTTTATAACTCCACACGAGATTGTTGAAACCCACTAAAGGAGATGCA
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GCAGCTGTAATGAATTGCTTGTGATGATCATGAGAAGAACACCACCGTACTTCAGAAACACATTGCTGCTACATGGCTTAA
GATGAAAGATCACCTAAGGTGCTCCTCCATTACCGATCCAAAACGTTGGGAAATGGAACGAGATTGAGAAGGGAGGAAAGCC

SEQ ID 326

MEKEТИLSVNLHVDFHTYAGEVKAIRDVNFELKGETLAIVGESGSGKSVTRTLIGLNAKNEISGNVQFKGRNLVELSEEWTKVRGNEISMI
FQDPMTSLDPTMKIGMQIAEPMMIHQKISKDDALKALELMKDVGIPNAAEHHNDYPHQWSGGMQRRAVIAALAADEPEIADEPITLADVTIQA
QILNLMKKIQAERDSSIVFITHDGVVAGMADRVAVMYAGKIVEFGTVDEVFYNPQHPYTWLNLNSMPTEDESGLSLESIPGTPPDLLNPPIKGDAF
AARNEFALDIDHEEPPYFKVSETHFAATWLDERSPKVLPLPPIQKRWEKWNEIEGRKA

SEQ ID 327

ATGACTGAAAAATCGAAAAAAATTAGTGAAGTCAAAATGTTCTTGACCTTCATAAAAGGAAAAGCTAATGAGTGAAGGAGCAATTGATAATGTT
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ATTCTGTGAGGAAATTACCTTAATGGAGAAGTGTCTCACATCTGAAAGGTTAACGATTACATAGTTCTGTAAGACGCTCAGATGATT
CAGGATCCTCAGGCTAGTTAACGGCGTATGAGAAGATTGCTGATATCGTAGCAGAAGGTTAGATATAACATAATTAGCTAAATCAAATCAGAT
CGTGTAGCAGTTAACGTTGAGGTTAAAGATGTTGAGGTTAACACGTTATCGCAGTGAATTTTCAAGGTTGAGCACAAG
CGTATCGGGATTGACCGTCTTAGCAGTAGGCTTAATTTTATCCTGCTGATGAAACCAATATGCTCTAGGTTCAATCCAAGGACAAGT
GTTAATTAACTGCAAAGAACAGAACAGGTTAGCTTATGTTATCGCAGTGAATTTGTTATGTTAAGGTTAACATTTCAAGTGT
GGTGTGTTATGCTTGTGGGAAACTGTTGAGGTTGGAAACATCTGATGATGTTATAACAACTCCACCCCTATACGAAGAGTCTATTAC
ATTCCAGAACAGATCCGGAGAGTGAACGTCACGTTACCCAGCGTATAATCCAGCTATTGAGCAAGACGCCAGAACAGTCAAATGACGAG
ATTACCCCTGGTCAATTGTTATCTACACCCAAAGAAGCTGAAGAATATAAAAACAAATATTA

SEQ ID 328

MTENRKKLVEVKNVSLTFNKGKANEVRAIDNVSFDIYEGEVFLVGEESGSGKTVGRSLIKLYDISDGEITFNGEVISHLKGKALHSFRKDAQMIF
QDPQASLNRMKIRDIVAECLDIHKLAKSKSDRSKVOALLDLVGLNKDHTRYPHEFSGGORORIGIARALAVEPKFIIADEPISALDVSIQAOV
VNLMQKLQREQGLTYLFIHDLSMVKYISDRIGVHMWGKLLEVGTSDVYNNPIHPYTKSLLSIAPEPDPESERQRVHQPNPAIEQDGQERQMH
ITPGHFVLFVLPSTPQEAEYYKKQJL

SEQ ID 329

ATGCTGAGAAAATTAGTCGAAGTAAAAGACCTAGAAATTCTCGGAGAAGGAAAGAAAAATTGTTGAGTTAAAATGCTAATTCTTATT
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CAAATTAACTGATGGAGAAGTAAATTAGGCAAGGAAATCAGAAGGCAATGAGCTCATTGCTAAATTCAAATGATTTCAGAAGT
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AAAATTAAAGAACATGATGGCGAAGTTGGTTGCTATCAGAGCATTGAGCAGCGTACCCCTCATGAATTTCAGGAGGTCACGTCAGCGGATCGG
ATCGCTAGGCCCTAGTAACTGAGCTGAACCGTATTGCTGATGAGCAGGATTTGAGCTTGGACGTTCCGTTGCGCACAGGTCTGAATCTT

CTTAAAAGAATGCAAGCCGAAAAAGGGTTGACTTATCTCTTCATTGCCCATGATCTTCAGTCGTCGCTTATTCAGATCGTATTGCGGTTATC
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 CCAGATCCAATTAGGGTCAAAAGAACACTTGTGTCTATCATCCAGACCAACATGATTATACATTAGATAAGCCATCAATGGTTGAAATCAA
 CAAATCACTTGTGCGAACCAAGCAGAAATTGAAAATATCAAAAGAATTG
SEQ ID 330
 MSEKLVEVKDLEISFGEKKKFVAVKNNANFFPIKKGETFSLVGESGSKTTIGRATIGLNDTSSQILYDGKTINGRKSKSEANELIRKIQMIFQDP
 AASLNERATVDYIISEGLYNFPNLFKTEERKEKIKNMMAEVGLLSEHLTRYPEFSGQRORIGIARALVMNPEFVIADEPISALDVSVRAQVLNL
 LKRMQAEKGTLTYLFIAHDLSSVRFISDRIAVIHKGVIVEVAEFEELFNNPIHPYTQSLLSAVPIDPLERQELVYHPDQHDYTLDKPSMVEIK
 PNHFVWANQAEIEKYQKEL
SEQ ID 331
 ATGACAAAAAAACAATAATCTGTCAAGCGAGACAGAAAAGAGCAAAGCTCAAACCTTTAATGAGAGTTGATCCTGGCTCAGGACGAACGCTGGCG
 CGTGC
SEQ ID 332
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SEQ ID 333
 GTGACGGTAACTAACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAAACGTAGGTCCCGAGCGTTGTCGGATTATTGGCGTAAA
 GCGAGCGCAGCGGTTCTTAAGTCTGAAGTAAAGGCAGTGGCT
SEQ ID 334
 MTVTNQKGTANYVPAAVIRRSRALSGFIGRKASAGGSLSLKLKAVA
SEQ ID 335
 TTGTACGGCTTGAAACTGGAGACTTGAGTCAGAAGGGAGAGTGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGAACACCGG
 TGGCGAAAGCGGCTCTCTGGTCTG
SEQ ID 336
 MYALETGGLCRRGEWNMSMCSEGMRYYMEEHRWRKRLSGL
SEQ ID 337
 GTGGCGAAAGCGGCTCTCTGGTCTGTAACGTGAGCTGAGGCTCGAAAGCGTGGGAGCAAACAGGATTAGATAACCTGGTAGTCCACGCCGTAAAC
 GATGAGTGC
SEQ ID 338
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SEQ ID 339
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 AAT
SEQ ID 340
 MLGVRFPPGLSAAANALSTPPGEYDRKVETQRN
SEQ ID 341
 TTGAAACTCAAAGGAATTGACGGGGCCCGACAAGCGGTGGAGCATGTGGTTAATTGAAGCAACGCGAAGAACCTTACCAAGGTTGACATCC
 TTC
SEQ ID 342
 MKLKGDGGPHKRWSMWFNSKQREEPYQVLTSF
SEQ ID 343
 TTGTTAGTTGCCATCATTAAGTTGGCACTCTAGCGAGACTGCCGTAAACCGGAGGAAGGTGGGATGACGTCAAATCATCATGCCCTTAT
 GACCTGGGCTACACACGTCTACAATGGTGGTACAACGAGTCGCAAGCGGTGACGGCAAGC
SEQ ID 344
 MLVAIKLGTLARLPVINRRKVGMTSNHHAPYDLGYTRATMVGTTSRKPVTAS
SEQ ID 345
 TTGTTAGTTGGAGAGGTCTGTGGGCTTAGCTCAGCTGGAGAGCGCCTGTTGCACGCAGGAGGTGAGCGTTGATCCCGCTAGGCTCC
 ATTGAATCGAAAGGTTCAATTGTTCAATTGAAATTGAATATCTATATCAAATTCCACGATCTAGAAATAGATTG
SEQ ID 346
 MFSFERSCGALAQLGERLLCTQEVSISIPLGSIESKGSNCNSLKIYEYLQIPRSRNRL
SEQ ID 347
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 GATATTGATTATTAAAGTCTGCTATTGTCATCAGATTATCAGTTAATGGTCAAATCTATGGGAAATTCACTCGAGGATATTACAATTACTAA
 AATCCAGTTAAAGTACAATAAAAGAACGTATGTTAAATTCTGGAGCCGATGTTGCTTAATGACAGGAAGTGGACCAACTGTTTTCAATGTG
 TCTACAGAGAAAAAGCTGATGTTTTAATAGTATGAAAGGTTTACAGGTTAGGTGAGAAGGTTAAAGTTAGGTGTTGAGA
SEQ ID 348
 MKIFEKAPAKLNGLDIKGRCDDGYHELMIMVSIDLNDYVTISELKEDCIVIDSSSKMLNNDNDVFKAADIKNQYGINKGVHIREKSIIPVC
 AGLGGGSTDAATIRALNRLWNLQMDYDEMVAIGFKIGSDVPYCLGGGCSVLGKGEIVKPLPTLRCWIVLVKPDFGISTKSIFRDIDCKSISRV
 DIDLLKSAILSSDYQLMVKSMGNNSLEDITIKNPVISTIKERMLNSGADVALMTGSGPTVFSMCSTEKKADRVLNFNSMKGFCKEVYKVRLR
SEQ ID 349
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 ATTTGGGCTGTTATCGCTTGGGTTGGTTAAACAGATTTGGTATCTCGACT
SEQ ID 350
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SEQ ID 351
 ATGACAGTTAGAACAAAATTAGACCAATTAGTGGAGTCAAATCTGCTTAAAGCAGAAAATCAACATGAAATTAGTGGTACTTGTCAAAGT
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 CAGGCAGCTGAACTAAAGCAGTAAAAGTTAACTCTCAGGATATGTTGAGAACAGCAAAACACATCATGACAATACGTTAGGGTTACGGAAGATTAGTAAATCATTGAG
 TTATGCAACTGCTAAACCCATTGCGAGATCACACACATCATGACAATACGTTAGGGTTACGGAAGATTAGTAAATCATTGAG
 GACGAAAGGTGTTAGAACGTTTCTGATCTTCTAGAGAATTAGAACGG

SEQ ID 352

MTVLEQKLDHLSQILLKAENQHELLFGTCQSDVKLTNTQEHLMLLSEQQLTNSDLAKKLNISQAATKAVKSLISQDMLKANKDSKDARITYFE
LSELAKPIADEHTHHHDNTLGVYGRLVNHFSDKEVVLERFLDLFSRELEG

SEQ ID 353

ATGGGGATTAGAAAAAAACTTGATAACTTAGTAAATACTATTTATTAAAAGCAGAAAATCAGCATGAGTTATTATGGAGCTGTCAAAGT
GACGTTAACGTTACTAATACGCAAGAACATATTAAATGTTACTATCTCAGCAACGCTCTACTAATACAGATTGGCTAAGGCATTAATATTAGT
CAGGCGGAGTAACTAAGGCTATCAAGAGTTGGCTAAACAAAGACATGTTAGCAGGAACTAAGGATACGGTTGATGCTAGGGTACTTATTGAA
TTAACCGAGTTAGCTAACGCCATTGGCTCAGAACATACCCATCATCATGATGAAACCTTAAATGTTACAACCGTTATTACAAAATCTCCGCG
AAAGAATTAGAGATTGTAGATAAGTTGTAACAGTTGCTGAGGAATTAGAAGG

SEQ ID 354

MGILEKKLDNLVNNTILLKAENQHELLFGACQSDVKLTNTQEHLMLLSEQRLTNTDLAKALNISQAATKAIKSLVKQDMLAGTKDTVDARVTYFE
LTELAKPIASEHTHHHDTLNVYNRLQKFSAKELEIVDKFVTVFAEELEG

SEQ ID 355

ATGCGATATATTACAGTTAGGGCTTACTTTCACTACGATAGCGATCCTGTGCTGGAAGGGTTAATTACCATTTAGACAGTGGGAGTTGTT
ACCTTAACAGGTAAATGGGCTGCTAAATCAACTTAAATAAAGGCTACTTTAGGTATTAAACGCCAAGTGGGTCAGTTAATATCTCTAA
GAAAACAAAAGAAGGAAAAAAATTACGTATTGCTTACCTCAACAGATTGCAAGTTAACGCTGGCTTCCATCGTCAGTTATGAAATTGTT
AAATCTGGACGATACCCCTAGAAATGGGTTAGAAGACTGACTAAACATGATGAAAGAACATATTAGGGTAGTTAGAAGGCTGTTGATGTTG
GATAATGCCATAAAAGATAGGAAGTTATCTGGCGGTAAAGCAGAGGGCTGTCATTGCTAGGATGTTGCTCTGATCCAGATATTGTTG
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ATGATTACTCACGATCTGATGAAAGTAAAGGGTATGCTGACCGAAATATTCACTTGTAGGAACCAATTACATGGCGTTCAATGTC
CATACAAAGGAAATGGAGGTTGAATCAGATGCTACT

SEQ ID 356

MRYITVSGLTQFYDSDPVLEGVNYHLDSEFVTLTGENGAAKSTLIKATLGILTPKVGTVNISKENKEGKKLRIAYLPOQIASFNAGFPSSVYEFV
KSGRYPRNGFWFRRLLKHDEEHIRVSLEAVGMWDNRHKIGLSGGQKQRRAVIARMFASDPDIFVLDEPTTGMDAGTTEKFYELMHNAHKHGKSVL
MITHDPEVKGYADRNIHLVRNQSLPWRCFNVHTNEMEVESDAT

SEQ ID 357

ATGAGATAACATATCAGTAAAAATCTCCTTCAATATGAAAGTGAGCCAGTTAGAAGGGATCACTTATCATTAGATAGTGGAGAATTGTC
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AAAATAAAGACCGTAAACAATTAAAGAATTGCTTACTTGGCGCAGCAAGTAGCTAGCTTAACGCTGGTTTCCATCACCCTGAGTTGTC
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GAAAACCGCTATAAGAGAATTGGTAGTTATCAGGTTGCTAAACACAGTGTGGTTATTGCGCTATGTTGCTCTGACCCCTGATATTGTTG
CTAGACGAGCCAACAACCGGAATGGATAGCGTACTACTGATACTTTATGAATGCTGACCCAGTGCACATCAACATGGGAATTCCGTTCTG
ATGATTACCATGACCCAGAAGAAGTGAAGGTTATGCTGATCGGAACATTCACTTGTAGTCAGAAACAAAAACTCCTGGCGTTCAACATT
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SEQ ID 358

MRYISVKNLSFQYESEPYLEGITYHLDSEFVTLTGENGAAKSTLIKATLGILQPKAGRVTIAKKNDGKQLRIAYLPQQVASFNAGFPSTVYEFV
KSGRYPRSGFWFRLNKHDEEHVQASLEAVGMWENRHKRIGLSGGQKQRVVIARMFASDPDIFVLDEPTTGMDAGTTEKFYELMHNAHKHGKSVL
MITHDPEEVKAYADRNIHLVRNQSLPWRCFNVHTNEMEVESDAT

SEQ ID 359

TTGTATAACAGTACGCAAATACTCTAAATACAACCTGCCCAAAGTAACAACGAAAATAGTTGACCATGTAGCGAGATACTAAAACAACGCTAAT
GCAACACCGGCTAAGGAAAC

SEQ ID 360

MYTVRKYSNTTAAKVTTKIVDHVGEIPKTPNPATPAKET

SEQ ID 361

ATGTCCATACAAACGAAATGGAGGTTGAATCAGATGCTACTTGATATGCTTTCTATGATTTATGCAACGAGCGCTTAGCAGTTGGCTATT
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TTAGCGTTTTAGGTATCTGCCACTACGGTCAACTATTGCTGTTACTTTGGCGCAGTTGCTGATTTGAGTATTGCTGACTTACAAA
CATTATGAGGAAATTAACGCTATCTGATGCTGAGGGTTGCTATATTGAGTAAAGCTATAATGTTGTAATGTCAGT
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GGTCAAATTAAAAGTGTATTGCTGGGTATGTTAATTGGATTGAGGATGGTAGCTGTTATTGCTTCTGTTATTGGAGACACCT
GCTAGTCAGGAAACATAACGATGATTGTTATTGCTGGGTATGTTAATTGGATTGAGGATGGTAGCTGTTATTGCTTCTGTTATTGGAGACACCT

SEQ ID 362

MSIQTKWRLNQMLLDMLSYDFMQRALLAVVAISIFAPILGIFLIRRQSLMSDTLHSVSLAGVALGVVLGISPTWSTIFVVTLAADVLEYLRTVYK
HYMEISTAILMSMGLAISLIVMSKAHNVGNVSLSEQYLFGSIIITIGKEQVIALFVIALITFILTFIRPMYILTFDEDTAFVDGLPVRLMSILFNV
VTGIAIALTIPAAAGALLVSTIMVLPASIAMLGRNFKTVIFLGMILGFVGMVAGIFLSYYWETPASATITMIFIGIFLVLVSLVGLLRKR

SEQ ID 363

ATGGTCATGCTTGATATTCTATGATTTCTGATGAACTGCAACGGCGGTAATGGCGTAGTTGCCATTAGTATTTTGCTCGATTAGTATTTGAGTGGCTATT
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ATCACTACTATTATTGTTGTTAGCTGCTATTGTTAGAATACCTGCGCTAGTTACAAACACTACATGGAGATTCAACGGCATT
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TTTGATGAAGAATGCTGTTGAGTGGTTGCGCTGCTGATGTTCTATTCAATATGCTCAGTGGGTGCTATTGCTTCTGACCATT
CCAGCAGCAGGAGCACTTTGGTTTACCAATTGGTCTTGCAGCAAGTATGGCAATGAGATTGGGAAAAACTTAAACAGTTACTTACTG
GGAATTGTCATGGTTTACGGTATGTTATCTGGTATTCTTCTTATTGAAACGGCAGCTAGTGCCTACTTACCATGATTTCATT
AGTATTTCTCTTAGTTAGTCTAGGTGGAATGCTAAAAACGGTTATT

SEQ ID 364

MVMDILFYDFMQRRAVMVVAISIFAPILGIFLIRRQSLMSDTLHSVSLAGVALGVVLGISPTWSTIFVVTLAADVLEYLRTVYKHYMEISTAIL
MSLGLALSIIIMSKSHSSSMSLSEQYLFGSIIITISMEQVVALFATAIILTVLFIRPMYILTFDEDTAFVDGLPVRLMSILFNVITGVIA
PAAGALLVSTIMVLPASIAMLGRNFKTVILLGIVIGFSGMLSGIFLSYFFETPASATITMIFISIFLVLVSLGGMLKRLF

SEQ ID 365

GTGACTCAAATATACGAAGGAAATAATTAGTACCTAGCCGAGTTGAACTTCAGTATGTTGAATTGATAAAACAAGGAAAATCTCTAGAAATCAA
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ATGCTAATCAAAGAACAGGAAACAGGCAAGAACAGGTGAAGATCCAATAGCGATGCTGATGAAACAGCAAGCAGCTATTGAAAGTGCATCTGAT

ATAGAAGAAAATACTAACACTAATACTTCTGAATCAGATAACAATAATGTAGCTCCCAAATAGAACATCGTCTACGTTGCAAATAAGGGTCGTTCA
AATACTTATTGGTAGTTAGAAAACATAAAAATGCAAATACCGCTAATATCGTTCAAATGACTGAACAAGAGCTTAATCAACACAAACAT
CACAGCACTACTGAAGCACA
SEQ ID 366

MTPYEGNNLVPSRVELQYVGIDKQGKLLIEKLGGGKEQVDEYGVTVTLENTSPLAKIDYKTGMLIKEDGKQAEEGEDPNSADENEAAIESASD
IEENTNTNTSESDTNNVAPQNIRIVVANKGRSNTYWYSLNICKANTANIVQMTEQEALNQHKHSTTEAQ
SEQ ID 367

ATGGATATGTCTAAATCAAATCGCTACTTGGCAAGGTTAGTTGTTATTTAATAGCTATTCTCACCACCTTTACACAGACTGTGTTACGGCA
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CTTAAATTCAATCTCTCGGCTGGCATAAATTACAAATTGACTGACGCTAATGGAAAACAACTGGTTAATGGACCGTGGCCATTAGTTGGTTAC
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TATTAGAAAATAGATTAGATAGCTGGTAGCTCTACACCTAACTCTGGCTAGACTAAAGTTACTCTGTGTTATCATAAAAATGAGTTAGTT
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GGAGTAACATCAGTTACATTAGATAACGTATCTCTTTAGCTGAATTGGATTACCAAACAGGAATGATGCTAGATTCAACTCAAACGAAGAAGAT
AGTAATTAGAACCGAAGAGTTGAAGAAGCGGCT
SEQ ID 368

MDMSKSNRRTWQGLVVILIAILTTFTSTVTAARKIRNFPDTTEILLGKATETPGILPFTGSYQLVLGDLNLQRPTFAHIQLKDQDEPNIKRG
LKFNPPGWHNYKLTDANGKTTWLDRGHLVGYQFSGLNDEPKNLVTMKTLYNLTGFSKDNPLGMLYENRLDSWLALHPNFWLDYKVTPVYHKNELV
PRQVVLQYVIDENGDLIQLGSEKESVDNGVTSVTLNDNVSPAELDYQTGMMLDSTNEEDSNLETEEFEAA
SEQ ID 369

ATGAATATTTTGATGAACCTCAAAGAACGTGGACTCGTTTACAGACAACGTGACGAAGATGCTTACGCAAAGCTTGAAGAAGGTTCTGCTCT
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TCTACAGGAAAATTCGGAAAATCTGAAGGAAATGCTGGTGTGATGCTGACAAAAACCTCTCCTTATGAAATGACCAATTGGTCAAT
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AATATCATAGACCTCTAGTCACTCAGGAGTTGTCATTCTAAACGTCAAGCTCGAGAAGATGTCCTCAATGGAGCTTTATATTAAATGGAGAT
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AACTTTAA
SEQ ID 370

MNIFDELKERGLVFQTTDEDALRKALEEGSVSYTYGYDPTADSLHLGHVLAILTSRRLQLAGHKPYALVGGATGLIGDPDFKDVERSLQTKKTVVS
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SDQWGNMTAGTELIRRKSNGVSHVMVTPLITDSTGKFKGKSEGNNAWLDADKTPSPYEMQFWLNVMDDAVRFLKIFTFLSLKEIEDIRIQFEEAP
HQRLAQKTLAREVVTLVHGEKAYKEAVNITEQLFAGNIKGLSVELKQGLRGVPNYHVQTEDNLNIIDLLVTSGVVNSKRQAREDVSNGAIYINGD
RIQDLEYTISENDKLENEITVIRRGKKYFVLNFK

SEQ ID 371

ATGAATATTTGAAGAACTCAAAGCTGTTGGCTTTCAAACGACTGATGAACAAAGCCCTGTCAAAGCATTAAACAGAAGGGCAAGTATCC
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CCTTACGCTCTGTGGGGGTGCCACAGGTTAAATTGGTGTATCTTCTTAAAGATGAGCGCAGGCTTCAAACAAAGAAAAGCTTGGAG
TGGAGTGACAAGATTAAGGGCACTTGTCTACTTCTTGTGTTAAAGGTTGAGTAAAGCAGGCTGTCAACAACTACGACTGGTCTCG
CAAATCAGCTTATTGACTTCCCGTGTGATGCGGTAATACTTACCGTTAATCATGATGAGTAAAGACTCTGTTAAAAACGCTTAAAC
GGCATTCTTACACTGAGTTGCTTACCAAATCATGCAAGGCTACGACTTCTACGAACTCAATGACAAGCATAATGTAACCTTACAAATTGGCGC
TCTGACCAAGTGGGTAATATGACAGCTGGTACTGAATTGCTCCGAAAAGGCTGATAAAACTGGGACAGTCATGACTGACTTACACTCATGAC
TCAACCGGAAAATTCGGTAATCAGAAGGTAATGCTGCTGGTTGATGCCGATAAGACGCTCTTACGAGATGACCAATTCTGGTAAAT
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CACAGCGCTCGCTCAAACATCTGGCACCGCAAGTGGTACCTGGTTCTAGGGAGAAGCTTAAACATTACGTTCAATGAGCAG
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AATATTGTCGAGATTAGTAGCTGCTAAGATTCCCCATCAAACGCCAGGGCGCTGAAGACGTCAGAAATGGAGCAATCTACATTAACGGAGAC
CGCGTTCAAGATTAGATTACCAATTAGTAATGATGATAAAATTGATGATCAATTACCGTTATTGCCCGCGTAAAGAAAAATACGCTGTTCTC
ACTTAC

SEQ ID 372

MNIFEELKARGLVFQTTDEQALVKALTEGQVSYYGYDPTADSLHLGHVLAILTSRRLQLAGHKPYALVGGATGLIGDPDFKDAERSLQTKETVLE
WSDKIKGQLSTDFENGDNKAELVNNYDWFSQISFIDFLRDVGKYFTVNYMMSKDSVKKRIETGISYTFAYQIMQGYDFYELNDKHNVTQIGG
SDQWGNMTAGTELLRKKADKTGHMVTPLITDSTGKFKGKSEGNNAWLDADKTPSPYEMQFWLNVMDDAVRFLKIFTFLSLDEIAEIETQFNAAR
HERLAQKTLAREVVTLVHGEAAVYKQALNITEQLFAGNIKGLSANEKLQGLSNVPNHYVQSIDHNIVELVAAKISPSKRQAREDVSNGAIYINGD
RVQDLDYQLSNDDKIDDQLTVIRRGKKYAVLTY

SEQ ID 373

ATGTTAAAGGAATAAGAAGTTGAATAGTTCTAAATTAGGTGATTACACCACTTGAATTGGTTCTATTAAAGAATTGTAAGCTTTA
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CCAAGTAAAGATGTTAGTAGCAGACAAGTAACTACACTTACTAGGGTGTCTAGGTTAACTTATTCTGATAAAATCACAAATTTCAGAGATTGCCACT
GATTACACCGTACACCGTACGGCAAAGGATGCTATCTGATAAAATTAAAAAGGCTATCTGCAACAGAGGAGCAAATTTCATGACCA
GGTAGTTCTCCAAAGCCGTTACGCTGCTGAGGGATCTGTTGGGTTGGAGAGAGTAGCGGTGTTCAACGCTGACACAACAAATTATTA
AAGCAGCAAATTGGGAGATGATCCGTATTAAACGCAAATCAAAGAAATTATTATGCTCTAGATTAGAGCTTACATGGATAAGGATTG
ATTTTATCAGATTATTAAATGATCACCGTTGGTCGAATAACAAAGGACAGAAATTGAGGTTATTGAGAAGAAGCAGACAAGGGATTGG
GTTTCCGCAAAGATTAAACATTCTCAGGAGCTTCTGAGGTTACCGCAAAGCTTATTGTTATTCTCTTATCTGAGATGCCAG
TTGAAATCAGATAAGATCTAGTTGGTATAAGCGCCAAAAAGTGTATACAAATATGTATAGAACGAGAGCTTAAACAAAGATGAGTAC
AAATCTCAGATAAGATCTAGTACAAACAGGTTATCAGGTTACCTAAAGGATAATGTTAGCGAGCATGATTCTTACTACTCGGCATTATCT
GAAGCTCAAAGATGATGATGACAAATTACCTCATTAAAGGATAATGTTAGCGAGCATGATTAAAAATGATGAGACTAGAGCGACGTACAGACAC
CGCGCTATTGAAGAGATTCAACAGGGAGGGTATACTTAAACACTATCAAAATCTGTTATCAAGCCATGCGAGGATGCTGAGCTCAAC
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AACTATAGTGAGAATCAAATAACCATGCTTGTACGGCACGGCTCCAGGGTAAGTTAACCGATATTACCTTACGGAATTGCTATTGATCAAGGGATGTTAGGAAGTGGTAGTGTCTTCAAATTATCCAACGACATATTCAAGTGGCAGAAAGATTATGCATGCGGATGAAGAAGGTACTGCTATGGTTAACCTTCAGAGTCATTGGACATTCTCAGCTTCTGAACTTACAAGATGCTACGAGATCGAGGCTTGATGTTAAAAACATATGGAGAAATTAGACTATCCAATGAAAATTGGTATAGAAAGTTTACCACTTGTGGTATTGATACGTCACTTGCTCAGCAAACAAACCTTTATCAAATGATTGCAAATGGTGTATTATCATAAAGCAGTATATGATAGAAAGTATAGAGGATACTAATGGGAAATGATTATAATCACGAAAGTAAACCTGCTCGTCTTTCGAAAGCACAACGCTACTATCTACAGCAGCTATTACATGGACCAATTAAACTCCGGAAGACTACAACTTTAAAAATCGCTTACAAGGTTAAATAGTGGTTAGCTGGGGTAGATTGGGATGGAAAACGGTACTACTAACCTCAACTTCTGTATTGGGTGATGCTTCTCACCTTAAAGTGCCTTAAAGTGGAGATGGGAGACATGATAATAATGCCCTTTAGCGAAATTGACAGGTTACAATAATAATGCTAATTATGCTCACTTGGTTAATGCTATTAAATGCAAGATGCAATAACTTTGCTAAGTGCAGAAAGGTTAGACTTGTGATGAGCGTTATAAAAGCTAAAGTTCTTAAGTCTACAGGTTACAGGCGAGGTGTAGTAAACAGTAAACGGCTCGAATCACTTGTGAGGTAAGCACAACAACTTATTGGGCAAAACGGACACTGGAAACGATGACCTATCGTTGCTATTGGGGAACTGATAGTGTATTGATCAAAGCTGGTCTACTTGGGTTGAAAACGAA

SEQ ID 374

MFKGNKKLNSSKLGDYTPLEFGSIFLRIVKLLSDFIYVIIILLFVMLGVGLAVGYLASQVDSVKVPKSNSLVTQVNTLTRVSRLTYSDKSQISEIAT
DLQRTPVAKDAISDNKKAIITATEDENPNFDHKGVVPKAVLRAAGSVLGFGESSGGSTLTQQQLLKQQILGDDPSFKRKSKEIYALALERMDKDS
ILSDYLNUSPFGRRNNKGQNIAGIEBAAQGIFGVPSAKDLDTIPQAFLGPQSPIVYSPYTADAQLKSDKDLFSGIKRQKNVLYNMRTRALTKE
KSYKYDVIKKDFIKPAVATTNNHDYLYYSALSEAQKVMYNLYIKKDNVSEHDLKNDTETRATYRRAIEEIQGGYTTINKTSVYQAMQDAAAQY
GGLLDDDGTVKQMVNLTDNSSGATIYFIGGRNYSSENQNNHAFDTARSPGSSIKPILPYGIAIDQGMLGSVSLSNYPTTSSGEGKIMHADEEGTA
MVNLQESLDISWNIPAFWTYKMLRDRGVDVKNYMEKLDYPIENFGIESLPLGGIDTSVAQQTNLQYMIANGGVYHKQYMIESIEDSNKGKVIYNHE
SKPVRVFSKATATILQQLLHGPINSGKTTTFKNRLQGLNGLAGWDWIGKTGTNSTSDVWLMLSTPKVTLGGWAGHDNNASLAKLTGYNNNANYM
AHLVNVNNADNGNTFGKSERFRLDDSVIKAULKSTGLQPVGVTNVGRRITVGGESETS YWA NGPGTM TYRFAIGGTDSDYQKAWSL LGGKR

SEQ ID 375

ATGAGGTATTTATGGAAATGGAACAGCAGAAAACAAAGCTATAAGTCATAAGCTCTGGATTGGGCGGTGCTATTACGTACG
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TCCAAAGACAATATCTTATGTGATTATCTTAATGTTTACCTTGGCCGTAACAAACAAGGGTCAAATATTGCTGGTGAAGAACAGCTGCGCGT
GGCATTTGGCCTTCTGCCAAAGATTTAACGGTCCACAGGCAGCATTGGCGGCTTCCCGAGAGTCCTATTGTTACTCTCCTTATTG
TCAACCGGACAACAGAACATGGCTTATGGCATCAAGCGTCAGCAGAACATGGTCTTTAACATGTCAGGTGTTCTGCT
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GCTTATGAAGAGAGAGCCTAACAGAACATTGCAACAGGGTGGCTATACCATCACCAACCAACCATTAATAAGCCTATTACAATCGCAGTCAGACAGCG
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CCTGCTATTGATCAAGGTTAATGGGAGTGCTAGCTTTGCTAATACCAACAACTTACTCGAGTGGCCAAAAATCATGCTAGCTGATAGT
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TGGTCCCCAAAAGGACGGGGGCTATGACTTACCGATTGCTATTGGTGGCACGGATGCCGATTATCAAAGCCTGGGGAACTTCGGGTTCAGA
AAAAAT

SEQ ID 376

MRYFMVKWNTKQKRISHQRLGLLDLGPVLLRTLRLLSNFFYIVIFLFGMMGFGMAFGYLASQIESVKVPSKESLVQKVSBLSMTISQMNYSDNSLIS
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SKDNILCDYLNVSFGRRNNKGQNIAGVEEARGIFGVSAKDLTVPQAAFLAGLPQSPIVYSPYLSTQQLKSEKDAMAYIKRQQNVLFNMYRTGVLS
KKEYEDYKAYPIQKDFIQPGSAIVNNHDLYYTTLADAKKAMYSYLIKRDVKSSRDLKNDETKAAYEERALTELQGGYTITTTINKPIYNAMEQTA
AAQFGGLLDDGTGTVQMGNVLTDNAIGAVLGFGGRDYALNONNNHAFNTRSPGSSIKPTIAYGPAIDQGLMGSASVLSNPYPTTYSSQKIMHADS
EGTAMMPLQEALNTSWNIPAFWTQKLLREKGVDVENYMTKMGYKIADSYIESLPLGGGIEVSVAQQTNAQYQMLSNNGLYQKQIVDKitASDGTVV
YKHENKPTRIFSAATATILOQELLRGIPITSGATTTFKNRLAAINPWLANADWIGKTGTENYTDVWLVLSTPKVTLGGWAGHDNTSLAPLTGYNNN
SNYLAYLANAINQADPNVGQRFNLDPGVVIKANVLKSTGLQPGBTNVNNGHTFSVGGEMTTSLSWQSQKGPAGMTYRFAIGGTADYQKAWGNGFGR
KN

SEQ ID 377

TTGGCAGGACATGAAGTTCAGTACCGAAAACACCGTACACGTCGTAGCTTCAAGAATTAAAGGAAGTCTTGATTTACCAAACCTTAATTGAAATT
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ACAGTTGCAACAGCCAACCTCAAGCTTAAAGAAGACGGTACATTGCAAGAAGAAATCGTATGGTGCATCAAGGTTAAACCAAGAGTTCTT

SEQ ID 378

MAGHEVQYGKHKRTRRSFSRIKEVLDLPNLIEIQTDSFQDFLDAGLKEVFEDVLPISNFTDTMDLEFVGYELKEPKYTLEEARIHADASYSAPIVTF
RLVNKGTEGEIKTQEVSFFGDFPIMTEMGTIINGGERIIVSQLVRSPGVYFNDKVDKNGKVGYSTVIPNRNGAWLELETDAKDIAYTRIDRTRKIPF
TTVLRALFGSGDDEIVDIFGDSELVRNTIEKDHNKPNSDSRTDEALKIYERLRPGEPKTADSSRSLLVARFFDPRRYDAAVGRYKINKKLNLT
RLLNQTAENLVLDGETGEILVEAGTVMTRDVIDSIAEHDGDLNKFVYTPNDYAVVTEPVILQOKFKVVAPFTDPDRVVTIVGNSNPEDFKVRLT PAD
I1AEMSIFYFLNLAEGIKVWDIDHLGNRNIRAVGELANQFRIGLARERMRNVRERMSVQDNELTPQ91INIRPVTAAVKEFFGGSQLSQFMQDHNP
LSELSHKRLRSALGPGLTRDRAGEVRDVHYTHYGRMCPETPEGPNGLINNLSSFGHLNYKGFIQTPYRKVRDRTGAVTNEIWVLTADEEDEF
TVAQANSKLNEDGTFAAEIVMGRHQGNQEFPSIIVDFDVSPKQVVAVATACIPFLENDNSNRALMGANMQRAVPLIDKAPVYGTGMEYQAAH
DSGAAVIAKHGRVIFSDAEKVEVRREDGSLDVYHQVKFRRNSNGTAYNQRTLKVGDVLVEKGDFIADGPMENGEALGQNPVVAYMTWEGYNF
DAVIMSERLVEKBDVYTSVHLEFESETRDTKLGPEEITREIPIVNGEDSLRDLDEMGIIRIGAEVKEGDLJLUVGVTPKGKDLSAERLLHAIFGDK
SREVRDTSI1RVPHGGDGVVRDVK1FTRANGDELQSQGVNM1LVRVYIAQKRKIKVGDKMGHGNKGVSVS11VPVEDMPY1FDGTPVDDIMLNPLGVPS
RMN1QVGMELHLGMAARNLGIH1ATPVFDGASSLEDLWETVQEAQMDSDAKTLYDGRGEPFDNRVSVGVMMYMIKLHHMVDDKLHARSVGPYSLVT
QQPLGGKAQFGGQRFGEMEVWALEAYGASNVQLB1ITYKSDDVTGRLKAYEAITKGKPIPKPGVPESFRVLVKELOSLGLDMRVLDEDDENEVELRD
LDEGEDDDDVMVDDLEKARVQKQEAEKQAEQVSEVQED

SEQ ID 379

TTGGCAGGACATGAAGTCGATACGGAAAACACCGTACACGTCGAGCTTCAAGAATCAAAGAAGTCTTGATTTACCAATTGATTGAAATT
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GAATTGGTGGTTACGAATTAAAGAACCTAAATATACCCCTGAAAGAAGCTCGTACCCAGATGCAAGTTTCTGACCCAATTCTGGTACCTTCA
CGTTGGTCAACTAAAGAACCTGGTAGATTAAACGATGCAAGAAGTCTTCTGGTATTCTGACCGGAAATGGTACCTTATTATCAATT
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ACAACACCTGGTCTGCCCCCTGGTTCTCAGGTGATGATGAAATTGTTGATATCTTGGTCAAAGGCACCTGGTACGATACCCATTGAAAAGAC
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CGTCTTTGAAACCAAACTATTGCTGAAACCTTGTGATGCTGAAACTGGCGAAATTGGTAGAAGCTGAGATGACTCGTAGCGTCATC
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CGTGTATCCGTTGGTGTGATGATGACAAACTCACCACATGGTGTGATGATAAAACTTCATGCCGTTCTGTTAGGACCATACTCACTTGTGAC
CAACAGCCACTGGTGTGAAAGCTCAATTGGTGTGACAAACGTTGGTGTGAGATGGAGGTTGGGCTTGTGAAAGCTTATGGTGTGATCAAAATGTTCTT
CAAGAACATCTGACCTACAGTCAAGTCAAGTCAACGGACGTTGAGGCTTAAAGGCTTATGAGCAGTACTAAAGGTAACCAATTCCAAAACAGGTGTA
CCAGAACATCTGACCTACAGTCAAGTCAACGGACGTTGAGGCTTATGAGCAGTACTAAAGGTAACCAATTCCAAAACAGGTGTA
CTTGATGAAGGTGAAGACGATGACATTATGATGTTGACGATCTGAGAAGGGACCTGAAAACAAAGCTCAAGAACACTCAAGAACGTTCTGAAACA
ACTGACGAAAAA

SEQ ID 380

LAGEHVRYGKHRRSFSRIKEVLDLPLNIEIQTDSFQDFLDSLKVFDVLPISNFTDTMELEFVGYEFKEPKYTTLERIHDASYSAPIVTF
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LSELSHKRRLSALGPGLTRDRAGYEVRDVHYTHYGRMCPPIETPEGPNIGLNNLSSFGHLNKYGFQTPTYRKVDRATGTVTNEIWLI
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DSGAIAQQNGKVFSDAEKVEIRRQDGSLDVYHITKFRRNSNQRTLVKVGDIVEKGDFIADGPMSENEMALGQNPVVAYMTWEGYNFE
DAVIMSERLVKDEVYTSVHLEEFSETRDTKLGPETIREIPNVGEALKDLEMGIIRIGAEVKEGIDLIVGVKVTPKBKEKDLSAERLHLAIFGDK
SREVRDTSLRVPHGGDGIIRDVKIFTRANGDELQSGVNMLVRVYIAQKRKIKVGDKMAGRHNKGUVSRIVPVEDMPYLPDGTVDIMLNPLGVPS
RMNIGQVMELHLGMAARNLGIHIATPVFDGASSELDWDTVREAGMDSDAKTIVLYDGRTEPFDNRSVSGVMMYMIKLHHMVDKLHARSGVPSLV
QQPLGGKAQFGQRFGEDEVWALEYAGASNLVQELITYKSDDVTGRLKAYEAITKGKIPKPGVPESFRVLVKEQLSGLDMRVLDEDNEVELRD
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SEQ ID 381

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ATCCGATCACTTACATGTAACATCGCCATGGTTGCTCAGCTTACGGTATTACTGAGGTTAACTGGCAACAGGTGATGGTGTGAGGTTGCTGAA
GCAGTGGTACTATTGAGCTCAATCTGGTGAAGGAGATCACGTTCTCAGGTTGAGGAGATGGCTGCTTCAATTACGGTGGTGTGCTTCAATTAGCT
ATTACACAAGGTCCTCCAGTATCAGGAAATCTGTTAAGGTCAGACAGGGAGGGAGAATACGGTGGTCAATTACAGCACGTATGAA
ATTGAAGAAGACTCTCAACACGTACTAAGGAAAGTATTGTTAAGGTCAGACAGGGAGGGAGAATACGGTGGTCAATTACAGCACGTATGAA
GTTGAAGTTGGTGTGAGTAGCTGCTGGTGCCTTAACGTTGAGGATCTATCCAACAAAACGTCTCTGAAGTCTGTAATTCTGTT
GAAACGTACCTACTGCTGAAGTACAAAAGTTACCGTAGCCAAGGGTAGAAATGGAGATAAACACGGTGGAGGTTAATGGTCTGTC
CGTAAAGTCTGTCATGGTACAGGAGATAACAGTCTCTCAGGTTACACTTATGGATATTTCAGACTTACAGGCTAACAAAGATATTGTT
ATTCTGGTGGAAATCCCTGCGACAAGCGCTCTGCTCTGGTATTACTAAGGCTCCCTGAAACTAATTCTTACAGCTGTCATCC
CAAGAAACACAGTGTCTTAACAGATGCTGTATCCGGTGAAGAACGATCTTACGGTCTTAAAGGAAATGTTATTATGGTAAACGAGTCT
CCACGGGTTACTGTTGAGGCTGTGTTACAGTGTGTTAACTGAGGTTGAGGATTTGAGGAAACTCTGTTGATGCAAGAGTT
ACCGAAGTATCACACACAGAAAGAT

SEQ ID 382

MMINRRKVVLVVDVNRFKSMQITLASPSKVRWSYGEVKKPETINYRTLKPREGFLDEVIFGPTKDWEACGKYKRIRYKIIICDRCGVEVTRAK
VRRERMGHIELKAPVSHIWFKGIPSRMGLTLMSPRALEEVYFAAYVVIDPMDTPLEPKSLTEREYREKLQEQYGYGSVAKMGAELQDLLKR
VDLDAETAVLKEILKSATGQKRVKAVERLDVLDAFKSGNKPEWMVLNLIPVIPPDLRPMVQOLDGGGRFAASLDNLDRYRVINRNRRNLRARLLELNAP
GIIVQNEKRMQLQEAVIDALIDNGRRGRIPTGGPSRPLKSLSHMLKGQGRFLRQNLGRKVRDFSGRSVIAVGPVLCMYQCGVPREMAIELFKPVFMRE
IVARDLAGVNKAICRMRVERGDERIWDLIEEVIEKHPVLLNRAPTLHRLGQAFEPVLDGKALRHLPLVCEAYNADFDGDQMAIHPVLESEAQAEA
RLLMIAAEHILNPKDGPKVTPSPQDMVLGNYYLTMEDAGREGEGMIFKDHDDEAVMAYQNGVHLHTRVGIAVDSMPNKPWTEEQKHKIMVTTVKG
LFNDIMPEDLPYLIEPNNNALTEKTDPKYFLEPGQDIQAVIDNLEINIPFKKNLGNIIJETFKRFRRTSETAFLDRLKDLGYYHSTLAGLTVGIA
DIPVIDNKAEIIDAAHHRVEDINKAFRRGLMTEEDRYVAVTTWREAKEALEKRLIETQDPKNIVMMMDSGARGNISNFSQLAGMRGLMAAPNGR
IMELPILSNFREGLSVLEMFFSTHGARKGMDTDALKTADSGYLTRRLVDAQDVIIREDDCGTDRLGLTTITADGKEVTELEERLIGRTYTKSIK
HPETGEILVGAUTLITEDMAAKVVKAGVEEVFTIRSFTCCTRGVCRHCYGINLATGDAVEVGEAVGTLIAAQSIGEPTQLTMRTFHGGVASNTD
ITQGLPLPRIQEIEFEARNPKGEAVITEVKGEVVAIEDSSTRTRKVFVGKQTGEYVVFPTARMKVEVGDEVARGAALTEGSIQPKRLEVRDLSV
FTYLLAEVQKVYRSQGVEIGDKHVEVMVRQMLRKVRVMDPGTDLLPGTLMIDSFTDANKDIVISGGIATPSRPVLMGITKASLETNSFLSAASF
QETTRVLTDAAIRGKDHLLGLKENVIIKGIIIPAGTGMARYRNIEPLAVNEVEIIEGTPVDAEVTEVSTPTTED

SEQ ID 383

GTTGGTTGACGTAATCGTTTAAAGTATGCAAATCACATTAGCCTCACCAGTAAGGTCCGTTCATGGCTTATGGTGAAGTTAAAAACCTGAA
ACAATCAACTACCGTACATTAAAACAGAACGTGAAGGACTCTTGACGAAGTCATCTTGGTCCAACAAAAGACTGGGAATGTGCGTGTGGTAAG
TACAAACGTATCCGTTATAAGGGATCGTTGTGATCGCTGTGGGTTGAGGTAACTCGTCTAAAGTACGTGTTGAACGTATGGGTCAATTGAG
TTAAAAGCTCCGTATCACATATCTGGTATTCAAAAGGATTCCATCTCGTATGGGATTTGACTCTTGTGATGGTCAATTGAGTCTCTGGCCCTTGAAGAAGTG
ATCTATTGCGCTTATGTGGTCAAGATGGGTGCTGAAGGCAATTCAAGAACGTTCTTGAAGAACGTTGGACTGGCAGCTGAATACCGCTGAATT
GAGTGGTGTGTTGAGGAGATGGTCAAGATGGGTGCTGAAGGCAATTCAAGAACGTTGGACTGGCAGCTGAATACCGCTGAATT
AAAAGAGGTTGAAATCTGCTTCTGGTAAAAGGATTAAAGCAGTTCTGCTTGTGAGGCTTGTGATGGCTTAAACAAATCTGGAAATAAACCA
GAATGGATGGTCTTAACATCTGCCGGTTATCCACAGATCTCGTCCGATGGTTCAATTGGATGGTGTGTTGCGGCATCAGACTTGAAT
GACTGTTACCGTCGTGTGATTAACCGTAATAACCGTTGGCACGTTGGTGTAGAACCTTAATGCCCCCTGGCATCATTGTCAAAATGAAAAGCAATG
CTTCAAGAAGCCGTTGATGTTGATTAATGTCGTCGTGTCATCAGGACAGGAAGTCGTCCATTGAAATCATTGAGGCCACATG
CTTAAAGGTTAAACACAGGGCTTCCGTCAAAACCTGTTGAGGTTGAGACTCTCTGCGACGTTGGCTTATGCTGTTGTC

ATGTATCAATGTGGTGTCCCACGTGAAATGGCTATCGAGCTTTAAACCATTGTAATGCCGAAATTGTGCAAAGAATATGCTGGTAACGTT
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 CCGACTCTCACAGACTGTATTCAAGGTTTGAAACCGCTTATTGACCGTAAGGCACCTCGTCTCACCCACTTGTGTGAGGCCCTACAT
 GCCGACTCTCACAGACTGTATTCAAGGTTTGAAACCGCTTATTGACCGTAAGGCACCTCGTCTCACCCACTTGTGTGAGGCCCTACAT
 TTGAAAGCTTAAGGTTAACCGTGTATTCTCATCTCAGGATATGGTTCTGGTAACTACTATCTACATGGAAAGATGCTGGTGCAGG
 GAAGGTTGATTTCAACGATAAAGACGAAGCTGTGATGGCATATCGTAATGGTTATGCTCATCTCATAGTGTGGTATCGCTGGTACAGC
 ATGCCAAACAAACCTGGAAAGACAATCAAAGACATAAAATCATGGTACAACTGTTGGTAAGTTCTTTAACGATATCATGCCAGAGGACCTT
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 CGCTTAGACATCAATGTCCATTAAAGAAGAAAACCTCGGTACATCATTGCGGAAACCTTCAACAGTTCCGTACAAACAGAAACATCAGCCTTC
 CTTGACCCCTGAAAGACCTTGGTTACTACCAACTCAACCCCTTGTGGTTGACAGTGGGTATCGCTGACATTCTGTATTGATAATAAAGCTGAA
 ATCATGTGCTGCTCAGCATCGTGTGAAGGAAATTAACAAAGCCTTGTGGTTGACAGATGACATGGTACAGGTTATGTCCTGTTAACACA
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 GCTGACCAATTAAATCACTGAAGACATGGCTGTAAGATTGATGACAGGTTGAAAGAAGTGACCTCGTCTGTCTTACCTGTGCGACTCGT
 CATGGTGTGCGTCAGTGTATTGATCAACTTGGCACTGGTGTGATGCTGTTGAAAGTGGGTGAAAGCAGCTTGTGACTATTGCTGCCAATCTATC
 GGTGAGCCTGGTACTCAGCTTACCATCGCTACCTTCAACGGGGTGTAGGCTCTAACGAGTATCAGGAAACGGTACAGGCTTAAACAGCCACTCAGGTAC
 CTTACTCGTGTGGTTGACAGTGTGATTCAGTGTGAGGAGCATTGTCAGTGTGGTACTGATGTGGTCTTCTTATCCGTGCTATTACAGAT
 GGTAAAGAAGTTACCGAAACGCTTGAAGACGTCTCAAGGTCGTTACACGTTAACAGTCAAACACCCGAAACTGGTGAAGTCTGATTGGT
 GCTGACCAATTAAATCACTGAAGACATGGCTGTAAGATTGATGACAGGTTGAAAGAAGTGACCTCGTCTGTCTTACCTGTGCGACTCGT
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 GGTGAGCCTGGTACTCAGCTTACCATCGCTACCTTCAACGGGGTGTAGGCTCTAACGAGTATCAGGAAACGGTAAAGGAAAGATGCGTCAACTCGTACCAAG
 AAAGTCTACGTTCAAGGAAAACGGTACAGGAAATATGTCATACATTACAGCAGTGAAGATTGTCAGGAGCAGAAGTTAATCGCGA
 GCTGCCCTACAGAAGGGTCAATTCAACCGAAACGCTCCTTGAAGTGCCTGATACCTTGTGAGTTGAAACGTTACCTTGTGAGAAGTACAAAAA
 GTTTACCGTAGCCAAGGGTAGAAATCGGAGACAAACAGCTGAGGTAAATGGTGCCTAAAGTCTGTGATGGTCAAGTCTGTGATGGATCAGGTGAT
 ACAGACCTCTCCAGGTACACTTGGATATTCCTGATTTCAGAGTCTAAAGGAAATGGTATCTCTGTGTTTACAGTGTGATCCCTCAAGAACAACTCGTGTGCT
 CCTGTTCTTATGGGTATTACTAAGGCTTCCCTGAAACCAATTCTCTTATCAGTGTGATCCCTCAAGAACAACTCGTGTGTTTACAGATGCT
 GCTATCGTGTGAAAGGAAATCTCTTGTCTAAAGAAAATGTTATCAGTGTGAAAGTCTGAGGCTGGTACTGGTATGGCTGTTACCGT
 AACATTGAACACAAAGCGATGAATGAGATTGATGATTGATCATACAGAAGTCTCAGCAGAAGCCGTTTACAGCAGAAGCAGAA
SEQ ID 384

VVDVNRFKSMQITLASPSVKRSWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWEACGKYKRIRYKGIVCDRCGVETRAKVRERMGHIE
 LKAPVSHIWFKGIPSRMGLTLDMSPRALEEVYFAAYVVIDPKDTPLEPKSLLTREYREKQLQEYGHGSFVAKMGAEEAQDILKRVDLAAEIAEL
 KEELKSASGQKRIKAVRRLDVLDAFNKSGNKPWVMVLNILPVIPDPDRPMVQLDGGGRFAASLDNLRYRRVIRNNRLARLLELNAPGIIVQNEMKR
 LQEAVDALIDNGRRGRPITGPGSRPLKSLSHMLKGKQGRFRONLNLGKRVDFSGRSVIAVGPTLKMYQCGVPREMAIELFKPFVMREIVAKEYAGNV
 KAAKRMVERGDERIWDILEEVIEKEPHVLLNRAPLTHRLGIQAFEPVLIDGKAIRLHPLVCEAYNADFDDGDMQAIHVPLSEEQAEARLMLAAEHI
 LNPKDGPVTPSODMLVGNYLTMEDAGREGEGMIFDKDDEAVMAYRNGAHLHSRVRGIAVDSMPNPKWPWDNQRHKIMVTVGKILFNDIMPEDL
 PYLQPNNANLLETPDPKVFLEPGQDIQEVDRLDINVFPFKKNLGNIAETFKRFRRTETSFLDRKLKDLYYHSTLAGLTVGADIPIVDNKA
 IIDAAHHRVEEINKAFRQLMTDDDRYVAVTTTWRKEAULEKRLIETQDPKPNIVMMMDSGARGNINNSFSQLAGMRGLMAAPNGRIMPELPILSNF
 REGLSVLEMFFSTHGARKGMDTALKTADSGYLTRLVDAQDVIIREDDCGTDRLGILLRAITDGGKEVTTLEERLQGRYTRKSVKHPEPETGEVLIG
 ADQLITEDMARKIVDAGEEVTIRSVFTCATRGVCRCYGINLATGDAVEVGEAVGTTIAAQSISIGEPTQLTMRTFHTGGVVASNTDITQGLPRIQE
 IFEARNPKGEAVITEVKGNVVEIEEDAESTRTKVVQGKTCMGEYVIPFTARMKVEVGDEVNRGAALTEGSIQPKRLLLEVRDTLSVETYLLAEVQK
 VYRSQVGEIJGDKHVEVMVRQMLRKVRVMDPGDIDLPGTLMIDSFTDANKDIVSGGIPATSRPVLMGITKASLETNSFLSAASFQETTRVLTDA
 AIRGKDHLDLGLKENVIIGKIIPAGTGMARYRNIEPQAMNEIEVIDHTEVSAAVFTAEE

SEQ ID 385

ATGTATCAAGTTGAAAAATGTTGGTATTGGGAAACCATGGTGTATTGAAAGGTTGGGAGGAAGATATTACTGAAATTGCTGAGTATGATACC
 TTATCAGAAGCTTGTCTATTTCAGAGGAGTGGGATAGGGGACAGGAAAGTGGCTTATTCTCAAAGTAAGTCTAGTTGTTGGCAAGCTT
 TGGAGTATAAAAGAAAACGTTGGTGTGAAAGATGTGATGAGTACCTCCAAAGTATCATTCTTAAATGTTATTGAAAGAATGGCAAGAAATTCT
 AAGGAAGAATCTATTGAGCGATTGAGTATTAAAGATAGCTGAGTTGCCATCGGCTATTGTTAAATTG

SEQ ID 386

MYQVKMFGDWEPWWFIEGWEEDITEIAEYDTLSEALLYFQEEWDRGQEKWPYFQSKSSLATFWSIKEKRWCEECDEYLQQYHSLMLKEWQEIP
 KEESIERFVNKIAEPLSACSLNL

SEQ ID 387

ATGTATCAAGTAATTAAATGTATGGTATTGGGAGCCTTGGTGTATTGAAAGTGGGAGGACTGTGAGGAGCTGGTCTTACAGGAGTATTTCTCTT
 TGGGAAAGAGATAAAAGATGGTGGAGGACTGTGAGGAGCTGGTCTTACAGGAGTTCATTCTCTTAAAGAATTTGTCAGGAGTATTTCTCTT
 AGCAATAATTATATCCCTGAATTGAAACACGAAATGATTCAACACAGGAGCTTATCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTACCA

SEQ ID 388

MYQVKMFGDWEPWWFIDGWQDDIIDEQQPSDWQEALDYFNQEWQRMKAIFPSYHSQKNLLATFWEKEDKRWCECDDEDLQQFHSLLLKNKDIVP
 SNNYIPEFQRNDSQPVAYLCKLNL

SEQ ID 389

ATGGTTCAATCATTAGCAAAGCAAGTCATTGATCAGGCACTGAGAAGTAAATGCTCAAGATATTATATCATTCCAAAGGTGATTGTTATGACTC
 TATATGCGTATTGATGATGAAAGGCGTTTATTGATGTTTTGAGTTAAATAGGATGGCTAGTCTTATTAGTCATTAAATTGTCAGGAGT
 AACGTTGGAGAAAAGACGAAGTCATTAGGTTCTGTGACTATGAACTGTCAGAGGAAAGACTGGTTTCAATTGACTATCGAGTGTGGGAGT
 TATCGTGTCAAGAATCTTATTGTTATTGATGTTATTGAGTCACTGGAGTAAATGTTGATAATATAAAGCAAATGAAGGAAGTA
 CTGGGTATAAGAGGGCTATATCTTTTCCGGCCCTGTGGGGAGTGGTAAACAAACTCTCATGTTATCAATTAGCTTCAAGTAAAGTAAAG
 CAAATTATCAGATTGAGATCCGGTAAAGATCAAGAATGACAAGATGTTACAATTGAAATGAGGATATTGAAATGACTTATGATGCTTTA
 ATCAACTGTCATTACGGCATCGTCAAGTATTTCATTGAGTCACTGGAGGAGTCAAGGACAGGCCGCTGTTATTGTCAGTAAAGTAAAG
 GGAGTGTGTTTTCTACTATTGTCATTGAGTCAACGTTATTGAGTCACTGGAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGT
 AGTCTAAATTAAATAGCATCAACGTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTAAAGAACACTCATCAGACAAGTGG
 AATAGACAAGTGGATATCTGGCTGAAGAAGACATATCAGTAAGAAACAGGACACAAGTCGAAAAAAATTACCCCTCAAGAAACACGGAAAGTACT
 CCAACTTTT

SEQ ID 390

MVQSLAKQVIHQAVEVNAQDIYIIPKGDCYELYMRIDDERFIDVFEFNRMASLISHFKFVAGMVGEKRRSQLGSCDYELSEGRLVSLRLSSVGD
 YRGQESLVLIRILYSGHQDLKYWFDNIKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQNLNEDIGMTYDAL
 IKLSSLRHPDILIIGETIRDQATARAVIRASLTGVMFSTIHAKSIPGVYDRILIELGVNYQELENSLKLIAVQLIIGGSLIDFETGNFKHHSSDKW
 NRQVDILAEEGHISKKQQAQVEKIIQPTTESSPTF

SEQ ID 391

ATGGTACAAGCATTAGCAAAAGCTATTCTAGCAAAAGCTAACAGGTTCATGCACAAAGATATTATTTGCCAAGAGCAGATCAATATGATCTT
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ATAGTTGGTAAAAGAGACGTTGTCAGGTGGGTTCATGTTAAGCTTAGAAGATAAGCAGTTATCTTGCGCTTATCTAGCGGGTGTAT
TATCGCGGAAAGAAAGCTTAGTGATTCTGCTCATCATCAAATAAAAGTGTACATTATTGGTTGATGGATGACAAAAGTAGCCAACTCAG
GTTGGCGGTAGAGGGTTATTTATTGCAAGGACAGTTGGGAGACACCTTGATGACAGCTGATTCAAGTCAATTATCATCAAGAAGCA
CAGGTATTAGTATAGAAGATCCTGAGAAAATAAAAACCAAAATTACAATTACAAGTGAATGATGATATTGGTATGACTTATGACAATTG
ATCAAACCTGCTTACGCCATGCCAGATATTAGTTAGTTATTGGAGATTGAGATAGTCACAAAGCAAGAGCCATTAGGGCTATTAGGGTAGTCAAC
GGTGCCATGTTTCAACGGTCAACGCTAAAGTATCTGGGTGTTATGCAAGATTGTTAGAACCTGGTGTAAACGAAAGCAGAACTGTCTAAT
TGCTTAGCATTAATTGCTTACCAAAGGTTACTTAATGGAGGAGCATTGATTGACTCTACTCAAACAGAATTGAAATTATTCCATCGAAGCTGG
AATCAACAAATTGATCAGCTTCTGAGGCAGGACATCTCAATCCAAAGCTAACAGCTAACAGCTAACAGCTAACAGCTAACAGCTAACAGCTAACAG
SEQ ID 392

MVQALAKIALAKAEQVHQAQDIYILPRADQYDILFLRIGDERRLVDVYQSDRMAPLISHFKFVAGMIVGEKRRQCQVGSDYKLSKDQLSLRLSSVGD
YRGQESLVLRLHHQNKSVHYWFDFGLTKVANQVGRGLYLFAGPVGSGKTTLMQOLISNYHQEAQVISIEDPVEIKNHQILQLQVNDDIGMTYDNL
IKLSLRHRPDILVIGEIRDSQTARAVIRASLTGAMVFSTVHAKSISGVYARLLELGVTKAELSNCLALIAYQRLLNGGALIDSTQNEFEYYSSSNW
NQQIDQNLLEAGHLNPQAKLEKII

SEQ ID 393

ATGGTCACCTTCTAAAGAGGAGTAAGTTATTGCTGATTGTTACAGATAGTATGAATAAGGATTATTAGAGGAAAGATTATCAAATG
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TATTAGTAACTCTTTGTTAGTAAAGTAAAGTAGCTACTTACCCATTGATATTGTTCTGTTGCTAATTATGATTGGC
CTTAGGAATTATTAATGCCAACTTGGAGGAAATAATTGCAACTAGACTGATTACAATGCGCAATTATTCTTATTACTTTAGCAGTT
GTACTTATTAGTTAGTTAATTATTGTTACAAAGCATTGCGCATTAAAGTAGCTTGTGTTTAACAAACATTCCATTAGTGGATCA
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TTTTCTTAAGCTGAGCTAGTTAATGATTGAAATGGCAAGTTAAGGCGAAATTAGGAACAGAGTTAGGATATATGCTGATGAGAAGTGGGAG
GATTTTTACAAAATTAGCTAGAGCGACCCAGTTAACCAACCGTTATTGTTAGTGTAGCTTATCATTGTTATGATGTTATGAGCAATG
CTGTTACCAATGTTACAAATATGGAGGATATTATCA

SEQ ID 394

MVTFLKRSKLLSDCYDSMNKALLGKDLSKMLGELGFSDTVITQVALADLHNISRSLLKIESYLANLLVRKKVIEWATYPLILLSFLVLI
MRNYLMPOLGENNFATRILITNPNIFLLLAVVLLIFSLIFYIIOQRLSRKVAFCFLTTIPLVGSYVKLYLTAYAREWGNLLSQGIELDQIVKVMQ
NQKSKLFRIGYDMEEGFLSGKAHQKVLDYPFFLTELMLIEYQVKAKLGETELIYADEKWEDFTKLARATQLIQPVIFIFVALIVMIAY
LLPMYQNMEILS

SEQ ID 395

TTGATCAGCTTCTGAGGCAGGACATCTCAATCCAAAGCTAACGCTAACGTTGAAAAATTATCTAGTAAACATCAGCATAAATTCAATTACTA
GCTAACTTTTATCTACAGGATTAGCTTCAGCAGAGGTTATTGCTTTTAAAGAAGCCAGTTGCTCAGTAGATTATGTTCTAAATGGAA
GAGCTTTTAAAGGCAAGGCTTAGCAGATATTGCTGGGTTAGGTTTTCAGATGCTATTCTACTCAAATTAGTTAGCTGATAGCAC
GGAATTATTGAAACAACTTAGCAGATCAACATTACTGAAACAAATGGCAAGGATCAGACGAAAGCTGTTGAAGTTATCACCTATCCTCTT
ATTCTTTACTTTCTTTGTTGATGATGCTAGGGTTGAGACGCTATTAGTCCCTCAATTAGAAACTCAAACATGAGATAACTTACTTTCTTAAC
CATTTCTGCTCTCTTATAGGTTTGTCTAGGTTATTGTTGCTGGGATGGTATGGCTACGATGGCGATCTCAAAGCCGCTGAAACTC
TATAGTCGGCTAACGGTTACCTTTAGTAAACTGTTAAACAAACTTAACTAGTTATTATGCTAGAGAATGGGTAACGTTAACAGTCAA
GGTCTGATTGATGACTATTAGCATTGCTAGGAACTCTACCCCTTTTAAAGAATTAAGTTAATGTTGAATACGGTAAATCAAATCGAAACTGGG
GCTGAGTTGAAATCTATGCCAGGAAGCTGGAAACAATTAGTCAAGTGTACAGTACACAACTTCAACCAGCTATTCAACCAGCTATT
GTTGCTGCAACATCGTCAATTGCTGTTATGCGGCAATTCTATTACCAATTACCAAAATATGGAGGTTAGTTT

SEQ ID 396

LISFLRQDISIPSKLSSLKSLKHQHKFIQLLANLSTGFSFAEVIAFLKRSQQLQDYVLKMEESLLKGQGLADMLSLGLGFDAILTQISLADR
GNIELTTLVAIQHYLNQMARIKKTVEVITYPLILLFLFVMMGLRRLVLPQLETQNQITYFLNHFPAFFIGFCGSLLILFGMVWLWRQSRLKL
YSRLSRYPFLGKLLKQYLTSYYAREWGLTIGQGLDMTILDIMAIKEKSSLMKELAEDIRMSLLEGQAFHIKVATYPPFKELSLMIEYGEIKSKLG
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SEQ ID 397

ATGAAAAATTATTGTTAAAGTAAAGGATAAGAAGGTTAACGCTTACACTTTAGAATGTTGGTAGCATTGGTTACAATCACAGGAGCTTAA
CTAGTTATCAAGGACTGACAAAATTGTTGGCTCACAGATAGTAGTGATGTTCTCTCCAGTCAGTCTGAATGGGTGTTATTAACTCAGCAACTA
AATGCAGAATTGAAAGGCTCATCTGAATATTAAAGACAGAACAAACTTATTACGTAAGAAGATAAGATTGTAACCTTTGCAATCTAA
AAAGATGATTCCGTAAGACAGGTTATGATGGTCAGGGTTATCAACCAATGGTTATGGTTAGACAATTGTCAAATGAGTCAGACAAAGTATG
GTAAAACCTGTTTATTGTTAAGGACGGGTTAAAGGACATTACTATGATTAAAGAAGAAACT

SEQ ID 398

MKNLLLCKDKKVKAFTLLECLVALVTITGALLVYQGLTKLLAQOIVVMSSSSQSEWVLLTQQLNAEFEAHLEYLRQNKLRLRKQDKIVTFGKSN
KDDFRKTGYDGRGYQPMVYQLDNCQMSQTKSMVLFYFKDGLKRTFYDFKEET

SEQ ID 399

TTGAGTAACAAATTAAAGTAAACATAAAAGCTTACCCCTCTAGAGGCCTAACAGCTAACGATTGAGAACCAATTAAACACTATTTATGATGCCCTTA
TTGACCCGAACCCCTCTAAACATAGCCATTATCTAGCCGCTCATGATCAAGATAATTGGCTTATTCTCATCAATTGCGAGGAGGAGTTAAGT
GGAGCAAGGTTTACAACAGTACTGATAAAACTATACGTTAAAAGGAAGAAAGTACTAGCTTTGGCAATTAAAGTCATGATTTCG
AAATCAGCTAGTAATGGAAAGGGTATCAACCCATGTTATTGGAATATCACCTAGTCATATTACATAGAGCAGTCACAGATTGCTATTACTTTA
AAGTGGAAAGTGGGTTAGAAGGACTTTTATTATGCCCTTCAAGAC

SEQ ID 400

LSKQLSNIKAFTLLEALIALLVISGSSLVYQGLTRLLKHSYHLARHDQDNLLFSHQLREELSGARFYKVADNKLYVEKGKKVLA
FQFKSHDFR
KSASNGKGYQPMFLFGISRSHIHIEQSOICITLKWKSGLERTFYAFQD

SEQ ID 401

ATGAATTGAAAAATTGAGACAGCCTATGAGCTGATTAGAAAATATCAAACAGATTGAGAACCAATTAAACACTATTTATGATGCCCTTA
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GAATGGCGTCGCACTTCCAGTTCAATTCTGCGAACAGAGCAATTACAAGCTAACATCAGTTACGCAAGCATTGCTGAAATTAGGTTCTAGT
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AAATAACGCTGAAAGAGTTAAATTATGGCATTGAGATTGATCTTGTGATCTACGCAAGCATTGCTGAAATTAGGTTCTAGT
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GGTATTGCTAAACGATATGCTGATCAAGTCTAAAGAGCACACCTATGCTCACCATCTATTGATGGAGCAATCTCTAAATATTGAAAGAAAGT
GGAATCGCTATATTGCTGACCCGAAACCTTTAACAACTGTCACAAAGTGTGAGGAGTGGTAAAGGATATGCGATGTCATTGCC

GTTTTAACTCTACCAGAAAATTTGGAAAGTCGTAAAATGCGAAATCTATATTGTTCTCAAGAAGCAAGCAGAACAAAACCAGAAACCTT
GTATATCCGCTGACAGATTCGAAATCGTGAGAATATGGCAAACCTTCATTGAAAATTTCAAAAATGGAGCAGAGAAAATAGTCATTACTCAAA
AATATGATAAA

SEQ ID 402

MNFKEIETAYELILENIQTIENQLKTHIYDALIEQNSYYLGSSCDLDMVVNNQKLRQLDLSQEERRTFQFIFIKSAQTEQLQANHQFTPDSIGF
ILLFLLEELTSQETVDLEIGSGTGMLAQTLNNSSKELNYMIEVDDLLIDLSASIAEIIGSSAQFIQEDAVRPQILKESDVIISDLPVGYPN
GIAKRYAVSSKEHTYAHLLMEQSLKYLKKDGIAIFLAPENLTSPQS DLLKEWLKGYADVIAVLTLPTIFGSRQNAKSIFVLKKAEQKPETF
VYPLTDLQNRRENMANFIENFQKWSRENSHYSKNMK

SEQ ID 403

GTGACACTCTTTCAAGTGTAAATTGGTATGATAAGGTTATGACTTTGAAAAAATTGAAGAAGCTTATCAGCTGCTCTAGAGAACTGT
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GCTCAAAATAGTGATAACTGAAAGCCTGTCGAAAAGAAGAATGCCCTGAGGCTTACAGCTGCTTCTGCTGATCTTGGAAACAATTGAGTAAAGATAGCCTAGGGTA
CAACTCCAAGCCAACCATCAGTCAGTCAGCTTCTGCTGATCTTGGAAACAACAGAGCAAGGCTGATTATGTAGGGATTGAACTTGTGATCTC
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GACATTGTATCAGTGTACTACCAGTTGGTATTATCCTAACGATGATAITGCCAAACGGTACAAGGTGGCTAGTTAGATAAGCATACCTATGCC
CATCATTATAATGAAACAGTCTTAAACTTGAAAAAAGACGGTTTGCAGTTCTGACCAGTCAATTGACAGGCTCAGTCAATTGACAGGCTCAGAGC
CAGTTGTAACAGTGGTAAAAGATTATGCTCAGGTGGTACCTGATTACGCTACCAGATTCTATTGGTCACTCCCAAATGCCAAGTCC
ATTATGCTCTACAAAACACAGACCACCAATGGAAACCTTGCTATCCAATTGGGATTGAGAATATTGATCTTGTGAGAGAATATTGATCTTATG
GAAAATTCAAAAATGGAAACTGAGTAATGTCAAT

SEQ ID 404

VTLLFISSIWYDKVMTFEKIEEAYQLLLENQLEIENDLKTHIYDAIVEQNSFYLGAEASPQVAQNSDKLKLALCLTKEEWRKAYQFLFIKAQTE
QLQANHQFTPDAIGFILLYLLEQLSKDSDLLEVLEIGSGTGMLAQTLNNNTSKLDYVGIELDLDLLIDLSASIAEIMDSAHFIQEDAVRPQLKES
DIVISDLPVGYPNDDIAKRYKVASSDKHTYAHLLMEQSLKYLKKDGFAIFLAPVNLLTSPQSQLLKQWLKDYAQVVTLITLPDSIFGHPSNAKS
IIVLQKTDHPMETFVYPIRDLKLAENIHDFMENFKWKLSNVN

SEQ ID 405

ATGTCAAAACAATAGCAATTATGCTGAAAGTTCAGTTGAAATGGCAATTATGAAATGCCAGAGGAGAAAGTAGTTGCCAAAGGGATTATC
GAACGTATTGGTTGAAAGATTCTATTGCACTGTAAATGACGATAAAAAGATGAAACAAATTAGATCTGAGTACATACCCAGCTGTT
AAAATCTTTAGAAGATCTAACAAACATGGTATTATCAAAGACTTTAATGAAATCACGGTGTGGTATCTGCTGTTGCTGGTGTGGTGAATAT
TTAAAGAGTCTGCTTAGAGTGTAAAGGTTAGAACAGGGTGAAGAATTATCAGCTTCTGCTTACAGCTTACACAAACAGCAGCTGAGCAGGG
ATTCTGCTGTTAGAGAAATCTTACCGATATCACGAGTGTATTTGATACAGCTTCTGCTTACACAACATGCAACCTCATACCTACTTATAT
CCAATCCCACAAAAGTACTATACTGATTATAAGTACGTAATACGGTGCACACGGGACAAGCCACCAATACGTTGACAAGAAGCAGCTAAGCAA
TTAGGACGTCTTTAGAAGAAATTAAATCACAGCACATGTGGGTAATGGTGTCTTCTATTACAGCAAATTATCAGGACAGTCTATTGATACA
TCAATGGGATTCACACCACTTGCAGGACCAATGATGGGACACGTTCAAGGAGACATTGATCTGCTGATTATCCTTATCTGCTAGTAAATGATCCA
GAATGGGAGATGAGCAGCTGTTAATATGCTTAACAAACATCAGGATGTGGTACAGGAACTTCAGGAACTTCAGGATGATATGCGAGAATTGAA
GCAGGTCTCAAAGTAAAGTCCAAATGCACTGTGTAGCTTATGCTTATGACCGTATTAGGAAACAAATTGAGAATATTGAGAATACTTGGCAGTATTAA
AATGGGGGGATGCTATTATTTACTGAGGTATGGGAGAAAATGCGCCATTATGCGTCAAGATGTTATGCGAGGATTATGAGGTTGGCATT
GAACTTGATCCAGAAAAAAATGTTTGGTATTGGAGATATCACAAAACAGATTCAAAAGTGAAGGTTAGTTACTGCTACTGATGAAGAA
TTAATGATTGCGCGTGAAGTGGAGCGCTTAAAGCTAA

SEQ ID 406

MSKTIAINAGSSSLKWQLYEMPEEKVVAKGIIERIGLKDSISTVKFDDKKDEQILDIVDHTQAVKILLEDLTKHGIIKDFNEITGVGHRVVAGGEY
FKESALVDDKVVQEVELSALAPLNPAAGIRAFREILPDITSVCVFDTAFTTQMPTHLYLPIPOQKYYTDYKVRKYGAHTSHQVVAQEAAKQ
LGRPLEELKLITAHVGNVSITANYHGQSIDTSMGFTPLAGPMGTRSGDIDPAIIPYLVANDPELEDAAVVNMLNKSGLLGVSGTSSDMRDIE
AGLQSKDPNAVLAYNVFIDRIKKFIGQYLAVLNGADAIIFTAGMGENAFLMRQDVIAGLSWFGIELDPEKVNFGYFDITKPDSDKVVLVPTDEE
LMIARDVERLKAK

SEQ ID 407

ATGTCAAAACAATTGCAATTATGCAAGGTAGTTCTAGTTAAAATGGCAACTTTATCAGATGCCAGAGAAGCAGTGTAGCACAAGGAATTATT
GAGCGTATCGGTCTCAAGGATTCTATTCAACAGTTAAGTACGATGCCAAAAAGAAGAGCAAATTCTGATATTCAAGATCATACAGAAGCTGTT
AAAATCTTATTGAAACGATTGATTCACTTGGAAACGTTCTGAAACAGATTGAAAGAATTATCAGGAGTTGGACACCGTGTGTTGCTGGTGTGAACCT
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CCAATCCCTCAAAATATTACGGAATACAGGTTCTGAAATGGGCGCATGGGACAAGTCATAAATATGAGCAGCAGCTGCTAAATG
CTTGGCTGCCATTAGAGAAATTAAAACATTACTGCTCATATTGAAATGGTGTCTCAATTACAGCTAATTACACGGTAATCAGTTGATAC
TCGATGGGCTTACACCACTTGCCTGCTGCTATGATGGGACACGTTCTGTTGACATTGACCTGCTTACATTCTTATTAAATTGAGCAAGACCA
GAGTTAAAAGACGCTGCTGACGGTTAATATGTTAAACAAAAATCAGGCTTACTGGGGTGTGAGGCTTCTAGTGTATGCGTATATCGAG
GCTGTTTACAAGAAGATAATCCAGATGCTGTTAGCTTACAAATATCTTATTGATGCGTATTGGGACAATATTTGCTGTTG
AATGCGAGCAGATGCTTGGTCTTACAGCTGGTATGGGAAATGCAACATTGATGCGTCAAGATGTTATGCTGTTAATCTGAGGTTGGCTTACATGGTCCGAATG
GACATTGATCTGAGAAAATGTTTGGGATACCGTGGTACACATTCAACTCTGAGTCAGGAAAGTGAAGGTTGGCTTATCTAACAGACGAAGAA
TTGTGCTCGCGCGTGAAGTGGTAAAGCTTAAACAAAAACAGATTCAAAAGTGAAGGTTGGCTTATCTAACAGACGAAGAA

SEQ ID 408

MSKTIAINAGSSSLKWQLYQMPEEAVLAQGIIERIGLKDSISTVKYDGKKEEQILDIDHDETEAVKILLNDLJHFIIIAAYDEITGVGHRVVAGGEY
FKESVVVNDKVLQEIELSVLAPLNPGAAAGIRAFRDILPDITSVCVFDTFSMAKHTYLYLPIPOQKYYTDYKVRKYGAHTSHQVVAQEAAKQ
LGRPLEELKLITAHVGNVSITANYHGKSVDTSMGFTPLAGPMGTRSGDIDPAIIPYLIEQDPELKDAADVNLNKSGLGSVSGIISDMRDIE
AGLQEDNPDAVLAYNIFIDRIKKCIGQYFAVLNGADALVFTAGMGENAFLMRQDVIGGLTWFGMDIDPEKVNFGYRGDISTPESKVVLVISTDEE
LCIARDVERLKNTK

SEQ ID 409

ATGAAAAAATTCTCTACAAAAGTTACGAAAATCTAGGAAATTAAAGTCAGGAAACTTGCAGTTGCACTTGGACTACTAGGCAAACATTATTCT
CTAGAAAAAAGAGAAAATACACGGCATCTTGGAGCTAGCTTAAAGATAGCGCCTTATTGATAAAACAAATTGAGGAAGTTTTATTACAGAA
AGTGAAGGAGGA

SEQ ID 410

MKNSLQKLRKSRKLSQAEALAVLGVTRQTIISLEKEKYTASLELAFKIARYFDKQIEEVFIYTESEGG

SEQ ID 411

ATGAAGGAGATGGCAATGGAGGTTATTCTTAAAATCGGCTAAAGAATTACGAGCTAGAGATGGAATTACAAACGGAAATGGCTAAACTGGCA
GGACTATCGAGGAGACCATCAGTCATGGAGCTAACGAGTACACCCCATCAGTTATAATTGCCATGAAAATTGCAAAGGTATTCAGGAACCA
GTTGAAGAGGTGTTCTAGTGGAGGTCAGGAA

SEQ ID 412

MKEMAMEVILKNRLKELRARDGINQTEMALAGVSQQTISLIERNEYTPSVIIAMKIAKVFQEPVEEVFRLVEVEE

SEQ ID 413

TTGGAGGTTTGTCTATTAGAAAAGGCAAATTTAGCTTGTCAATAGCATTAGTTATAATCAACTTGTCCTATATTGGCT
 GTGTGGCTCTAAAGAACACTATCAAACGCCCTTACTAGTATATTGTTGATTGGCTTAGAATTACTTATTGCTCTTCTTATTATGCC
 AAGGTTAACAAATACTAGATGGAAAGCATTATTGACAAGGAAGCATTAGTTACTATTCTTAGGTTGTTATCATTGAGGGTCCACAAATT
 ATTGGTTACCTCATTATGACTATGCAAGGGTTAAAGATAACAGCAAATCAAACAGTAATTATGCAATTAAACAGCAACTTCAACTAGCTTTGATG
 TTAATTGGCCATAATTGGTGCCTTATTATGAAAGAAATTATATTGCTATATTATCCCTAAAGAACCTTGGCGAAACATCAAAAATGGGT
 TTTGTCATCGGTACTTTAGCTTCTATTCTACCTCCCTCTGATATAGGTAGTTTATTATGCTGGGATGGGTGCTATTATCTT
 GTTATTATAAACTGAGCACTAGAATATAGTATAATGATTCACTTAAACATGCTTGTCTAGCGTAAATCAGTACAATGATGAAT
 AAC

SEQ ID 414

MEVFVFSIRKGKILALLIAFLVINQLPILAVWLKNHYQTPFTSILLIGLELLIIFLYAKVKQIIRWKALLTRKALVTLILGWLSLRVPQI
 IGYLIMTMQGVKDTANQTVIMELTQLPLALMIFAIIGAPIMEIIIFRYIIPKELFAKHQKWGFVIGTLAFALIHSPSDIGSFIIYAGMGAILS
 VYYKTEHLEYSIMHFINNALAYSVLISTMMNN

SEQ ID 415

ATGAAAGGATTCACTAATTATTTAAAAATAGCAGTGCTCATTCTGGCTATGGTTTCAATGTCCTCCGATGATTTATTGCAAAAGCAACAC
 GATATTCTATGGTACTTAATTGGGAATTGGTATTTCTACTGGTTATTGTTGAAAGTGCCTTATTGTTATTGGGTCTTATCAAGCTAAG
 CAAGCACCTTATTAAACAGCAAATGAGATTGGTACTGGGGTTATTAGCATTATTGTTAATCATCGTGTGATAGCTATTGTAAGGT
 ACCCTTGTAAACAGCTATGGTCTGGTCAACAAGTGAGTGACTACCTTAAAGGTGGTTCCCTATCAAGGTGGTTCCCGCTT
 TATACTGCCCCTATTGTAAGTGTGATAGCTTATCGCTCTATTGAAAGAAACTAGTCTTAGAGGAGTTCTATGATTGATCTTCAAAGGA
 AAATCACTAAAGGGCAGGTTAGTGCACCTCTTGTCTTACACATGCCACCAATAGTGTGAATTATCATGTACAGCTGTATGGC
 ATTTTCTCTTGTGCTCTATCAAAGACGAGGAACITTTAAAGATGCTATCTGTTACATATTTAATAACTTGTGATTGAAGTCATTGTTAATG
 TCAATAGGCTTAGGAGTCATA

SEQ ID 416

MKGFINYLKIAVLIILAMFVNVLPMILLQKHDIPMVNLNWGIGIFYLVIVGSVLIVLWGLYQAKQDFTIKQQKMRDVWGLYALFWLII
 RVIAGVTLVNLWSQQVSANDAIIHTLARLIKGFPLYTALFVLVIAFIAPIMEELVFRGFPMDLFKGKSLKVAGLVTSLVPHATNSVEFIMSCMG
 IFLFVAYQRRGNLKDAIILHIFNLLIEVILLMSIGLVI

SEQ ID 417

ATGAAAATGGAATTATCGCGTGCAGAAAATGCCAGTGCATTATTCAAGGCCCTCAAACAAACCCACATGACATTATCATATCCGATCTGC
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 ATTAACACCTCAACTATTGAAAAGGTTCTTCTTCACTTGATATCACAAACCAATCATCTAATGGCAGCAGGAATCTCTTAGCGCTTAAAC
 CAATTAAACTCGTTCTGATTACATTGATTCGTTATTGCAAATATTAAACGCAAAATACTTCAAGTCAGCTATTGTTACAACAACTCAT
 GTATCAGATGAGTTACGACAATTAGCCAAGAAATTACGGTAGTTGGAGTAGCTTGTATAGCAGAAACCAATTGATACCTTCACTGCT
 CTACAGGGTCTAGCCCTCGCTATATCTATTGAGCCTTAGCTAAAGCAGGTTAAAATATGGATTCTCAAAGAACAGCAACTCT
 ATTGTTAGGACAGACTGCTTAGCTTAGTCAAACACCTATTACAGGACAAATAGCACCTCTGACTTATCGACAAACATTGTA
 ACTACTATTGCTGGCTTTAGACTTAGAAAAAAATGGTCTGACGCATAGTGTATTCTGCCATTGATGCTACTATTGAGAAAGCAAAACTT

SEQ ID 418

MKIGIIGVGKMASAIQGLKOTQHDIISGSCLERSKEIAERLDVTYAEHSQSLINQADIIMLGKIPQLEKVLPLDITKPIISMAAGISLARLS
 QLTRSDLPLIRIMPNNQAQILQSCTAICYNHHVSDELRLQLAKEITDSFGSSFDIAETNFDTFTALAGSSPAIYLFI
 EALAKAGVKYGFPKEQALS
 IVGQTVLASSQNLLQGQNSTDLDNICSPPGTTIAGLDDLEKNGLTHSVISAIDATIEKAKL

SEQ ID 419

ATGAAAATGGCATTATTGGTGTGGCAAAATGGCTAGCGCTATCATCAAAGGCCCTAAACAAACACCCATGAACCTTATCAGGATCATCT
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 ATCAAGCTCAACTATTGAAAAGGGTACTCAAACCGCTTCACTTCAAACAGCCTTATATATCATGGCAGCAGGCTTCCCTCAAGCAGTAGCA
 ACATTGCTAGGACAAGACCTCCGCTGCTACATGTCATGTCACATGTCACAAATCTCCAAAGCAGCTTACCGCTTAAACGGAAATGCTT
 GTGCTCCAGGAAATTACAACGACAGTGTGAGACTTAACAGATAGCTTGTAGCACATTGATATTAGTGAAGGATTGACACCTTACCGCT
 TTACAGGGTCAAGTCTGCCATTATCTTATTGAGGTTGGCTAAGGCTGGCTCAAGAATGGCATACTCAAAGCAAAGCGCTGGAG
 ATTGTTACTCAAACAGTATTGGCTAGGCCAGCACTCAAGACCAGTCTCAAAGTCCGACGATTCTGACGCTATTGTAGGCCCGTGGC
 ACAACTATTGCTGGTCTGATGGAGTTAGAACGCCCTGGCTCACAGCTACTGTCAGCTGCTGACAAAACATCGATAAGCTAAAGCTT

SEQ ID 420

MKIGIIGVGKMASAIKGLKOTPHELIISGSCLERSKEIAEQLALPYAMSHQDLIDQVLVILGKIPQLEKVLKPLHFKQPIISMAAGISLQRLA
 TVGQDPLLRLIMPNNQAQILQSSTALTGNALVSQELQARVRLTDTSFGSTFDISEKDFTFTALAGSSPAIYLFI
 EALAKAGVKNQIPKAKALE
 IVTQTVLASASNLKTSSQSPHDFIDAICSPGGTTIAGLMELERLGLTATVSSAIDKTIKAKSL

SEQ ID 421

ATGTCAGATTTTAAACAAAATTAAACCGTAACCTGAGCTTGTAGGGATTGCTGGCTATGAAACACAATATCCGCAACTTCTTCGTCAGGAAATA
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 GCCCATATGGATGAAGTCGGCTTATGGTACTGTCATACTCAGCCAGATGGAACATTCTGTCAGTTGAGGTTGGAGGATGGAATCCCTAGTAGTC
 AGCTCACAAACGCTTACCCCTCTACACACGTTCTGGTACTTCTGTTATATCAGGCTCAGTTCTCTCTACTTCTCTGTCAGGAAAGCGGT
 GGAACAAACATTACCCAAATTAGTGCACATTGTTGAGGATTACAGATAAAAGCTGAAGCTGAAGCTTGGCATTGCTCCCTGGGATATC
 ATTGTTCTTAACTCTGAAACCATTTACTGCAAACTATTATGTCACAAAGCTTGGGATAATGCTTGTGCTTATGGTGCAGGAA
 TTGCTAAAAGCTTAAAGATCAACAGCTTCTGACACACATTTACTGCTGGGGAAATGTCAGAAGAAGCTGGACTTCGTCAGGCACTGTC
 ACAACTAAATTCAACCCAGATATCTTCTGAGCTGTCAGTTGAGGAGATATTGAGGAGATTTCTACTTACAACAGCTGAAGAAGCAGG
 ATATACTGTCACATGCTGGTACCGATGCTGGGCTGCTCACCTAAAGTGGTATTCTCTACAACACTATGGGTCTGTCAGCCTACATTCT
 CATCAAACACTCTACGCTATGGATGATTCTACAAGCACAAGCTTACCTCAGGCCATGCTTAAACAAATTAGACCGCTCGACGGTGGATATT
 AAAAGCTTAT

SEQ ID 422

MSDLFNK1KTVTELDGIAGYEHNIRNFRQEITPLVDQVETDGLGGIFGVNTHETNAPKVMVAAHMDEVGFVMSHIQPDGTFRVLVEGGWNPLVV
 SSQRFTLYTRSGDAIPVISGSVPPHFLRGQSGGTTLPK1SIDIVFDGGFTDKNEAESFGIAPGDIIIPKSETILTANQKIMSKAWDNRYGVLMVTE
 LLKSLKQDSLNTLJAGANVOEVLGJAHVSTTKFNPDIFLAVDCSPAGDIYGEQKGKIGEGLIRFYDPGHIMLKDMRDFLTTAEAGIKYQYY
 AANGGTAGAAHLKNNSGIPSTTIGVCARYIHSQHLYAMDDFLQAOQAYLQAVNKLDRSTVDIICKY

SEQ ID 423

ATGACAGACTTCTAAAAATCAAAGAAGTTACCGAAGTGGATGGCATTGGGGCTATGAAACATAGCCTCGTACTACCTACGCACCAAAATA
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GGCACATGGACGAAGTCGGTTTATGGTCAGTGATATCAAAGTTGACGGAACGCTACCGTGTTGGATCGGTGGTTGGAAACCACCTGGTGC
AGTTCACAAACGGTTACCCCTTACACACCACTGGCAAGTTATCCCCCTATTTCAGGATCGGTACCTCCCCATTTCAGTGGGCAATGGC
TCTGCTAGTCTACCACATATCGAAGATAATTGTTGATGGCTTACGGATAAGGAGCTGAAAGATTTGGTATTACACCGGGCTGATATT
ATTATCCTCAATCTGAAACGATCCTAACAGCAATCAAAAAAATTATTCAAAAGCTGGACAATCGCTATGGCTCTCATGATAACAGAA
ATGCTGAAAGCTTAAAGGACAAGACCTAACACCCCTAACGTTAACAGAAGAAGTTGGTCTGGCAGGACCCACGTCTAAC
ACCAAGTTGACCCACTCTTCGAGTAGATTGTTGCCGCTGGTATTTTACGGCAATCTGGAACAACTGGAGATGGTACCTG
TTGCTTACGACCCAGGCCATGTCATGCTCAAAGATAATGCGGACTTACTGACTACTGCTGAGGAAGCTGGTCAATTCAA
TGTGCAAGGGAGGCACAGATGCAGGTGTCACACCITCAAATGGTGGTCCCATCAACACCATGGAGTGTGACGCTACATTCA
CATCAAACCTCTACGCTATGGATTTCTAGAAGCCAAAGCCTTACAAGCATTCAAAGGATCGCTAACCGTTGACTT
AAATGTTAC

SEQ ID 424

MTDLFSKIEVTELDGIAGYEHESVRDYLRTKITPLVDRVETDGLGGIFGIRDSKAEKAPRII.VAHMDEVGFMSDIKVDTLRVVGIGGNPLVV
SSQRFTLYTRTQVPIPLISGSVPVPHFLRGANGSASLPHIEDIVFDGGFTDKAABERFGITPGDIIIPQSETILTNQNIISKAWDNRYGVLMITE
MLEALKGQDLNNTLIAGANVQEEVGLRGAHVSTTKDFPELFFAVDCSPAGDIYGNPGTIGDGTLRLRFYDPGHVMLKDMRDFLLTAEEAGVNQYY
CGKGGTDAGAAHQNGGPSTTIGVCARYIHSHOTLYAMDDFVEAQAFQLQAIKKLDRSTVDLJCKY

SEQ ID 425

ATGGTTAACATTCAAACAGAAAGAAAAACATGAAAGAAAATTATTAGTACCTGCTTTAATTGTTGCTAGGTCTACTCTTCTAGG

SEQ ID 426

MVNHSNRKKHERKIISTCFKL FARSTLPR.

SEQ ID 427

GTGTCTAATCCGGGGGGTATGGTATAATAACAGTTATGAAAAAATAAAAAAACTTATTTGGACTGGCTTGCTGGTGGGTTACTGGCAGGT
GCTGGTTATACCTAACAAAAAGTAACAGATTAAACGTCAGCAAATCACTCAGACCTTAAGAGAATTTTTAGTCAGATGGTGTATATTCA
GTATTATTATTAAATGAATTCTGATATTAAATGACCAGTGGTGGTCTGTCTGGAGATGGCAGAATTTCGAATTATCGTCAA
GGTGGTCTGATTATGTGGAGGTGAGCAA

SEQ ID 428

MSNSGGYIITVMKNKKILFGTGLAGVGLAAAGYTLKKVTDYKRQQITQTLREFFSQMGDIQVFYFNEFESDIKMTSGGLVLEDGRIFEIYRQ
GVLDYVEVSK

SEQ ID 429

ATGAGGGATATGAGTAAAAAGAAAATAGGTATGATTCAGGTATCTTGGATTAGTTAGCTATTGGCTAGGAATAGTTATCAAAGATTATTG
CAAGACAGCAGCGTCGACAAATGACAAGGGATTACGCACCTTTTCACCTTAAAGACAATCGAAGTTTATATATCAATCCTGTCAGGTC
AAACAAGATTATATTTCAGGTGGGGTTGTATGTCAAACGCAAAACAGTACCAATTACACAGTCGACAAATTAGTTGAGGAGGACAAG
GGA

SEQ ID 430

MRDMSKKKIGMISGIFGFSLAIGLGIVIKDYCQDRQRQMTRDLRTFFSPLGQIEVLYINPCQVKQDYISGGVMSNGKQYQFTYHRSRQISFEEDK
G

SEQ ID 431

ATGATTTTACCAAGAATCTTATGAAGAAAATAGCAGCCTATATTGATAGCACTAAGAAAGTTGTTCTTTTACAGCAGATTGGTGCAGATTG
CAATTATATATCCAGTAATGCCATCAATTGAAAAAGATTCTCAGATTGTTGCTTGTACGTGTTAATCGTGTACTATAGAATTAGCTCAG
CAGTGGAAATTGGGATTCCGAGTTCTGTTGTTGAAAATGGTCAGGAACCTGGTCGTTGGTTAATAAGAATCGCAAAACAAAGGCTGAA
ATTACTAAATTCTCGTCAAATTAAACTATAAA

SEQ ID 432

MILPESYEETIAAYIDSTKKVFFTADWCPDCQFIYPVMPSEKDFSDFVFRVNRDDYIELAQOWNIFGIPSFVVENGQELGRVLNKNRKTAE
ITKFLAEINYK

SEQ ID 433

ATGATCACAGCGACTTCTTATGAGTCATTAGCAGCTTATTGAAAAAGATAAGCTGGTGTATTTCACGGCAGACTGGTGCAGACTGT
CAATTATCTCTATTATGCCAGAAATTGAAGCAGAACTTACAGATATGACTTTGTTGTTAATCGTGTACTATAGAGGTAGCACA
AAGTGGAAATTGGTATTCTCTAGTTGTTGTCGATTGAAAAGGTCAAGGAAGTAGGGCCTGGTTAACAAAATGAGAAAGACAAA
ATTATGATTGTTAGCTGCTTATCAA

SEQ ID 434

MIRPTSYEETLATLIEKEDKLVLFADWCPDCQFIYPIMPEIEAELDMTFVCVNRDQFIEVAQKWNIFGIPSFVVIEKGQEVGRVLNKNRKTAE
IMHFLAAYQ

SEQ ID 435

ATGATTTTACTTATAATAGAGAGCATGTTGGTACCTTAATGGTTATTGTTAAGGATAGTCAGGAGCTAAGCTAGATGTTGATCGTCGCGGA
CAAGTAGCACCGCTATCTGCAAGATAGTAAAGAACAGTTGCTTGGAAATATCTTGAAGGTGTCAGTTAATGTTATTGAGGGAGCAGGTCAA
ATAATTTTATCTGATCAAGATATTAAACCTTAAATGCAAGACTACTGAAAGAAGGATTCGAAGACTCTCTGTTAATAATATTGAACACTATT
GTTGTCGGCACAATTAAAGAAAATTGATCATCCAGATAGTGCACCTTACATATCTGTCAGCAGAAATCAACGATGGGAAGACGGTCCAATC
GTTGTCGGCACAATTGCTTCAGTAGGTCTTAAACAGTTGCACTCTCAGGAGCTATGTCAGCAGAAATGGTAGCTTACATTGAAATTCTGAT
CTTCAGTAGGTTGGAGAGCTTCTGACGCCAATAAACATTGGAAAAT

SEQ ID 436

MIFTYNREHVGDTLMVIVKDSQGAKLVDRRGQVARVYLQDSKETVAWNIFEVSSLIVIEGAGQITLSDQDIKILNAELLKEGFEDSLVNNIEPTF
VVAQIKEIILHDPSDHHLICQAEINDGKTVQIVCGAPNASVGLKTVAlPGAMMPNGSLIFPGKLRGEDSFGLCSARELALPNAPQVRGIIELSD
QVIVGESFDANKHWKN

SEQ ID 437

ATGATTTTGCATACAATAAGAACAGTTGGCAGTGTCTTGTGGTTATCTTACAAGACACCAAAGATATCAAACGTCAGTAGAACGAAAAGG
AAAGTAGCCCGTGTGTTGGCAGAAGAACGCGAAACCCCTGCTTGGAAATATCTTGAAGGTGTCAGCTGATTACTATTGAAGGCAATGGACAG
ATTTTTTGACAGACGAGAACCTTGCAGATTAAATGCAAGACGTTGCTAAGGAAGGATTTCAGAAAGGCTTGAACCGATTGTCGGACTGTTT
GTGGTTGGTCAAATTGTTGAGATGGTGGCTCATCCAGATAGCAGGACCATCTTAATATCTGCCAAGTGGCTATTGGTGAAGATCAA
CTGAGCAGGGCACCACAAATGCTGGCTGGTTAAAACGATTGTCGCTTACCAAGGTCTATAATGCCAATGGTAGTCAGAGGTATCATTGAATTATCTGAT
CTTCAGCTGTCAGTAGGAGAGCTTCTGACGCCAATAACATTGGAAAAT

SEQ ID 438

MI FAYNKEQVGDVLMVILQDTPDKI KROVERKGKVARVFAEESGKTLAWNIFI EASSLITIEGNGQIFLTDENLARLNAAEIAKEGFSERLEPIVGPVF
VVGQIVEMVAHPDSDHHLNICQVAIGEDQTVQIVAGAPNAALGLKTI VALPGAIMPNGSLIFPGKLRGEESYGMCMSPRELALPNAPQKRGIIIEFDE
SAVVGAEFDAKHWKG

SEQ ID 439

ATGACAAATGTAACTAGTTATAAGAAAATGCTGGCTAACCTGGGGAAAAATACAATATGAAATAACTTTGCTCAATTAGCCATATCAAAATC
CAGAACGTTTGTAGATTGGAGCTGGTTTGTCTACCGAACACATCTAGAAAAGAAAACAATGTAACGCTATTGAACCCAATCTAACTG
CTTACGATAATCAAAGTGACAATATTATAAAATCCTAGGTTCTACGAAGCATTAAAGAGATTGCTGTCAAAGCTTGATACTATTATTG
CATATAATGTTCTGAAATATAGACAAACATAATCCTGTTATTTGACGAATTTCCTGACTCTAAACCCAATGAGAACTATCTCTCATC
AAACATAATACCGGTTAAATTACAACTCAGTTATTGCAATGATACTCCACTGGATGGAACCTTAAACAGGAGAAGCAACTTTAAA
AGTGCCTAGTTGACCAGGGAAATATTATACCTTAGAAGAACTAAACAAACAAATATTAGTGTAAACGTTATCAGGGTATTCTGACCTTC
TATTCTTACACCAACCAACCAATTAAACTGAACTGGTTGGCTAAACAAATGCTTGCTATCGAGCTAAGTGTGCTGACAAGCTCCTTATAAA
GATATTGCTTTTGCAACACATCACACTTAAAGTCATTG

SEQ ID 440

MTNTVTSYKEMLAKPWGKIQYEITFAQLSHIKNQNVLDFGAGFCILTEQHLAKENNVTAEPNPKLLYDQNQSDNIYKILGSYEALRDLPDQSFDTIIC
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YSLQPNNHFKTETGWLNKMLAIELSVADKAPYKDIAFLQHITLKKSL

SEQ ID 441

ATGTATAATAAGTTATTATGATTGGCGTCAACAGCAAAGCTGAGATGGTAAAAACACAACCTGACAAGTCAGTGACGCGTGCACTGTTGCT
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GGGACAAAGGGCTCTTAAATTCAATAGATGGTGAATTGCGTACCGCAGTAACGAAAAGGATGGTCAAACGCACTATATCACTGAAGTATTAGCA
CTCATCTTCTAGTTGCTAGAAAGCCGTGCCAACCTGCTATGCGTGAACGTTCTGGTGAATTGTCAGATTAGTATTGGAAGAAGAGGGAG
CTCCCCCTTT

SEO ID 442

MYNKVMIMIGRLTAKPEMVKTPTDKSVTRATVAVNRNFKGSNGEREADFINVVMWGRLAETLASYGTKSLISIDGELRTRKYEKDGQTHYITEVLA
SSFOLLESRAORAMRENNVSQDLSDLVLEEEEELPF

SEQ ID 443

ATGTATAATAAGTGTAGCAATCGGTCGGTAGCTAACCCAGAATTGGTAAAAACAGCTACGGATAAGCATGTAGCACGTCCTCTTCTTTAGCT
GTTAATCGAAGATTTAAAATGCTCTGGAGAGCGAGAAGCTGATTTATTCAGTTGTTGGGAAAGTTAGCAGAAACTCTGGTTCTTAT
GCTAGCAAAGCTAGTTGATGTCATTGATGGCAACTTAGGACCCGCAAGTATGATAAAAGATGGGCAAGTGCATTATGTGACAGAAGTCTCTGC
CTTCACTTCAACTGCTGAAAGTCGTCAGCGCGTATGAGAGAAAATATGTTACTAATGATCTAGTTGATTTAGTCTTAGAGAAGATACT
CTTCCCTTT

SEQ ID 444

MYNKVIAIGRLVAKPELVKTATDKHVARLSLAVNRRFKNASGEREADFISVVVWGKLAETLVSYASKGSLMSIDGELRTRKYDKDGQVHYVTEVLC
QSOFOLLESRAORAMRENNVTNDLVDLVLEEDTLPE

SEQ ID 445

TTCGTTTACAGAAAGCAACCTTTTATTGAAAATAGAAAGGCAAACGATTACAATAAAGGGATAGAAAGCAGGTTAACATGGAAAAAGTC
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GTCTCGTATCAATACCAGTACATGGGACTACTTGTGATTGTGGCAAGCTATGAAAGAGGAGTTGGCTTACCGAAAACAGTAAAGAGTAT
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CATGGCTATGGCTTAGCGATTGGCTCTCATCTCCTAAAGCTATCTAAAGGCTATCTAAAGACTTGGGTGTACAGAATGCTTGAATACATG
GTTACAGGAGAAGATGTATCTCTAAACAGCACCGAGATGTTCTAGAGCTGCAGAGCTTCTAGATGTAGACCCCTAAAGTTGTATAGTT
ATAGAAGATACTAAGAAATGGAGTTAGCTGCTAACGGCAGCAGGAATGTATTGCTTGGCTTGTAACTCTGATTATCCACCGCAAGATTATCA
ATGGCAGACAAGGTTATTCAGATTATCAAGATATCTATTTTCTTCCGGAG

SEQ ID 446

MLFTESNLFLLKIERQTITIKGIESRFKMEKVIFDMGVIVDSEYTFLDNKTEMLREEGIDTDVSYQYQYMGTTFEFMWQMKEEGLPKTVKEY
IAEMNRRQAIVARDGVRPIKGQAQLIHLWHLHQHGYRLAVASSSPMVDIKRNLKELGVTECFEYMTGEDVSSSKPAPDVFLRAAELLDVDPKVCIV
IEDTRNGSIAAKAAGMCFGFANPDYPQPQDLMSADKVISDYQDIIYLPE

SEO ID 447

ATGGTGATGATTAAAGGAATTATTTTGATATGGACGGTGTGTTATTTGATACAGAACCTTTTATCTGAGGCAGCAGAAGATTTTTAAGACAAAGGGAATTCCCATGATCATTGAACTCTAAAGATTTTATGGGGCAATCTCAAGAATTATGAAAGAGTTGTTAGGTAAGGATGATGCTATCGTTAAGGCAATTACAACGTACTGACATGACGCCAACAAACAGCGCATAAGCCTCTTATCAAAAAACTGTTGATTACAGAAGTGAACCTCTGCTTGAACAGCTGGAAAAAAACAGGTTAATAAACTGGCTGTGGCATTCAAACATCGAAGCGTCAGGATGTTGTGGCCTGGAGACAACGCAAATAAAAAAGATTATTTGAAAATCTACCGCTGAAGATCTTCTAGAGGCAAACCTTATCCAGGATTTATAAAAGGAGTACAAAAACTTAGGATTACAAACAAAAACACTGCTTGAGTAGAGGCCAGGCAAAAGGCATTGCTGCCGCAAAGCAGCCAATCTGACAGTTTGGCATTACCGGACTACCGGATATGGCATTGATCAGAGTCAGCTGATCAAAGATAGATCATTAGGACAACGTGTGTTAAATCGGGTTGGATCG

SEQ ID 448

MMLMKIGIIFDMGVLFDTEPFYLRREDFFKTKGIPIDHLNSKDFIGGNLQELWKELLGKNRDDAIVKAITTDYDAYKQAHKPPYQKLILITEVNSCLEOLEKQGIGLAVASNSKRQDVLLAETTQIKDYFEIILAREDVSRGKPYPDIVNKAVQKLGQLQQQLLVVEDSQKGIAAKAAANLTVAITDYRGIDQSQADHKIDHLGQLCVKIGCFGSS

SEQ ID 449

TTGGTGGACCTCTGGTGGATCAATTGGGTTTATTGGAGGAGTCATCGCTTTCAAGGAAGCTTTCAGGTTCTTCTATATTGTCAGTT
CAGTTC

SEO ID 450

MVDLWLDQLLVLLEEFIAFFKEAFOVLSILSVOF

SEQ ID 451

GTGGAACTAAACTATTAAAAATCATCAITGGAATGACAATCATTGACAAGTTCCATCCTGTAAAAATGCCAACAAATAGCATCTGGATACTT
TCGGCAATAACTAATTAAAATCAACTTGGCTTGTTGAGGG

SEQ ID 452

MEPKLFKIIIGMTILTSSHPVKMPTNSIWILSALLIKITWLVEG

SEQ ID 453

ATGTTGATGGTGTGTTATTCAAAGGCTAGGAATTATTATGATTTAGCCTTTTATTGGAAATAATAGTTATTTAGACAGTTAATTGAAGGCGGTCTAACAGTGAACGGTAGTCCTGTATCATTCGGCTTGTGTTATTATCTAAATAACAGGAATTGAAATAAAGGGGATCGAAGTTGGTCAGGCCCTTTCTAACACGATTTCTCATCTGACTCACTTGCTAAACAAGGACTTTAGTTTACACGGCAAGTTGGTGGACCTCTGGTTGGATCAATTGGTTTATTGGAGGAGTTCATGCCCTTTCAAGGAAGCTTTCAAGGTTCTTCTATATTGTCAAGTTCTA GTCCGCATTGTTAGCGGAAAGATTGGTGTAAAGCTTAAGGAAAACCCTCTCACCTTCAACAAGCCAAGTTATTAAATTAGTATTATTGGCCGAAAGTATCCAGATGCTATTGGTGCATTTCACAGGATGGGAACTGTCAAATATTGTCACTTCAATGATGTTAAATAGTTAGGTTCCCACATTTCTTCGATTTGAAACTATTGTCAATGAAACTGTCACTTACGGCAGTTCAACAGAGATGTTCTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGGTTGACACCGCAATCTGCTAGGAGCGTTGCGAAATTATAAGAGGCATACTTGTGCTGTGGGATAAACAGAT

CGGTCAAACGTATTAGCTATGGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTTATCTAAAAGTGTATTTTGAT
GGCGAACCAAGAATTGCGCAAGATAAAAGCGCGATTCTTGTCCAGATCACAACGTCACTGTCAAGTAAATTCTGCTATTGTAGTCTCTCTAA
GATAAAAACTGTGGGTGCTTAAATGTAATTGGCAGGAGATAAGACAATGTCAGGTGGAGGAAACCTAGTCCTTGTTAGGCCAAATATT
TCAGGACAACGGCAATGGGATAACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAAGCCTTACAAGCACAATCAACCTCATT
TCCTTAAATGCCATTAAACACAATTAGTCGATTAATCGTATTGATTCTGATAAAAGCAGCTATGCACTGTCAGTTAAAGTACTTTTTAGAAC
AGTTGCGGGTGGTCAAGGATCGTGAGGTAAACGCTTGAGCAAGAAAAATCACATGTTGATGCTTATGATGAGTGTGAAATTACGTTCCCTGAT
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TCAGATACTATCATGATAAAATTAGGTCAAGAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAACAGGGTGAATT
TTATATGGTAGTGTAAAGTTGCCTCATTTTCAGCGACAAGAATGGTACAAAGTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCAT
GAAAATTCTAATTCT

SEQ ID 454

MLMVLLFQLGIIMILAFLLVNNSYFRQLIEERSKRETVVVLVIIFGLFVIISNITGIEIKGDRSLVERPFLTTISHSDSLANTRTLVITASLVGG
PLVGSSIVFIGGVHRRFFQGSFSGSFYIVSSVLVGIVSGKGKIDKLKENHLYPSTSQVILLISIAESIQMLFVGIFTGWEVLMKIVIPMMLNSLGST
LFLAIIKTYLSNESQLRAVQTDRVLELTROTLPYLRQGLTPQSARSVCETIIRKHTNFDAGVLTDRSNVLAHIGVGHDHIIAGQPVKTDLKSVID
GEPRIAQDKAAISCPCDHNQCLNLSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVLGLAQIFFGSQLAMGITEEQNKLASMAEIKALQAQINPHF
FFNAINTISALRIDSKARYALMQLSTFFRTSLQGGQDREVTLQEBKSHVDAYMNVEKLRFPDKYQLSYDISAPEKMLPPFFGLQVIVENAVRHA
FKERKTNDNHILVQIKPDGHYYCVSVSNSDNGQGISDTIIDLKGQETVAESKGTGTALVNLNNRLNLLYGSVSCLHFSSDKNGTKVWYRIPNRIREDEH
ENFNS

SEQ ID 455

TTGACAGACCTTGCACACAGTTAATGCGCTTAGATCAAATGATAGCTGGATGGTGGCGTGGGATAAGGAAAAGGCATTGGGAGTAT
AGGTTCACAAGCCTGGCTAGTCAGATTAACCCGCTTCTATAACACCTGGACACTATTATTTGGATGGCAGAATTAAATGACAGCAAGCGC
GTGGTAGAAGTGACCAAGTCTAGCTAAGTATTTCTGGGCTTAATCAGGGGAACGAATAACATTCTGGCAGATGAAGTGGATCACGTT
AGCCAAATACCTCTTTATCAAAAAACAGCGCTATGGAGACAAGCTAGTTATGGAGTCAGGCTTACGCAAGGCTTACGCAAGCTTGTATTCCCTAAG
CTTATCTTACAGGCCCTAGTAAAGTCATCTACATGGCATCAAAGAAGTCATCGCAAGGGCATGATCAAGGTTACGGTATCTGATACAGCT
CAGCATCTGATGTTGACTGTTGGGATAATGGTAAAGGCATTGAAAGACTCTTCACTGACCAATAGTCAGAGCTGTTGGCTAGGGGGAGGTGGGC
CTTAAAGTGTGACAGCGGGTAAACATTCACTATGGTGAAGGCTACCATGACCATTGACCATTCAGGCAAGTCAGACCAGTCAGGAAATACAATTA
AGCCTTCTAAATGCGATGAAATTAATGGCAGACGACACACAGGGAAAACGAG

SEQ ID 456

LTDLAQQFNALLDQIDSLMVAVADKEKAIGQYRLQALASQINPHFLYNTLDTIIWMAEFNDSKRVEVTKSLAKYFRLALNQGNEYIRLADELDHV
SQYLFIQKQRGYGDKLSYEVQGLDVFYADFVIPKLLQPLVENAITYHGIKEVDRKGMIKVTSVSDTAQHMLTVWDNGKGIEDSSLNSQSSLARGGVG
LKNVDQRLKLHYGEFYHMTIHSQSDQFTEIQLSLPKMHELMADDTQE

SEQ ID 457

ATGAGCATGAAAATTAACTTGTGATGAAATGTTGCCAGACAAGAATTATCGTTTAGTTGAACATAGCCAGGAGTTGACAACCCGTGAG
ATTTTCAGGCTGAGGATATCAGTGAAGCCGAAAAATCTTATTAGACAGCAAATTGATTAACTTTTTAGATATTTCGCTTAGTGAAAGAAAAT
GGCTTACTTGGCTAACAGTGGACAGCCAACCTGGCACATCCCCCACTTGTGTTTGCAGCAGCTTATGATAACTACCTCTGTGAAAGCTTTGAA
AGTAACGCTGTTGATTATATCATGAAACACCAGCGCTTGAACAAACAGCGCGTGTATGGCTCTATCAGAAAGGAAATTGAGCCAACCTCACCTGCT
TCAGATGTAGAGCAACGAACTACCTTAAAGGCCAGTGTGAAATTGTTAACCTTGACATTATCAGATCGCAGTGTGTTGTTAAAATGCAAGATATT
GTTGCAGCTAGTGTGAAAGATGGCGAATTAACTGTTAGTACAGTTAGAAAACCTACACTATTGGAGACACTCAATTGTTAAGTCACGCGCT
GTAGCACCATAATTCTCCAGATTCTGAAACACAGTGATTAACTAGAGATGATTGAGGAATTCAACCTGGTTAATCATACTTTGTTACTA
ATTATGTCATAATGGAGAGAAATTCCAGTAGGTGCGATCGTATTAAAGACCTAAATGAGCATTAAACCATG

SEQ ID 458

MSMKILILDDEM FARQELSFLVEHQSEVDNPEIFQAEDISEAEKILFRQQIDLIFLDISLSEENGFTLANQLSQLAHPPLVVFATAYDNYAVKA
FESNAVDYIMKPFEQQRVDMALSKVKKLSQLTTASDVEQAIPKKASVELLTTLSDRSVVVKMQDIVAASVEDGELTVSTVQKTYTIRKT
LNWFKSRAVAPYFLQIHRNTVINLEMIEEIQPWFVNHTLLLIMSNGEKFPVGRSYLKDLNEHLM

SEQ ID 459

GTGTACTCATTGTTAATTGTTAGAAGACGAATACCTTGTGCCAGGGTATTGTTCTTGTTGATTTAGCCAGTTCAAGATTGATCGGGTCAAC
GAAGCAGAAAATGGCAGATTGGCTTGGGACTTGTGTTTCAGAAAGAGCCTTATGATAATTGTTTGACGGATATCAATATGCCAAATTAAATGGGATT
CAACTAGCAGAACTCATTAACAGGAATCCCCCAAACCTCATCTGGTATTGTTGACGGCTACGATGATTAACTATGCCTTATCTGCTTTGAAA
TTTAGGGGAGATGATTACTGTCATTAACCCCTTCCAAGGCAGATGTTAGAAGACATGTTAGGAAAGCTCCGGAAAATTAGAACCTTCCAAGAAA
ACAGAACACATTGCGAAATTGGTTGAGCAGCTTAAAGAAGTATCAGCAATAGCAATTGCTATTCTAGCGGTTGGCAGATTCTGATTGACC
CTAAAAAGCTTGGCTCAGCAGCTTGGTTTAGCCTAATTACCTTAGCGCTTGATTAAAAAAAGAGTTAGGGATGCCCTTCAGGATTATCTGGTA
CAAGAACGGTTGAAAAAAGCCAAGCTCTTGTAAACCAGTAATCTTAAATCTATGAAATTGCAAGAGCAGGGTGGTTGAGGACATGAATTAT
TTTCTAGCGCTTAACTGGTAGCGTTACCCCAAGTCAGTATAAAAAGGAGGCCAGGCA

SEQ ID 460

VYSLLIVEDEYLVQRQGIRSLVDFSQFKIDRVRNEAENGQLAWDLFQKEPYDIVLTDINMPKLNQIQLAELIKQESPQTHLVLFTGYDDFNLYALSALK
LGADDYLLKPKFSKADVEDMLGKLRRKKLELSKKTETIQELVEQPQKEVSAIAMATHERLADSDLTLKSLAQQLGFSPNVLSQLIKKELGMFPQDYLV
QERLKKAKLLLTSNLKIYEIAEQVGFDNMYSQSRFKQLVGVTPSQYKKGGQA

SEQ ID 461

GTGACACTGAGTTCTGATAGCAAGTATTAAATCGTCAACATATGCTACCACTACCAACATAACAACAGTTGAGATTGTAATAACAGCAACTAGT
TGCAAGCCCTTCAGGATATCTAACAGATTGCTCTACTGATATTCTGGAGGGGCCAAACATAAAACCATATCGTTTATCATCAAAGCCCCA
AAAAGACTCAACCCCACTCTACCTTGATAATTCTTAGCAGTTAGCAATACATACATTAGCACCACCAATAACCGTCGTTGGGATTGGTAGTGTATTG
GGTAATAACATTGAAATCATTTGTGAAACTAATAGAAATAGCTGCATATATTGACATT

SEO ID 462

MTLSSIASINRATYATTTNITTVEIVITATSCKPSAFRISRAATDIPEGTNIKPIMLIKAPKESTHSTLILAVSNTYISTKPITVVGIGSDF
GNNLICETNRIAAVIDI

SEQ ID 463

GTGACTATGAAACACACCGTAAAGAAAACAAAACAAAAGCTCCAATGTTATTCAATGTCATAATATGCAGCTATTCTATTAGTTTACAA
ATGTTCAATGTTATTACCGAAATCACTACCAATCCCAACGACGGTTATTGGTTGGTGCTAATGTATGTTATGCTAATGCTAAAATTATCAAG
GTAGAGTGGGTTGACTCTTTGGGGCTTGATGATAAGCATGATTGGTTTATGTTGTCCCCCAGGAATATCAGTAGCAGCGAACCTTGATATC
CTAAAAGCTGAAGGCTTGCACACTAGTTGCTGTTATTACAATCTCAACTGTTGTTATGTTGGTAGTGGTAGCATATGTTGCAACGATTAACTTGCT
ATCAGAGAACTCAGTGTACAGATTTAATTAAGGATATTACCTAACCACTATAGTAAGAAGTAGAGGAAAAAA

SEQ ID 464

SEQ ID: 404
MTMKHTSKETKTKEAPMFIQMSIYAAIILVSQLMISMLPKSLPIPTTIVGLVLMVLLTAKIIKVEWVDSFGALMISMIGFMFVPSGISVAANLDI
LKAQGQIVAVITISTVVMLVVVAYVARILIARELSTVTDLEKKILPNHYSKKVEEK

SEQ ID 465

ATGGAACCTTAAACACCCATCTTGGTATTTGCTTTCTTAATACTCTATACGATAGGAGAACATTATTTAAGAAGAGTAAAGGTTCTTC
 CTTTTGCAGCCTCTTCTTGCAATGGTAGTGTATTGTCATTCTTGGCTTATGTCAAAAGGTTAGGAACCGATGTTAAGACATTITATACA
 CAAGCTTAAACCAGGGTGTGATTAAATTTGGTTTAAATCCAGCAGCAATTGCTTGCAGTCCCTCTATAAGAAAAATGACGTTGTT
 AAAAATATTGGTAGAAATTCTCAGCAAGTTAGTAATCGGTATGATTGTTCCCTTAACTTATGTCGCTATTCTAAAATGGTTGGCTTAGT
 CAAGTCGGAATTGCTCAATGTTGCCAACAGCAGCAACAGCAATTGCTTCCAATAACAGCAGCAATTGGAGGAACACAGCTGTGACAGCA
 ATGGCGTGTATCTTAAATGCACTTATTGTCATTAGTAAAGGTTAGTGTCACTTCCATTGAAATGGAGAACACTGCAAGGTGCGATGGCAGCTAGT
 GGTCTAGGGACCTCTGGTCATACAGTCGGAGCAGCCTTGCATTGGAAATTGGAGAACACTGCAAGGTGCGATGGCAGCTAGTGTGGTGGTTATC
 GGTTGGTAGTTGATTGTTCTTATCCTTACTGTCATTGATTGGTTGCT

SEQ ID 466

MELLKTPIFGICFSLILYLTIGEHLFKSKGFLLQPLFFAMVSIVILWLMSKGLGTDVKTFYTOAYKPGGDLIFWFLNPATIAFAVPLYKKNDVV
 KKYWVEILSSLVGMIVSLLILIVAIASKMVLSQLVGIASMLPQAATTAAIALPITAAGGNTAVTAMACILNAVIIYALGKLVSFFHLDNSKIGAGL
 GLGTSHTVGAFALELGELOQAMAAIAVVVIGLVVDLVIPIFSLIGLL

SEQ ID 467

GTGACTAAATATTGAGTACATCTTTGTTGCTTCTGGCAGTATCTTTAGTAGCTTGTCAAATCAAAATCACAACCAAGGAG
 CGAACCGAAAACAACGACCCAAAGATGAATTGGTTCTATGGGGCAAAGCTTCCATGAATTGCAAAAGGACCGTATGGAATCCAT
 AATGAAGGTAATATTACTCATAGCACCCATTGAAACGTTCTCTGAACAGATAAAAAGGAGAGCTTCTAAAGGAAATATAAAATCTCTAAGGAT
 GGCTTAAACGCTGGTGTGACTTAAATGATGATTAAATCTCAATGGTAGGCTGTACTGCTGAGCAGTGTAAAGTTACTTATGATATGTTG
 AAAGCAGATGGAAAAGCTTGGGATTGACCTTAAATGAAATGGTAGGCTTAAAGGCTTAAATCTGACTGAGGCGCATTG
 ACATTACAGCACAGTGGACAGAAATCCAATCTCCCTAAACATGATAAGTAAAGCAATCTATCGGTCAGGACCTTACAT
 GTGAAAGAATATAAGGCTGGAGAACAGCAATCTCGTTGAAATCCCATTGGCACGGTAAAAGCCTTATTTAAAAGTGGACTTGGGTTATTA
 CTTGATGAAAATACGACTAGCTGTTAGAATCTGGTAGTTGACATGATTACGCAACGCCAGAGCTTGTCTAGCAAGAAAAGTCAAAGGAACA
 CGTCTTCTAGATATTGCTTAAACGACGTTGCGGACTGTCTGGCTTATGTGAAGAAAGGTTGTGAAAATTCCACAGACGGTATCCAGTA
 GGAAATGATGTCACTAGTGTGATCCAGCAATCAGAAAAGCCTTGACTATTGGTTAAATAGACAAAAGTCTGGGAACTGTGTTAAATGGTTATGGT
 AAACAGCTTAACTTAAATGATGAAACACCATTGGAATCAAAACAGCAATTAAAGATAATAAGTAGCTAAAGCTAAGCAACTTTTGACA
 AAAGCTGGATGGAAAAGAACAGCAGCTGGTAAAGGAAATCTTAAATGGAATTGACCTTACTACCCACTAATGATCAATTACGA
 GCAAACCTAGCCCTTAAAGCAGGGAGCTAAAGCCTTAAAGGCTAGTAACTGGGATGAAATGGCAACTAAGTCA
 CATGATTGCGCTTAACTTATGCGGGAGGAGCTCATGCGCAGCAATTATGAAATCACATTACCAAGTGTGTTAAAGGTTGGACCAAT
 ATTACTTTATAACAACTACTGTGACTAAGTACCTTGACAAAGCAATGACATCTCTGACCTTGATAAAAGCTAACAAATATTGGAAGTTAGCT
 CAGTGGGATGGCAAAACAGGTGCTTCACTCTTGAGATTACAAATGATGGTTGGTAGTCTAACCTACTTATGGTGTGATAAACGATTC
 AATGTTAGTAAACAAGGTTGTCATAGTCATGGTCATTGTCATTGACTAACATTGCTGAATGGACTTGGGATGAATCTGCTAAC

SEQ ID 468

MTKYLKYISFVALFLASIIFLVACQNQNSQTKERTRKQRPKDELVVSMSGAKLPHEFDPKDRYGIHNEGNITHSTLLKRSPLEDIKGELAKKYKISKD
 GLTWSFNDDFKFSNGEPVTADDVFKFTYDMLKADGKAWDLTFIKNVENVGKQVNINLTEAHSTFTAQLTEPIVPKHYNDKYKSNPIGSGPYM
 VKEYKAGEQAIIFRNFWHKGKPYFKKWTWVULLDENTALALESQDVDMIYATPELASKVKGTRLLDIASNDVRGLSLPVVKGVVKNSPDGYPV
 GNDVTSDFPAIRKALTIGLNRQKVLDLTVLNGYGPAYSIIIDRTPFWNPKTAIKDNKVAKAQQLLTKAGWKEQADGRKKGNLKSEFDLYYPTNDQLR
 ANLAVEVAEQAKALGITIKLKASNWDDEMATEKSHDSALLYAGGRHHAQQFYYESHYPSSLAGKGWTNITFYNNPTVTKYLDKAMTSPDLDKANKYWKLA
 QWDGKTGSTLGDPNVWLVLNSNHTYIGDKRINVGKQGVHSHGHWDSSLTNIAEWTDWESAK

SEQ ID 469

ATGACTGGATCAACCGGTGATTGTTTAGTAAATAAGGTCAAAATTGATACTCCAAAACGAGTGACAAACACCTAAGTATCTTCAGATAACT
 ACAGTGGTAATATGTTACAGATAATCTCCT

SEQ ID 470

MTGSTGDCFSKIKVKIDTPKTSKHLISIQITTVVICFTDKSP

SEQ ID 471

ATGGAACGTGCAATTATGACACGTCACTAACCCCTGTTAGTACAAGCAGATTGCTCACCACTATGGTTGGATAAGGCCAGCTCCGGTCCAGTAT
 TTTATTGGTTAAAAAATTATACAGGAGCATTAGGACTTCAGTGTATCGGCAACCTGTTATTGATATTAGATCACGGCAGGTG
 TCTTTCATACTTATGGACTCTCCTGGTCTTATGGGTTATCTAGGAACTTATCAGCTTCCATCAAGGAAATTGCTTGAT
 CGAATTGTAAGGTGGTTCTACCTCAGATATCAGTACCAACTTTGGATTGGCTCATTTTATTAAATCTTCTGTCAGCTGGGTTGG
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 AGTATTCTAGGCAATTGCAATGTAACCTTCATAGAACTTAAAGTGTGCGGACTTTCTAGTGAATATGCTTATTGCCAGAGCGCGCTGGG
 GAAACGGGAATGGCAATTTTAAATGTTAGGCTATCTGTCAGCTATTACACTGCACTTCCATTTGGGAAATTGTTGG
 GGATCCGTCTTGTGAGCAAGTTCTCATATCAGGACTAGGGTCTACCTCAACTGAAGCAGGACTTAAAGTGTACACCGCTACTCTGACT
 ATTGTGATGATAGGGACATTATTGTTGGGAAATTGCTTACGGGAAATTAAACAGCATAATCAACAGCTTAAAGGAGAAAAGTA

SEQ ID 472

MASVNYDTSLTPVQYKAIHHYGLDKPAPVQYFIWLKNFIQGHLGTSVLYRQPVIDIIRSAGASFILMGLSWLVSGLIGFILGLTLSAFHQGKLLD
 RIVRWFSYLQLQISVPTFWIGLIFLFLIFSVQLGWFPIGISSPIGTLQSDITLADRIKHLILPVFTLSILGIANVLTHTRKMMSSVLSSEYVLFARARG
 ETEWQIFKNHCLRNAIVPAITLHFYSFGELFGGSVLAEQVFSYPGLGTLTEAGLKSDTPLLLAIVMIGTLFVAGNLIAIDLNSIINPQLRRKV

SEQ ID 473

ATGATATTGGAGACGTGCAACTATTGTTTATGGCAACTGGGATCTGCCATTCTCTCATCTTAGTATTCTAGCCTTAAATCTTATTTCCATAGT
 ACTCTTGTGCAAACCAATGAGCTTACGGAACCTTGCCTTCACTAAACCATCTTTGGGACAGATGGTTAGGTAGGGATATGTTGTCAGA
 ACGATTAAAGGACTTTATCTCTACAGTCTGCTTATTAGGTGCGCTTATGGGGCTATTCTGGCGACAGTTTGGAGTGCTTGCAAGTT
 GGAAATAGCATTATTGATAAAATAAGCATGGTAGTTGATTGTTATTGGTATGCCTATTGCTATTGATTTTATGATTCTATTCTTGTGTT
 GGGAAAGGTGCTCAAGGGGTCATCTGCAACGGCTTACACATTGGCTTCTTAGCAAGGCTTATCCGAATGAAGCTATCATCTAAAGAAT
 AAAGAATTGTCACCTTCTAAAGTATGGGAAAAGCCTTATTATAATTGAGGCTATCATCTGGCTTGTGCTTCAATTTCATT
 GGTTTTATCTCTTATCTCAGATGTCATCCTACATGAGCATAATGACTTCTTAGGATTGGGCTCTGCGCAACACCTCGGTTGGTATC
 ATTCTGTCAGAGGAGCAGCTAACATCTCTTGGAAATTGGGGTTATCTTCCAGGACTTATCTTGTGCAATGCATTG
 ACTATCGGAAATCTTAAAGAAACTCTTACCTCAAACGATCTT

SEQ ID 474

MILRRRTIVLWQLGIAISLILSILALNLYFHSTPLQTNAAALRNLAQSLNHLFGTDGLGRDMFVRTIKGLYFLQVCLLGLMGVILATVFGVLAGL
 GNSIIDKIIAWLVDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYHLKRNKEFVQLSKSMGKTPYYIWRHILPLIASQIFI
 GFILLFPHVILHEASMTFLGFGLSAEQPSVGIILSEAAKHSISLGNWWLVIFFPGLYLILVNVNAFDTIGESLKLKFYPQTDFH

SEQ ID 475

ATGACAGAAACATTATTAAGCATTAAAGACCTCTCCATCACCTCACTCAATACGGAAGATTAAACCCATTCAATCAACACCGATAACAGC
 CTGAATTAGAAATTAAAGGTTAGGTTAGCTATTAGGTGCTAGTGTGCTCAGGAAAGAGTTTATTAGCACATGCTATTATGGATATTCTT
 CCTAAAAATGCATCTGTAACAGGAGATGATTCTGTTGCAATCACTAAACCCATTAAACAGTTGCGAGGAAAGATATTACGTTG

ATTCACAAATCAGTTAATTATTTAGATCCATCTACGAAAAGTCAACACATCAGGTGCGTTAGGTATCTCAGAAAATTCAAAGGCTACTCAAGAAGGA TTGTTCAACAGTTGGTTAAAAGAAAAGTGTGACTTGTATCCTTCAACTTCTGGCGGAATGCTCGACGTGTTGTTACAACGCTGTT GCAGATAAAAAGATAAGCGTTATTATTCAGTACAGTCTGCAAATGGTTAGACCAACTACGCTCTT ATTGAAACAGCTCCAGCTAGTTCTTAGCGGAAATGGAGAGCAGTTACAAACAGAATTGCTAGAAGTTATGGCCTCTCCCACAGCAAGAA TTTTGAAAGGAGTTACTCATGACCTAGAGGC

SEQ ID 476

MTETLISIKDLSITFTQYGRFLKPFQSTPIQALNLEIKKGELLAIIASGSGKSLLAHAIMDILPKNASVTGDMIYRGQSLNSKRIKQLRGKDITL IPQSVNYLDPSMKVHKQVRGLISENSKATQEGLFQQFGLKESDGLYPFQLSGMRLRVLFTTCISDKVSLIIADEPTPLHFDALQMVLDQLRSF ADKGIVSIFITHDIVAASQIADRITIFKEKGKAETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTSDLRG

SEQ ID 477

ATGACAGAAAATTATTAAGCATTAAAGACCTCTCCATCACCTCACTCAATACGGAGATTTTAAAACCATTCAATCCACACCGATCCAAGCG CTGAATTAGAAGTTAAAAGGTGAGTTATTAGCTATTAGGTGCTAGTGGTCAGGCAAGAGTTATTAGCACATGCTATTATGGATATTCTT CCTAAAAATGCAGCTGTACAGGAGATATGATTATCGTGGTCATCACTAAACAGCATCAAACAGTTGGAGAAAAGAAATGACGTTG ATTCCACAATCCGTTAATTATTTAGATCCATCTATGAAAGTCAGCATCAGGTGCGCTGGGTATCTCAGAAAATGCTAAGGCTACTCAAGAAGGA TTGTTCAACAGTTGGATTAAAAGAAAGTGTGACTTGTATCCTTCAACTTCTGGCGGAATGCTCCAGTCAGTTGTTTACAACGTTG ATTAGTGTACGGTTCTTGATTATGCGGATGAGCCACCCCTGGATTACATCCAGATGCTGCAAATGGTTAGATCAACTACGCTCTT GCAGATAAAAAGATAAGCGTCATATTATCACCCATGATATTGTAGCAGCTAGTCAAATTGCGGATCGTATTACTATTAAAGAGGAAAAGCT ATTGAAACAGCCCCAGCTAGTTTTAGCGGAGGTGGGGAGCAATTACAAACAGAATTGCGAGACGTTATGGCAGACTCCCTCAGCAAGAC TTTTGAAAGGAGTTACTCATGACCTAGAGGC

SEQ ID 478

MTETLISIKDLSITFTQYGRFLKPFQSTPIQALNLEVKGELLAIIASGSGKSLLAHAIMDILPKNAVTGDMIYRGQSLTSKRIKQLRGKEMTL IPQSVNYLDPSMKVHKQVRGLISENAKATQEGLFQQFGLKESDGLYPFQLSGMRLRVLFTTCISDTVSLIIADEPTPLHFDALQMVLDQLRSF ADKGIVSIFITHDIVAASQIADRITIFKEKGKAETAPASFFSGNGEQLQTEFARSLWRSLPQQEFLKGVTSDLRG

SEQ ID 479

ATGACCTTAGAGGCTAAAAGCTTGGCTTTATCATAAAAAGATCAATGGCTTTAAGGAGATTATTAGAGGTAGCACCTGGTCAAGTTTTA GGTATATTGGACAAAGTGGTGTGGAAAAACTAGTTTATCCAGGGTGTGGCAGGTTTTTACATCTCAAATCTGGTGAAGTTAGTTGATGGC AGTAATTGCTCTAGCAAAAGCATTAGCTGTCAGTACACTTATCCAAACACATCTGAAACAAACATGTAATCTTTATGGCTATGAAAAAAAGTTG GAAGAACGCTTACCCAAGTCAGGATTACTAGATGCTTTGGAAATTGCAAGAAAATGGCTAAAGCGTCGCTCTAGTGAACCTCGGGAGGGAGAA TTACAACGCTTTGATTGTGCTTCATTACATCCAGAGACTAAACCTTATTGAGATGAAATGACTACTATGTTGGATAGCATTACACAAGCT AGTGTATGAAAAGCCTGTTGGAGATTGTAAGGATAGAAATTAGGTCTCATCGTTATTAGTCATGATTGCTATGTTAGAGAAAACCTTGTAAAC CAATGCTATATGATTGAAGAGAATGCTATGCTATCTTCAATGGAGAT

SEQ ID 480

MTLEAKKLGFYHKKDOWLFKEINLEVAPGQVLGIFGQSGCGKTSLSRVLAGFLHPKSGEVLVDGSNLPSKAFRPVQLIQQHPEKTMNPLWPMKKS EEAAYPSQRDLDAFGIQEKWLNRPSLESGGELQRFSIVRSLHPETKYLIADEMTMLDSITQASVWKSLLIEVKDRNGLIISHEFDMLEKLCD QCYMIEENRIVSFNGD

SEQ ID 481

ATGACCTTAGAGGCTAAAAGCTTGGCTTTATCATAAAAAGATCAATGGCTTTAAGGAGATTGATTAGAGGTAGCACCTGGTCAAATCTT AGGATATTGGACAAAGTGGTGTGGAAAAACGAGTTTATCCAGAGTGCTGTTGTTTGCAGCCTAAATCTGGTGAAGTTAGTTGATGGC AGTCATTGCTCTAGCAAAAGCATTAGACCTGTACAACACTTATCCAAACACATCTGAAACAAACATGTAATCTTTATGGCTATGAAAAAAAGTTG GAAGAACGCTTACATCCAAGTCAGGATTGCTGAGATGCTTTGGCATTCAAGAAAATGGCTAAAGCGTCGCTCTAGTGAACCTCGGGAGGGGAA TTGCAACGCTTTGATTGTGCTTCATTACATCCAGAGACGAAATACCTTATTGAGATGAAATGACTACTATGTTGGATAGCATTACACAAGCT AGTGTATGAAAAGCCTGTTGGAGATTGTAAGGATAGAAATTAGGTCTCATCATTATTAGTCATGAGTTGATATGTTAGAGAAAACCTTGTGAC CGGTGCTATATGATTGAAGAGAATGCTACTCAACTGTTCAAGCATTAC

SEQ ID 482

MTLEAKKLGFYHKKDOWLFKEIDLEVAPGQVLGIFGQSGCGKTSLSRVLAGFLQPKSGEVLVDGSHLPNKAFRPVQLIQQHPEQTMNPLWPMKKS EEAAYPSQRDLDAFGIQEKWLNRPSLESGGELQRFSIVRSLHPETKYLIADEMTMLDSITQASVWKSLLIEVKDRNGLIISHEFDMLEKLCD ACYMIEENRTQLFKHT

SEQ ID 483

ATGAAACATTAAACATGATGCCAAGCCTGTTAGAGGCAATTGGGGTAAAGAAAATATTAGTCAGTGACACATTGTGCTACACGCATGCGA TTTGTTTGATGACAGTAGTAAAGCTAAGGTAATTGAGGAGTACCATCAGTCAGGTTACCTTACCATGCTGGCAATTCAAGT ATTATTGGTAATGATGCTCTATTTTTATACTGCTTTGTAGCCGTTCTGGTATTGAGGGTGTCTAAAGAGGCGCAAATCGCTGCCAA AAAATCAAAACCTTACACCGTGTGTTGACAATGCTGGTCAAATATTACACCGTATTTCAGCCATTATTGTTGCTGTTCTGATCTTGGT TTTCGTAATATTAGTCAGGTTCAATTGTAAGGTTAGGTCAAAGGTTGATGGTCAAGGCAAGTAGACTCTTATGGCATCCAATTGG AATACTCTAGTAGATGTTCAACGTTGGAGCGGAGTAGACTCTTTTATGGTACCGAGGTAGGCTATATTCTTACCGAGTTGGTATT GTATGGTCTGTGACTCGTAAGATGGGACTACTCAAATCCTCGGATTGTTCTAGGTATCTGCTAGTGTGCCCACAATTACTTAATGCTTATTCT GTAGCTAGTACTTCAGCAGCAGACATTGCTAAAATTGGTCTGGAATTGGTACTTTACAGTACAAAAAATTGGTATCAAGCTCAAGTTATT CCAGCTCTGTTAGCTGTTGAGCCTGTTACTTAGAAATCTCTGGAGAAAACATATTCTGTAAGGTTGTTCAATGATTGGTCTGCAATTCTA TCCTTAGTCCAGTATTATCTGGCTCATACTGCTCTGGACACTAGGTTACGGTAAATGGATTCTGCTATCGTTCTATTGGATT ACTGGTCTGTAAAATGGCTTGGTGTGCTATTGGCTGCTGTTGAGCTTACCGAGTACAGCTTACGACAATGCTAGTGTGACTAGCTTACTCGA ACTCAACTCATAGCAGATAAAAACACATACAACACTGGCTTGGCCGATGTTCTGCTTCAATTGCTCAGGGTTCAGCTGACTAGCTTAT TATTGGTCTGATGTTGAGGAGGCTCAAATATCAGTCTGGCTGTTACAGGCTGCTGTTACAGAGCCGGCTTTTGGT GTAAACGTTAAATACATTATCATTGGTCTGGTATGATTGGTCAAGTGTGGCAGGTCTTGGCACAATTAAATGTCAAAGCTAACTCT ATTGGTGTAGGCGGTCTCCAGGCTTCTGTCATTAACTGTTAAATATGGATATTCTTATCTGATGGCAGTGGCTATCTTATTGCTTTA TTTTGACACTATTCTTAAAATCAGGTATTGGACAAAAGTCAAGGAGAAAATTAGTACCTGATGGTCACTGGCTTCAACACAGAAACA AAATCAGCAAAGAAAAGCTGTCGATCAGGTAACAAAGCTTAGTGTAGTAAGCCCTTATCAGGTTAGCTAAACACTGGATCAAGCTAGTGT CCTGCTTTTACAGGAAATTGGGAGTGGTTATCGATCAGGAGACTAGTTCACCGGTCATGCCAGTGGTCTAGTGTGTTTTAGCTTACGTTCTT TCCCTACGAAACATGCTATTGGATTGTTAACATCAGAGGGGTTGAGTTCTATTGATGGTACTGTTAATTAGAAGGAAAAGGG TTTACCTCTCATGTTGCTCAAGGTGACACTGTTAAAGTAGGGAGATAAAACTCATTACTTCAGTATTCAATGATAAAAAGAAGGATACATTG TGAAACTCTTATCTGATTACTAATCAACAAGAATTCCGACCAGAGAATTGATAGATTACCAACAGATAAAACGTTGACAGCATTAATGGTT GCCAAGAAAATT

SEQ ID 484

MEQFKHDAKALLEAIGGKENISAVTHCATRMRFVLNDSSKAKVVKIEELPSVKGFTNAGQFQVIIGNDPVIFYNAFVAVGIEGVSKAEAKSAAQ KNQNPLQRVLTMLAEIFTPIIPAIIVGGLILGFRNILDADVPEFLGQKVVDGVROVDSSGHPIWNTLVDFVSTFWSGVDSFLWPGEIAFHFLPGI VWSVTRKMGTTQILGIVLGICLVSPQLLNAYSAVTSAAIDIANKNWSWFQGYFTVQKIGYQAQVIPALLAGLSLSYLEIFWRKWHIPEVVSMIFVFPFL

-50-

SLVPATIILAHTVLGPIGWTLGKWI SAI VLV LIGL TGPKVWLFGAIFGALYAPFVTI GLHMHMTNAIDTQLIADTKTHTTGLWPMIALS NIAQGS AVLAY YFMHRHDEKAQISLPAAISAYLGVTIPEALFGVNWKYIYPFVGAGMIGSSVAGLLATT FNVQANSIGVGGLPGFLSINVKYMGYFFICMVAIFIPL FFLTFKKSGILTKEEKLVPAVIASSTTETKS AKEKAVVSGTKLSVSPLSGLIAKPLDQASDPVFSQGIMGKGVVIDPSDGELVSPV DATVSVL FPTKHAIGLLTSEGVEFLIHIGMDTVNLEGKGF TSHVAQGDTVKVGDKLITFDIPI MKEEGYIVETPILITNQQEFRPEELIDL PKQIKRGQALMV AKKI

SEQ ID 485

ATGGGAAATTGGAACAGGATCTAACAGTCTTCTAACAGTCTATTGGGGTAAGAAAACATCAAGGGTCACACACTGTGCAACCGCTATCGCTTTGGTGAATGATAATAAAGGCAAATGTCAGGAGATTGAAAAAAATCTGTAGTTAAAGGGACATTACCAATGCTGGCAGTTTCAGGTAATCATTGGTAATGATGTTCCAGTTTTAATGACTTACAGTGTTCTAGTATTGAAGGGGTGCTAAAGAAGCTCCAAATCAGCAGCTAAAAGTAATCAAAATGCCTAACAGGGTGTGACCATGTTGGCTGAGATTTCACACCTTATTCCCGCATTATTGGGGGGCTTATTAGGTTCGGTAATTTCTGGAGAGTGTGCCCTTGAATTCTTGGGCCAGGGTCGAAAAGGGAAATTAGTTGTGACGTGGGATCTGGTGGGAAATACAGATTGTGAGGGTATCTCTTGTGTCAGGGTTAACCAATTCTGGGTATCAGGGGAAGCTTACCTTCACTTACAGTGGGATTACTGGTCTGTGACCGTAAGTGGAAACCACACTCAAAATTAGGGTCTGTGAGATTGCCAAAACGGGTTGGGATTGGTCTTACCCATTATCGTATTGGGTATCAGGCACAGGTTATTCCAGGCCCTTAGCTGTGCTGTGCCCTGTTATCTGAAATTCTGGCTAACGGATTCCAGAAGTGGTTCAATGATTGTGCCATTCTTCTCTTGTGATTCCAGCTTGATTTAGGCCATCGGTATTGGGCCAATCGGTTGGACTATTGTAAGGGATTCTTGTGTTAGCTGGATTGACTGGTCTGTAAATGCTATCGGTCTATCTGGTGCCTTGTATGCTCCGCTAGTTACCTACATCACAGACAAATGCCATTGTGACCCAAATTATGCTGACTGCAACTCGTACAATGGGTTGGCCAATGCTCTTCAAATATGCTCAAGGGTCAAGGGCTAGCTTGTACATTAAATGCTGAGGCTGAAATATGCTTCCGCAAACTTGTCTTACCTGGGTTACTGAGCCTGCCATTGGGTTAAATGTTAATGTTAAATACGTTTATCCCTTGTAGCCGAATGATTGGCTCAGGTATTGGGCTCTTATCACAAACCTTAAATGTTCAAGGAAATTCTATTGGGTGTTGGGGTTTACCGGTTCTGCTATCAATGTGAAGTACATGATTCCATTCTCATGTTAGGCAGTAGCCATTGTGGTGCCTGATGTTTTAACCTCTTTCCGTAATCACATATCATGACTAACAGACAGAAGATGAAGCTAAACACTGAGACACCCGTTGGATGCTCTGTAGCAACTGCTCACATAAGACTATGCAAGGAAACAGTTACCTTAAACAGCCCTTAAACGGGTGAGGTTAAAGCGTTGCTGAAGCTGTTGATCTGTTGGCACAGGGAGTTGGGCAAGGGTCTCTTCAACCGACAGAAGGGGTTAGTAGCCCTGTGATGCTGAAGCTGTTGATCTGCTTCCCAACTAAACACGCTATTGGGTTGGCAAGGACTGAGGTTGGAAATTATGATGCTATGGCATGGACAGGTTAACCTAGGATGGCTAACCTAGGATGGTCAAGGATTGAACTGGGGTGAAGCAAGGTGATCAGGTTAAGGCTGGACAAACATTGATTGATCATTAGCAGCAATTCTGAAGCTGGATACGCCACTGAAACGCCCTTGTTGGTACTAATCAAGATTTACGGTAACCTGTTACGGTGAAGGTTAGTTACCCGTCAGGATTAAGGTTAATGATAAGTGTAGCAGTGGCGGTAAAAAG

SEO ID 486

MGKFEQDAKSLLITAIGGKENIKVVTHCATRMRFVLNDNNKANVKEIEKISVVKGFTFTAGQFQVIIIGNDPVFYNDFTAVSSIEGVSKAAKSAAK
SNQNALQRVMTMLAEIFTPIIPAIIVGGILIGFRNILESVPFEFLGQQVEKGKLVFDAAGDPVNNTIVRVSPFWSGVNHFLWLPGEAIFHFLPVGI
TWSVTTRKMGTIQILGIVLGICLVSPLLNAVAGTPAAEIANKWNWDFGFFTINRIGYQAQVIPALLAGSLAYLEIWFKRRIPEVVSMSIFVPFL
SLIPALILAHTVLGPIGWIGTGKGSFFVLAGLTGPVKWLFGAIFGALYAPLVITGLHHMNTNAIDTQLIADTATRTTGLWPMIALSNSIAQGSASFAY
YLMNRHEEREEAISLPAIASYLGVTEPALFGVNVKYVYPFVAGMIGSSIGIAGLSTTFNVQANSIGVGGLPGFMAINVKYMIPFFCIMAVAIVVPM
FLTFFFRRKSHIMTKTEDEAKLPETPVSDAPVATAHKTMQGTVILTSLPLTGEVKALSEADPVAQGVMGQGALLQPTEGVLVAPCDAEVSVLFP
TKHA1CLVTTTEGLELLMHIGMDTVNLDGQGFALVKQGDQVKAGQTLIQFDIAAISEAGYATETPLVVTNQDVFVTVEGSLPRQIKVNDKLAVAV
KK

SEQ ID 487

ATGACGATTGATAAACGTTAAAGTGTCTATCAAATTATCAAACATACAAGACACAACGGTAATGGGGTTGGTATCTCGGGTATTATC
AAAAAATTACCCATTAGCAGAACCTGGTATTGATATGGTTGGCTAACCCATTATCCAAGTCACACGAGATAATGGATATGATATCTCT
GATTATACAGCTTAAACCTGATTTGGAACGATGGACGATTTGAAGAAATGATTGAGGTGGGACGTCATAACCGTATAGATTTATGCTGAT
ATGGTGCTTAATCATTGGTCAATAGAACATGAGTGTTTAAAAAAGCACTTGCAAGGAGATCGCTACTATCAAGATTTCTTATCTACGTTGATAAT
CCAACAGATTGGGTATCTAAATTGGTGGAAATGCTGGGCACCATTTGGTACAGGGAGTATATCTTCATCTTTGATATCACTCAAGCT
GACCTTAATTGGGCCAATGCGATTTGCAAGGAACCTTTAAAGTGTCAATTGGCTGATAAAGGGGTTAAAGGTTTCTGATTTGATGTG
ATTAATTAATTGGGAAAGATGAGATACTTGAGAATGCCCCAAATTATGATGGAAAACAGCTTATAGTCGTCATAACACATGATTATCTC
AAGATGTTGAAATAATGCTAGTTTGGCAAGAACATGATTCTTCATGAGCTGGTAAATGCTTCAACGACAATTGCAATTGCAATTCTTACACT
GCACCCAGAACGTTGAGAGTTATCCATGGCTTTAATTTCACCACCTCAAAGTAGATTATAAAGATGGGCAAAAGTGGACCATTATGGCTTTGAT
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CGAGCATTAAATCGTTGAGACGTAAACGTTGCAATGAGGGCAACCATGTTAGCAGCATCTATCCACTATCGCTGGTACTCTTAT
ATATATATGGGTAAGAAATCGGAATGCTTGTATCCCATTACAGTTCTATGGATGATTATGTTGAGATGGCTACCAATAATG
CTTGATGAGGCAAGTCACAAGAAGAGGCATTAGCATTATTCGAGCGAAATCTGAGACAACTCTGAGTACCAATGCAATTGGGATGATAGTACG
AATGCGAGGTTTCTGAGGCGCTCATGGTTGAAAGTAGGAAATCATATAAAGAAATCATGTCGAAAGGAGAAAACAGGGCTGATATTACT
TTCTATCAAGAGTTGATAAGGGCTACGTTAAACACTGCAAAATATAGCTGACGGGAATTATAAGCAGCTTCAAAAGATAATGAAAAGTATATGCT
TTTGAACGCCATCTGATAAGGAAAATTCTTGTGTTAAATAATTCTTGTGAGGAAAGTTAGGATAAATTAACCGGAGATTATCTCCAGGA
CAAGTTCTCATCAAATTATAAGGATGTTACTCTGATGAAACGGTTACTTTGCAACCTTATCAAACCTTGTGATCTTAGTGTCA

SEQ ID 488

MTIDKRKVYQIYPKSYKDGTGNGVGDLRGITIEKLPYLAELGIDMVWLNPFPSPQRDNGYDISDYTAINPDFGTMDDFEEMIEVGRQYRIDFMLDMVLNHCSEHEWFKKALAGDRYYQDFFLRDNPTDWVSFKGGNAWAPFGDTGKYLLHFDITQADLNWRNADVRKELFKVVNFWRDKGVKGFRFDVINITLIGKDEILENCPIINDGKPAYTDREITHDYLKMILNNASFGQDDSFMTVGEMSSTTIANCILYTAPEREEELSMAFNFHHLKVDYKDQKWTIMAFDFPALRDLFHSGWEGMSENGNWYQFVNNHDQPRALNRFDVVKRNGEATMLAASIHLRSRTPYIYMGEETGMLDPDYSSMDDYVDIESLNAYQIMLDEGKSQEAEFSITRAKSRDNSRVPVMQDDSTNAFGSEGAPWLKVGSYKEITNAVEKTGLTIFTYQELIRLRKQLPIIADGNYKAFFKDNEKVYAFERHLDKEKLLVLNNFFAAEKVVKILEPENYLOGOVILLSNYKDVTLDFTVLOPYOTLAILVS

SEO ID 489

ATGACAATTGATAAAAAGAAAGTCGCTATCAAATTACCCAAAATCCTATAAGGACACGACTGGAAATGGTGTGGGAGACTTGTCTAGGGATCATT
GATAAATTGCCCTACTTACAAGAACCTAGGAATAGATATGATTTGGTAACCCCTTCTACCCCTAGTCCACAACGAGACAATGGCTATGATGTTCA
GATTATACCGCGGTCAACCTGTATTTGGAACATGGCTATTTGAAAGCTGCTAAGGAGCATCAGATTGAGTTAATGTTGGAC
ATGTTTGTAATCACTGTTCCACAGCACGAGCTGGTTCCAAAAGCTTCTAGCAGGAGACCCTTATTATCAGGATTCTTATCTGGAGAGATCAG
CCGACTGATTGGTTCCAATTGGGGAAATGCTGGGCGCTTGGGAGATAACGGGAAATACTACTACACTTGTGTTGATGTGACACGAGCT
GACTGTAATTGGCGAACCCACATGTCGAGGAATTGCTTAAGTGTGTTAATTGGGAGATAAAGGAGTGAAGGGTCTCGTGTGTTGATGTC
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CATGATCTCAATCAAGCCAGTTTGGTCAGGATGATTGTTATGACAGTAGGGAAATGCTGCAACGACTATTGACAACGTCTTTATACACG
GCTCCGAACGTGAGGAGCTATCCATGGTTTAATTCCACCATCTAAAAGTGATTATGAGAACGGTCAGAAATGGACTATTATGGCTTTGAT
TTTCAGCAGCCTGGAGACTTATTCCATGCTTGGGGTGAAGGCATGACTCAGGGCAATGGCTGGAATGCCCTGTTCTACAAATAACCATGATCAACCA
CGTCCCCCTGAATCTGTTGATGTAACACATTCCGAAACGAGCTGGCAGCTGGTGTGAGCTTCCACATCCATTGTCAGCAGGAAACGCCCTAC
ATTATATGGGTGAGGAGATTGGCATGCTTGAAGCTTGTAGTATGGATGATTATGGTGTGGAAAGTCTCAAGCTTACTCAAGCTT
TTAGTCTCAGGTTAAAGTGCAGAAGAACCTTGGCATTATCAAGGCCAGTCAAGGCCAGAACACCAATGCAATGGGATGCTAGTGAA

CATGCTGGCTTACGACTGGTAAGCCTGGTAGAGGTTGGCAATCTTATCGAGACATCAATGCGAACAGAAAAAGAGGGACGTATTTCCCT
TTCTACCAACGCTTGATTGCTTGCAGGAAGGAACTCCCTATTATTGCTGAAGGGACTATCGGGCTGCTTAAAGATAGTCAGGCTGTCTATGCC
TTTGAACGCCATTAGGTGACCAGTGGTCTGTTCTAACATCATTCTATGCTGATGAGGTCGAACGTGAAATTACCTCACGTTACAACATGGGA
CAGGCTTAACTCAGCAACTATGAGAAAGTTCTATTGTGAAAAGTGTACTGAAACCTTATCAGACACTTGCTATCTTAGCTGATAAC

SEQ ID 490

MTIDKKVVYQIYPKSYKDGGNGVGDLLGIIDKLPLQELGIDMIWLNPFPSPQRDNGYDVSDYTAVNPDFGTMADFENLVKAKEHQIELMLDMVLNHCSSTDHEWFQKALAGDPYYQDFFLIRDQPTDWUSKFGGNAAWAPFCGDTGKYLYHLFDVTQADLNWRNPHVREELAKVVFWRDKGVKGFRFDVINLIGKDEELDCPVDNGKPYATDRPIITHYLHDLNQASFQGDDFSFTVPMGEMSATTIDCNCLLYTAPERELMSMAFNHFLKVDYENGQKWTIMAFDFAAFLDLFHAWGEQMSQGNGWNALFYNNHDQPRALNQRFVTHFRNEGATMIAASIHLSRGTPYIYMGEEIGMLDPDFDSMDDYDVSLENAAYSSLVSGKSAAEFAIIKAKSRDNARTPMDQWASEHAAGFTTGPKLPLEVQGKSYRDINVETEKEGRIPFPYQRLTALKELPIIARGDYRAAFKDSQAVYAFERHLGDOCLLVLNFHYADEVELELPPRYQHGQVLISNYEVKSVICEKVILKPYQTLAILADN

SEQ ID 491

GTTGCTGCTGTGGAAAGGAATCTTGCCTAGATTTCGCAATTCTTCTTTCTTACTCTATAACAATAGCCAAATTCAATTGATAGT
AGTGCAGATTGGGCTAACATGACCTAGAAAAATGTAACCGTTACTA

SEO ID 492

MLLVERNLALDFAISSFFFLYSITIAQIHSIDSSARLGSNDLEKCKRLI

SEO ID 493

SEQ ID 494

MVDNKTVVIMLVFLARKNLNSLYELTVQTFKS1KV1IEQINYLNSFLAKNHLP1AHSAGRYQLLGDEKEHDK1IVSLLEAQFYLTQE1ERVCL1YLY
SFCRREFVSNVHYQDFLKVSNTTLD1KMLRSKLAKRG1SLTYTRAKGYS1VGDEM1DKHQVA1FQM1TQ1LLESP1GFWSLN1Y1LS1SWKF1ALSYEKL
EKTVEYFY1ESFQLSP1QDR1LEK1S1Y1L1L1LCR1Y1QR1S1VDR1L1QG1SP1V1SEQ1L1K1EL1TT11V1N1L1SQD1L1SKP1LD1Q1K1E1D1Y1T1L1L1SGC1F1GEG1T1KD
DDFF1EALAK1AV1DEM1T1V1L1N1FS1K1E1LL1Q1G1L1K1H1I1P1F1R1K1Y1G1L1T1G1D1G1S1G1Y1T1N1K1E1H1Y1S1D1F1L1V1K1A1R1P1L1E1Q1V1G1L1P1D1S1E1I1Y1F1V1H1F1G
GYLR1QSGGT1QMS1Y1K1L1L1CP1G1V1S1L1V1K1E1K1L1R1G1L1F1P1Y1H1F1H1R1V1S1K1E1Q1L1K1D1N1Q1Y1D1M1V1F1S1T1F1V1E1T1K1P1N1Y1L1S1M1M1T1A1E1Q1V1Q1K1L1V1S1
DFPK1AC1L1D1F1Q1D1Q1I1A1T1K1Y1A1H1V1C1E1E1L1K1A1R1T1M1V1Q1D1L1R1K1D1P1R1L1H1Q1L1T1E1Y1Q1T1S1E1Q1N1W1K1A1R1L1A1K1P1L1A1S1G1K1T1E1S1Y1P1E1M1
EKV1EEFGP1F1N1L1G1K1G1A1P1H1A1R1P1E1D1G1V1N1S1V1G1M1S1M1V1L1E1Q1P1R1R1T1H1E1N1F1L1F1I1L1C1P1D1I1N1F1K1P1F1

SEQ ID 495

TTGAGTCCAATTGCGACTAAAAATGACATGAGACAATTGGACTCAATTATCTTGAATAAGCCTTCATTAACTGACATTATAGGAGGA
GATGACATGCTATCTCATGAGCTCATCGAAACTATCAACTTTCTAAATATAAAGGACATTCACTGGAGGCATTGAATCCATTAAAGGCA
AGCAAACGTCATATACTGGCAGATATTGCTAAATCAATGACACGGTGCACCTATCAGTTACCCCTTATTGCTCTGGACAGGCAGCTGGTTAT
CCGCGAGACCTTACTGAAAAGGACTTGTGAATCGCATGCTACCTACCTTAGCAGACTATCCTTCAAGATGAGCGTCTGATATGATTATCATT
TACATCATGATGGCTAAAGAATTATCTCCTTAAACCTTGGAAAGCTTGTACGGCTCAGCAGAAATCTGTTATTGCTGATTTAACCTGGTG
CGTGTACGGTACAAAGCTTTCAGGTAACTTCTAGCTTACATGCCAGGATGGTTATTTTTGAGGGAAACCTTACGGCTTGCCTCTCTTA
GAATCAGGGTCACTTCTTGCAGTCACATCTGGACCTTGGGTGTTCACTTATTGCTGATGAACTTGGTTGGCCAGCAGAAAAGGGT
ATGGCAGCAACGGTGGAGGAACCTGAGCAGGGAGAACCACTTAACTTTATTCCGAGAAATGAGGGATTGATTATTCTGCTTCTCGCT
CATCGACCATTTCACCGAACGTAAGGGCTGAAGCAGTGGATACTTTCTTAGCTCGCAGCTGTGAAACGATGGGAGCAGTTGGTC
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TATGACATTATGGAGGAATCATCAATTGGCTGGCGTTAACCGGATTGCTATCACCGATACCCAGAACCTCGTCAAGAACCTATAAGTCAC
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CAGGCCCTAAGAAGAGGCGAACGCAATCAGCTGGTACGTTTACTGGCTCTGCTCTGATGGGAGCAGCTTGGAG
GAACCTTCCACAGCTACAGTTATTAGGATTCAACAGCTGGACAAAATAAGTGTGGATCCAGCATCTTGTGATTGATTTTCAACAGTA
GCTTTGACTGTCTAACCTGTTTATGTGACGCAAGCTTGTGGACCTGTTGAAAAAAATGATGTTGAAAAAGATGGTCTGTGATGACTTTCTAT
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GTTTCGGATTGGCAGGAGCATTGCTGGCTCAGCCTTACTAGAACACCACTGATTGAAACATCTTATATCATGGCATGATTGATTG
GTCAATGAGCTTGGGGCTATATTGTTTAGCCCCCTAAGGGTGGCTTCTCATGGCGCCTGAAAAGGAACGGCAGTTAGGCATGTCCTC
TTACAATAAAAGAACCTGTCACTTGTGAAGCAAGAAGGTGATCCAGAACAGCAAGTGCATTGATTGTTGTGCTGTTGGATTCT
AGTTCACATTGAGGGCTTGCAGGAAGTCTGCTTGTGATTGATGATGAAACATATTGAGCAATTAGGCTAAGAACATACTGAGGAAATA
ATGAGTCTGATTAGCCATATGATTGAAAAGGAGACGAATCACATGAT

SEO ID 496

LSPIAVKNDMRQLDSIYLENENASFYTDIIGGDDMLSHELIRNYQLFSKYKGSLEAFESTILKASKRHILADIAKINDTLSLYQLPLIALDRQLVY
PPDLTEKDLLNRMLPTLDDYLFDQDERLDMMI~~I~~YIMMAKFISINHLESLLRISRNSVIADLNLRDVRVQAFQVTLAYNRQDGYFFEGEPLALRRLL
ESAVSSLLQVTSGPWFVSYLLHEGLPDQKKVMAATLEELSRNHLTFI~~E~~KLRLDLYFFCCLLAHRPFSRNRAEA~~V~~DTFPLASPAVETMDQLLV
NFPSLITEKSYLVQSRLLGCIGQDLELFVQPOQPIYDIMEIIINSVA~~N~~TCLSITDTPELRQNLYSHLLPAYYRLLYDINLTPLKEQIKQDYESLFY~~L~~
VKRSLSPLKEQOLGKS~~V~~NEDDEVAYFTIHFGRWLQAPKKRPSNQLVALSPCNGISSMLEATL~~K~~ELFQDQFIRIHQD~~K~~IKL~~D~~PASFDLIFSTV
AEFDCAKPVYVTOALMGPEVKMMI~~I~~KKMVICDDEHT~~H~~PLS~~E~~OFAR~~A~~DLL~~S~~TH~~H~~KHTT~~T~~LN~~E~~IGL~~G~~WS~~D~~TP~~V~~LC~~N~~HT~~T~~LE~~T~~EG~~G~~CL~~I~~LD~~T~~LP~~R~~BO~~D~~

VSDWQEAIRLAAQPLLEHQMIETSYIDGMIDSVNELGAYIVLAPKVAVPHAAPEKGTRQLGMSLLQLKEPVSFDLKQEGDPDKQVQLIFVLSAVDS
SSHLKALQELSLILDDDEHIEQLIEAKNTEEJMSLISHMIEKGDESHD
SEQ ID 497
TTGGAGAAAGAGGCTAACGAGATCATTGATTAAAAAGGAATCTTTCAAAATTGATGTCCGGGCACAAAAGGATGAAGAGAAAGTTTCATGCGT
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SEQ ID 498
MEKEAKQIIDLKRNLFKIDVRAQKDEEKVFMRTAWLFQNKH
SEQ ID 499
TTGGAGAAAGAGGCTAACGAGATGATTGATTAAAAAGGAATCTTTCAAAATTGATGTCCGGGCACAAAAGGATGAAGAGAAAGTTTCATGCGT
ACGGCGTGG
SEQ ID 500
LEKEAKQIMIDLKRNLFKIDVRAQKDEEKVFMRTAW
SEQ ID 501
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SEQ ID 502
MTTMDFIISIDDCAVELDQRSWKRYPPLSTILFLVFVCQLAGIETWKEMEDFIEMNEPLFATYVDLSEGCPSEHDLERVISLVNSDRLKE
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KGKA
DYCLAVKGQETLYDDIALYFSDVNLEELQENAQQYQTVEKSRGQIEVREYWSSDIKWLQHPKWHKLRGIGMTRNTIDKDQQLSQENRYF
SFKPVDLTFANCVRGHQWQIESMHWLLDVYVHEDHHQTLDKRAAFNLNLIRKMCLYFLKVMVFPKKDLSYRKQRYISVHLEDYLVQLFGER
SEQ ID 503
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TACGTTGATTGAGTGAAGGTTGTCCTCATGATAACCTTAGAGCGTGTAGTCTTGTAAATTGAGACCGTTAAAAGAGCTTAAGGTTCAA
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GACTATTGCTTAGCGTCAAAGGAAATCAAGAAACACTTTATGATGATATTGCTCTTATTGTTAGTGTCAACTTATTGGAAAGAACTCCAAGAA
AATGCGCAGTATTACGACTGTTGAAAATCTAGGGGACAGATTGAGGTTAGAGAAATACTGGGTGCTCCGATATCAAATGGTTGTCAAA
CATCCCAAATGGCATAAGCTACGTTGATTGGGATGACTCTGTAACACGATTGATAAGGATGGTCAAGGATGTTGTTATCATGAA
AGCTTTAAGCCGGATGTCCTCACATTGCCAATTGTTGACAGGTCATTGGCAGATAGAGGATGACTGGTTATTGGACGTTGTTATCATGAA
GATCATCATCAGACATTGGATAAAAGAGCCGATTAACTTAACTTAACTGCTTATTGGACGTTGTTATTTCTCAAAGTGTGTTATT
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SEQ ID 504
VTTMDFIISIDDCAVELDQRSWKRYPPLSTILFLVFVCQLAGIETWKEMEDFIEMNEPLFATYVDLSEGCPSEHDLERVISLVNSDRLKE
FEQSLTSLSDAVHQLISVGDKTIRGNRGNQPKPVHIVTAYDGGHHLSLGQVAVEKSNEIVAIPOLLRTIDIRKSIVTIDAMGQTAIVDTI
KGKA
DYCLAVKGQETLYDDIALYFSDVNLEELQENAQQYQTVEKSRGQIEVREYWSSDIKWLQHPKWHKLRGIGMTRNTIDKDQQLSQENRYF
SFKPVDLTFANCVRGHQWQIESMHWLLDVYVHEDHHQTLDKRAAFNLNLIRKMCLYFLKVMVFPKKDLSYRKQRYISVHLEDYLVQLFGER
SEQ ID 505
GTGAAACAGCCTATTATTGATGACCCCCAACAGGAAATTATCTTATTGATGACGCTATTGATAATGAAACGCTATTGAAAG
CTATCGCATTGACAACAATACTTCGTGATAATAATAATGTTAAAGCTTGTAGCTTCACGTAGGTTATCAAGATATTGAAATGATT
AAGGAT
SEQ ID 506
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SEQ ID 507
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CTGGGGATGTTGTTATTAAACAGTATCATTGATATGGTGAATTGAGAGAATTAGTGACAGGTATTGCAAGAAAAGGCTTAATC
SEQ ID 508
MLRIGTACGSGLGSSFMQMNIESILKDLGVSDVEVEHYDLGGADPSAADVWIVGRDLEDSAGHILGDVRILNSIIDMDELRELVTGICQEKGLI
SEQ ID 509
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AAAGATATTTCAGAGGATGCCAAGGTTGTTATCGTTAAAGCTATACCAATCGTAAAAAAATTGAAAGAATTGGTTCCGGTCTCAAGGAA
ATGAGTGGCAAGGAA
SEQ ID 510
LKKETNHMIKIVTVCGNGIGSSLLRMKVEAIASSLGIDVDAESCDNSAAVGKGADLFVTVKEFKIDFPEDAKVCIVKSYTNRKIEEDLVPVL
MSGKE
SEQ ID 511
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SEQ ID 512
MTVVPVTIMTIILTNPPKLEIKPINTALGA
SEQ ID 513

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 CGCAGATTCTGTGATGCTGACTAGGTGGACTTGGTCAACATTCTCAGATGCTGATTGTTGACCGGTATCATTGGCCT
 CTTAACATGTCGGCGGTGCGATAGCTATTGGTATTGTTAGTTAATGGACTTTGGCATTTCAGGAAAGGAAATCAACCCAT
 AAGGAAGGT

SEQ ID 514

MKGLLDFLVIASTPAILVALIAIIGLVLQKKGPDIVKGGIKTFVGFLVVSGBTIVQNSLNPFKGKMFHAFHLVGVPNEAIVAVALTKYGS
 TALIMLAGMIFNLIARFTPKYIIFLTGHHTLYMACMIAVIFAVAGFTSFSLILFPGGLALGIIMSVSPAFVQKYMQLTGNDKVALGHFGSLGYWL
 SGFIGGIVGDKSKSTEDIKFPEKSLSLFLRDTVSITISMIAIYLIVAVFAGEAYAKEISNGVNLVYALOLAGQFAAGVFLAGVRLILGEIVPA
 FGKISEKLVPNSKTPALDCPVIPYAPNAVLLGFISSFVGGLVSMIVMTGTTVLPGVVPFFCGATAGVIGNASGGVRGATIGAFVQGILISFL
 PIFLMPVLLGLGFKGSTFSADFGLTGIIILGALNHVGGAIIAIVIGIVVILIGLFGTSFVGKSTHKEG

SEQ ID 515

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 CTTGCCAACACTATTGAGCACGGTTAGCATCAGGCTAGTGCACAAATAAGAACGGCTCAGTCTGCTCAAAAGATTCTGGTGTGGAA
 ACTATGTCATCTGGGGTTATTGCTCAATTGGCTTACCCGCTCAAAATACATTCTAAACAGGACATCACAGCTTC
 TTTATGGCTGTCTTGTCCGGCGCTGGAGCTGGTTTCAAGGAAGTCTTTGATTCTAGATGGGTTCTCTGGAGCTTGGTCA
 GCTTATTCGCCCAGCCATTGGTCAACAGTATACCTGAAAGTGCAGGAGATGAAATCCTGATGGGACACTTGGTAGTTGGCTATTACCTT
 TCTGCTGGGGTGGTAGCAAGGTTGCAAAGACAGTAAAGACATCCGAAGACCTTCTGAAATTGGAGTTCTGCGCAACACCACCAATT
 TCAACAGGACTTATCATGGTATTCTGGGCAACAGTGGCTCTGTTGAGGAATGCTCAGTAGCAGAAGATTAGCAGCAGGTCAA
 AACCCATTATTGGCATTAAAGAGTGGCTTACCTTGCGGTTGGTGGCAATTGCTCACGCCGTTGCGATGATTGGCTGACTGATT
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 ATCGGTTTGTGCTCAAGTTGGCTTACTGGGATGTTAGTTAGGAGTTGCGAGGTTGCTCTGATTATCCAGGTATGCGCTCAT
 TTCTGCGGTGCAACAGCAGAGATTGGAAATTCAACAGGTGGCTGCGATGATTGGTGTCTCGCTAATGGCTTATTACTCGCCT
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SEQ ID 516

MEALLSFIRDILKEPAFLMGLIAFAGLVALKTPAHKVLTGTLGPILGYLMLVAGAGVIVTNLDPLAKLIEHGSITGVVPNEAVTSVAQKILGVE
 TMSILVVGLLLNLAFARFRPKYIIFLTGHHSFFMACLLSAVLGAVGFKGSLLIILDGFLLGAWSAISPAIGQQYTLKVTGDEIAMGHFGSLGYYL
 SAWVGSKVKGDKSDTEDLQISEKWSFLRNTTISTGLIMVIFYLVATVASVLRNASVAELAQNPFIFAISGLTFAVGVIAIVAGVRMILADLI
 PAFQGIANKLIPNAIPAVDCAVFPYAPTAIVIFGASSFVGGLGMLILGVAGGVLIIPGMVPHFFCGATAEIFGNSTGRRGAMIGASLMAYSP
 SCQPCFYLVLNVLFQTRPLEMWISVF

SEQ ID 517

ATGACATCACCAGAAGAAAGATATTCTCTAAAGACGATTGCAACGGAGATTGTTAAATACTCTAGAAACGCTAACCCATTAGGATTGCGT
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 GATTATACTGGCTTATCAAAGGACATGCTGCCAGCTTGTATAGTACACTCTATTAAAAGGTTTTGATAAAACATTCTCATTGCTC
 AATACAAACGGTACCAAACCTACCTCGCATCTGACCGCAATTAACTCCTGTTAGATGTAACGACAGGCTGTTAGGTCAAGGCTT
 GCAACGGGAAATTGCTTATGCTAAAGATTGAGAATTCAAGCTTATATACTATTGAGGTGATGGTGAATTAAATGAAGGACAATGTTGG
 GAGGCTATACAATTGCTGCCATCATCACTGACCCATTAAATTGTTTGAGATGATAATAAAAACAAATTAGATGGTTGACAGCTGATATT
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 AAAACTTCAAGATTCAAATAGTGTGAGACCAAAATGTTAGATGACATCAAGGGACAAGGTGTGAAAGAGTTGGAGGAGTTAGCTCT
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SEQ ID 518

MTSPEERYSSLRRFATEIRLNLETLNHLGFHGYGGSLSIVEALAVYGDIMINPEKFKESDRDYMVLSKHGHPALYSTLYLKFFDKTFLHSL
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 CNPGDFVAKFEAFGFDAVRVKGDDIEAIDKAIKTFQDSNSVRPKCIVLDSIKGQGVKELEELASNHHLRPDLQKTMLERALISLRESLEVVE

SEQ ID 519

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 GAGGTTTACTATGACATTGCAATTGACCTTGGAGCTGGAGTAAACACTGTCGCCACCCCTATCAAGGATGCCATTCAAGCGGAAATTCTGGA
 CACCCAGGACTTCCAATGGGAGCAGCACCATGCTCATGGCTTACAGGTTACATCAACATCCTTCAACAAACAGCGTAATTGGTCAACAC
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 TTTGGTGCCTTAAACAGGAAACTTCACTGCTTCAAGGCTCTTGGAGCAAGGAGTGGCTTGGCAAAAGCTTACCAATGGACTCAT
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SEQ ID 520

VATVSTGSLIFIVKKNPPMSKLVFFWQNREKEFRDFGGFSEKS VYFCDTIDNRKRLILVVINREVLLMTFDAIDQLA VNTVRTLSMDA IQAANSG
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ANAVGMAMAEAHAAKFNKPGFDIVDHYTFALNGDMLMEVS QEAAS MAGHLKLGKLVLVLYDSNDI SLDGPTSMASFTEDVKG RFEAYGWQHILVKA
DGNDLEEIAAAIEAAKATEKPTIIEVKTIIGFGAEKQGTSAVHGA PLGAEGIAFACKAYQWT HDQFEPVAEVTERFAQGLQARGEKA EQAWNDLF
AAYEAYPELAA BYQKAF TNEAAQV ELEAH ELCSSMASRVSQS QAIQI SEQVAS FWCGSADLSASNNTMVKAETDFQPHYEGRN IWFGVREFAM
AAEAMNGIALHGGTRVYGGTFFVFSNYLPAVRMAALQNLPTVYVMTHD SIAVGDGP THPIE QLQAS VR SMPNLNVIRPADGNETNAAWKR KRAI AET
DRPTMLVLTRO NLPVLEGTKELAEDGLSKGAYILSEAKG DLDG ILIATGSEV KLMADTQE AEEG I HVRV SV SMPS QN IFDEQSAEYKESI LPAAV
TKRLAIEAGSSFGWAKYVGLSGKTLTIDTWGASAPGNRIFE EY GFTVANATELYKSL

SEQ ID 521

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SEO ID 522

MRCSTKEMRLVYRDFLLQANQENKQITVLEADLSSSMSTNALASEFGKRYINLGIMEAMVGLAAGLAIKGYPYLHTFGPFASRRVFDQVFLSLGMRSLATIIGSDAGISAEMLNGGTHMPFEELGLRLIPKATIFEVSDDIQFEAILKQTLSIDGLKYIRTIRKAPTAVEYEGREFDSKGFIQLRGKDITLVASGIMVSRAIEAADYLKELGIEASVIDLFKIKPLPEELKPLLIDQSIVTIEHNHRIGGIGSALCEWLSMEKDTTVSRMGIDERFGQVGQMELYEEYGLAVKDIVOHCKSTIYKS

SEO ID 523

ATGCTAGATAAAATTAAAAACAATACCTTTCCAAGCTCGATAACGCCACCCTTTATTTTTA
AACTTTAAAATTTCAAGAAAAATAACAAAAAGGCACCTCAATGTTGCCTTTTGTTATGTTTA

SEQ ID 524

MLDKIKTIPFOARITTPLEFLVRIKYHKILIONLKISENNKKATPMLPFCYDL

SEQ ID 525

SEQ ID 526

MTSLSLTFLSTKFRILESYFQGIENMYFYHKVMAVFSMILLLHKGIGLQGQGHGSEFAKTIGSAGLYLFLSIVFVAYFGNFLKYEIWRFIHRFVY
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SAAHFPSISGGHDRVIFLTVKASGDTKSIFYQLKVGTKIALDRAYGHMLFDKDKKEQVWIAGGIGITPFIISFIRENSILTKRVDFYFTFSNQDNL
IYQDMLESYAKANPNFKLHLNNSSLKGRLDFSQSVEFGQPTIFMCGPTSMSTYAKVFRQDAKSRLVYEGFSFRDSWLSIFLCLKTFDKVYSNLIK

SEQ ID 527

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AACTTATTAGCATACCTACGTCGTACAGATGTTAACCGTTACCGTGAATTCAATCACTTGGACTTCGTCGT

SEQ ID 528

MAISKEKKNEIIAQYARHEGDTGSVEVQAVLTWEINHLNDIKQHKKDHATYRGLMKKIGHRRNLLAYLRRTDVNRYRELIQSGLGLRR

SEQ ID 529

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AACTTGGTGGCATACCTACGTCGTACAGATGTTAACCGTGTACCGTGGACTTCGTCGT

SEQ ID 530

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SEQ ID 531

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GGACAAACCCAAGCATTATCAGTATTAACGTTAGCACCTATGGGTAGAACACAAATCATTGATGGGCTAACACCAGAGTATAAGAAACGCCTTATGCCCACTATACTTCCCACAATATTCACTGGTGAGACGGGACGTTATGGAGCTGCAGGGCTCGTGAATTGGTCACGGTCTTTAGGAGAGCGTGCATAGAACACAAGCTCCAGATTGGAGGAGTTTCCGTATGCATTCGACTAGTTGCAGAAGTTTAGAATCAAACGGTCTCATATCTCAGGGTCTCTATATGTGCTGGAAACGCTTGTCTTATGGCAGGTGGTGCCTATAAAAGCTCCAGTTGCTGGTATTGCCATGGGCTCATATCAGATGGAAACAACATACAGCTTCACTGATATTCAAGGATTAGAACACCATTGGCATATGGCTTAAAGATTGCGGGTACACGTAGAAGGGATTACAGCATTCAAATGGATATTAAAATTGAAGGTATTACCCCTCAAAATTGGAGAGAGCTCTTGCCTAACAGCTAAAAAGCACGCTTGGAAATTCTTGTGTCCTTCACTGGAGCTATCGCAGAGCCACGTCCACAATTAGCACCAACGGCACCTAACAGATTGATATGATAAAATCGATGTTGATAAGATTAAAGTTGTCTCATCGTAAAGGTGGCAGAAACTATCGATAAAATCATCGTGAACAGGGTAAAGATTGATATTGATGAAGAAGGAAATGATCTATCTCTAGTGATCAGGGTCTGATTGATCGACGAAAGACATTATTGCAAGGTTAGTACCTGAAAGCAGAAAGTGGGAGAATTACCTGCTAACAGTAGTTCTGATCGAGAAATTCTGGCTTCTGCAACCTTTGATAAAACAGATGCATTGGTACATATTTCAGAAATTGCACTGGACACGTACACGAAATGTAAGCTGATGTTCTTGAATTGGTGAAGAAGTTGATGTTGAAAGTCAAAATTGATGATAAAGGGCAGTTGATGCTTCTATGAAAGCATTGTTACACGTCCTCCAAGAGCTGACAATCCTAAAAAGGAATCT

SEQ ID 532

MENNNMSKQVFEMI FAGKKL VVETCQVAKQANGSVVRYGDESTVITAAMS KMMSTGDFPLQVN YEEKMYAAGKFPGFNKREGRPS DATLTARL IDRPIRPMFAEGFRNEQVINTVLSDENASAPMAAMFGSSLALSISDIPNGPIAGQVAVDGNFIINPTAQEQEASALELTVAGTKEA INMVE SGAKELSEEIMLEALLKGHEAVCELIAFQEEIVTAIGKEKAEVELLQVDPELQAEIIATHNIALQAAVQEVEKKAREAA TEAVKEVVI GEYEAR YA EHHEYDRIMRDVAEILEQMEHAEVRLITEDKIREDGRRVDEIRPLDAEIDFLPQVHGSGLFTRGQTQALSVTLAPMG EAQIIDGLTPEYKKR FM HHYNFQPQSYVGETGRYGAAGRREIGHALGERALEQVLPRL EEFYAIRLVAEVLESNGSSSQASICAGTLALMAGGVPIKAPVAGI AMGLISDGT NYTVLTDI QGLEGDHFMDFKVAGTREGITALQMDIKIEGITPQILEE ALAQAKKARFEILDVLHGAIAEPRPQLAPTA PKIDMIKIDVDKIKVV VI KGKGETIDKIIAFTGVKIDIDEENGVSIFSSDQAAIDRTKDIIASLVREAKVG EVYHAKVVRIEKF GAFVNLF DKT DALV HISEIAWTRTANADV LEIGEEVDVKVIKIDDKGRV DASM KALLPRPPKA DNPKKES

SEO ID 533

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GGGACCCCTGCCATTGGCTGGTGTGCCATTAAAGCGCTTGTGGCAGGGATTGCCATTGGCTCTATTCCGATGGGACGAATTACAGTC
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AAGATTGCAAGGAATTACCCCTCAATCTAGAAGAACGCTTGTGACAAGCTAAAAAGCTGCTTGTGAAATTCTTGTGATTGAG
GCTGAAACCACTGCTGAGTTAGCCCCACTGCACCCAAAATTGACACCCATCAAGATTGACGTAGACAAAATCAAAGTGGTTATCG
GAAACTATTGCAAGGATTATTGCGGAACGGGTGTCAAAATTGATGACGAGGAATGTCCTATCTACTCAAGTGCACCAAGCTGCCATT
GACCGCAGTAAAGAAATTATTGCGACTTGTGCTGAGCTAAGGTAGGGCAAGTTTACCATGCTAAGGGTTGCTGTTGAGAAATTGGTGC
TTGTCAACCTCTTGTGCAAGACAGATGCTTGTGTTCAATTCTGAAATTGCTGGACGAGAACGCCAACGTGTCAGATGCTCCTG
GAAGACGTTGATGTTAAGGTCATTAAGGATTGATGAGAAGGGTGGTGGATGCCCTAATGAAAGCTTGTGATTCCACGCCAC
AAAGAACAGGAAACATGAC

SEQ ID 534

MSKQTFTTFAGKPLVVEVGQVAKQANGATVVRYGDSSTVLTAAMSKMATGDFPQLQNVYEKMYAAGKFPGGMKREGRPSTDATLTARLIDRP
IRPMFAEGFRNEVQVINTVLSYDENASAPMAAMFGSSLALSISDIPFNGPIAGVQVGYIDGEFIINPDKEQMEASLLELTVAGSKEAJINMVESGAK
ELSEDIMLEALLKGHQAIQELIAFQEQIVAVVGEKAEEVLLQVDVLQADIVAKYNAQLQKAQVQEKKAREAATEAVKEMVKAEEYERYAEDEN
LATIMRDVAEILQEOMEHAEVRRRLITEDKIRPDGRKIDEIRPLDAVDFLPKVHGSGLFLTRGQTQALSVLTALPGETQIIDGLAPEYKKRFLHHYN
FFQYSVGETGRYGAAGREIGHGALGERALEQVLESLEEFPYA1RLVAEVLESNGSSSQASICAGTLALMAGGPVIKAPVAGIAMGLISDGNTNYTV
LTDIQLGEDHFMDKVFVAGTREGITALQMDIKIAGTIPQ1LEEALAQAKKARFEILDVIEATAEPRLPELAPTPKIDTICKIDVDKIKVVIGKGG
ETIDKIIAETGVKIDIDEDEGVNVIYSSDQAAIDRTKEIAGLVREAKVGEVYHAKVVRIEKGAFVNLFDKTDALVHISEIAWRTTNTVSDVLEV
GDVDVKVIKIDEKGRVDASMKALIPRPPKPEKKEEKHD

SEO ID 535

ATGACAAGTACAAACGAGTTAGACATTAGATTCGGCTTTATCAATGCACCGGATAATTTTTAGATAGTATAGGTCTTGTGAATGCCCTGCAC
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TTCAGAGGAGCAAGAACGTGCTCGAGATATGTTGGAGAGTCGCTGAGTTAGCCTTGTAGAGCTATTACATGGCTTAGCAGGA
TTGGCTATAATTAAAAAGAACGCCATTGGAACTCGACTATTTCTACTGTAGAGATATGGCCTTGTAGATAATTACACCACAAATC
TTAAATCAGTTGTTAAATGAAGATAACATTGGTCCGATATCGGATAAAACCTATGGTACCTGCCTTGTCCATCCACGTGAAGAAGGGTAGT
TTTGACCGCTTTCCTTCCACATGTCACCCCCGAGGGAAAAGTTAGTGGTCAGTATTCTCAAACCTTTAAGTTGGAAAAATGGTATAACCCAT
AATGATTGGTGGTGTCTTTAGGAAAGCACAAAGGAGCAATTAGCTGGCCTGGACGATTGACGATTAATTAAACGGCTGATGGAGAAAATGAGATT
GATGATACTTTGGAGTAGGCCATCAATCCATTGAAACAAAGTTAGTTGATTGGCTGTAGTGTAGAAAACGAT

SEO ID 536

MTSTNELDIIRLRAFINAPDNLDSIGLVNALHHSTVWASKEPYAIQVDGQEVPVFDTIDLNHFKEEQESARDMFWECSRSLDVDLDEAISHGLAG
LVYNLKKEGDFGNSTIFYCEDMVQFMNNYTTILNQLLNEDNIVADIMDKTYLVPAFVHPREEGSFDRLFPTMSTPEGKSYVPVFSNLLSFEKWYNH
NDFFGAFRKAQGVILAWTIDDIYKPRNGENEIDDTFGVAINPFDQEQQVLVDWSDVEND

SEQ ID 537

ATGACTAAATCAAATGAATTAGATATTCGCTTAAGAGCTTATCAATGCGCTGTATACTTTGGATAGCCTTGCCTTGTCAACGCCCTTCCAT
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TTTAAAGAAGAACAAAAGAGTGTCAAAGTCAGTATTGGCTGGAGCCTCAGCTTGCAGTGCTAGAAGAAGTCATTACATCTGGTCAGCAGGT
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TACGACCGCTTCTTCTTACCATGTCAACGCCCTGAAGGGAAAAGCTATGTCGGCTTCAAAATCTTCAAGGCTTGGCAAGATGGTACAACCAA
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GATGAAACGTTGGCTGCTGCCATCAACCTTGTGATGACCAACAAATTCTGTTGATGGTCAGAATTAGATAAGTC ...

SEQ ID 538

MTKSNELDIIRLRAFINAPDNFLDSLALVNAFHNFVWAKEPYVIEVEGVKVTVPFTDKEDMARFKEEQKSAQSQYWLERSALAVLEEVITSAGAAG
LIFNLKKKGDFGNSTIFKSSDMIQFMNHYTTVLNTLMSDDNVAAATMKEKVLPFVYPKDNHHYDRLFPTMSTPEGSYVPAFSNLQSFAKWYNQ
DDFGGLFRKAEGVILTWIIDYQPRNGENELDETGFVAINPFDDQOILVWDSELDKS

SEQ ID 539

TTGAGGATAACTATGGGGTGGAAAGAAAGTATAGCTATTGTCAAAAGAACAGATCCAGCTGCTCGTAGTTCTCTAGAAGTTATTTAACCTTACCA
CCAGGAATAAAAGCTCTGCAGCTCATAGGTATCTCATTTTATGGAATCATAAATTAAATTGTTAGCACGCTATGCACAGTCATTGGCGT
TTCTGGACACAAATTGAAATTCTACATCCCGAGCGACATTGGAGGGTTTTATTGACACAGGTTAGGATTTGCTATTGGAGAAACTGCCATT
GTAGAGAAGGTGCTATGCTATACCATGGGGTACATTGGGTGGCACAGGTAAAGACAAAGGCAACGACACCCAACCACATCGTAAAGGAGCGCTA
ATTTACAGCACATCTCAAATCATGGTCAAATTGGGTTGGAGAAAATGCTAAAGTCGGTGTGCGAGCAGTTGTCCTGAGATGTGCCAGCAGAC
GTAACAGTAGTTGGTGTCCAGCTAAAGTTGTCGTCCATGGTCAAAGGATGATCTCAAATCGAAGTATTGAACATGATGAGAAAG
TATTATTGCTCCAAACTT

SEQ ID 540

MRITMGWWKESIAIVKEQDPAARSLEVILTYPGIKALAAHRLSHFLWNHNFKLLARMHSQFWRFWTQIEIHGPATISEGVFIDHGSGLVIGETAI
VEKGAMLYHGVTLLGGTGDKDGKRHPTIRKGALISAHQSIIIGPIEVENAKVGAAAVVLADVPADVTVVGVPAKVVVRHGQKDDLQIRSIIEHDREES
YYSSKL

SEQ ID 541

ATGGGTTGGTGGAAAGAAAGTATAGCTATTGTTAAAGCTAGACCCAGCTGCTCGTAATAGCTTGGGTTATCCTAACCTTATCCAGGCATCAA
GCCCTAGCTGTCATCGTTGTCATTTCTTGGCAGCATCATTAAATTACTAGCCAGAACATGCATAGCCAATTGGCGATTGGACACAA
ATTGAAATCCATCCTGGAGCACAAATCGCTCTGGAGTCATTCATTGACCAGTGGCTGGTCTTATTGGAGAGACAGCAATTGGTAAAAAGGT
GTGATGCTTATCATGGGTGACCCCTAGGTGGAACCGGAAAAGATTGTCAGGTCATCCACGGTTGACAAGGTGCTTAATTGGCAGACAT
GCCAAAGTGGTGGACCTATTGACATCGGAGCAAATGCTAAAGTAGGGGAGCAGCTGTTGTTATCAGATGTTCTGAAGACGTGACAGTTGTA
GGTGTGCCAGCTAAGATAGTACGAGTGCATGGGAAAAGATAATGTCAAATTCAAAAGTTACAAAACAACAGAGAGGTCTTATCAGTGTCA
AAA

SEQ ID 542

MGWWKESIAIVKALDPAAARNLEVILTYPGIKALAAHRLSHFLWRHHFKLLARMHSQFWRFWTQIEIHGPQAQIAPGVFIDHAGGLVIGETAIKEKG
VMLYHGVTLLGGTGDKDGKRHPTVRQALISAHQVIGPIDIGANAKVGAAVVLSDVPEDVTVVGVPAKIVRVHGQKDNRQIQSLQKQREVSYQLSK

SEQ ID 543

GTGAAGGAAATATGTAACAACCTCAAATATTATCAATCTTAGGTACTAGCAGCAGCTTGTAAAGCTATTAAAGTTGCAACAAGTAACCCCTCTC
TTAGGAATTATTTGGGCTGTTGTTAAATGTTAGTGTGTTCTGTTATAAAGCTTATCAGAAACAGAAAAGGAAACACCA

SEQ ID 544

MKDVTTCILSILGILAAACLSYLKFAQGNPLLGIIWAAFVLMYVVRLYKAYQKQKKEKP

SEQ ID 545

ATGATAAAAATTTACGACACTATGACTCGCAGTTACAAGAATTATACCTCTCAATGAAGGTAAGTCACATGTCAGCTGTGGCCAACAGTT
TATAACTATACACATCGGAATGCCCGCAGTGTAGTAGCTTTGATACTATTGCTGTTATTGAGTATTGTTGTTACCAAGTCATTATATT
TCTAACTTTACTGATGTTGATAAAATTATAAAAGGTGCAAGCTGAAGCAGGTTAGGATACAAAATCCTCGAGTTATTGACTATATGGATGAGTT
ATGGAAGATGTTGTCGATTAGGTGTCAAACCTGCTACAAAAATCCTCGAGTTATTGACTATATGGATGAGTTATTGTTGTTAAAGTT
GTTGATAAGGAATTGCTCATGAGCTAATGGAGATGTTTATTAGAGTAAGTAAACATCATTATGCAAAATTAGCCAATAAAACTTGGAA
GATTAGAGATTGGTGCAGCTGGTGTGTTAGTGTGAAAGGAGAGATAAAGAGAATCCTTTGACTATTGCACTTTGGAAATCAGCTAAATCTGG
GAAGTCTCATGGGAAAGTGGTGGGGGAAAGGGCGCCCAGGGTGGCATATTGAACTGTTCTGTTAGTGTGCAACTGAGATCCTGGTGTAACTATTGAT
ATCCATGGTGGAGGAGCTGATTAGAATTTCACATCACAGAATGAGATTGCAACATCTGAAGCTAAAACAGGTAAGACCTTGTCAAATTACTGG
ATGCATAATGGTTGTTAACGTTGATAACGAGAAAATGTCATAATCTTGTGAACTTTTACTGTTGACGATATGTTGAAGAGCGTGTGACGGA
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GATTTGCACTGCTGATGTTAGAGATGAATTGCAAACAGGAATTAAATTGTTAGATACGAAAGGATGGCGTGGACTCGTGT

SEQ ID 546

MIKIYDTMRSLSQDFIPLNEGVNMYVCGPTVNYIHNARSVAFFDTIRRYFEYCGYQVNYISNFTDVDDKIIKGAAEAGMDTKFSFDKFISAF
MEDVAALGVKPATKNPRVIDYMDEIIFVVKLVDFKEFAYEANGDVYFRVSKSHYAKLANKTLDELEIGASGRVDGEGEIKEPLDFALWKSASKG
EVSWSPWGKRGPGWHIECSVATEILGDTIDHGGGADLEFPHHTNEIAQSEAKTGKTFFANWVHNGFVNVDNEKMSKSLGNFVTVDMLKSVGD
QVIRFFLATQQYRKPVNFTEKAVHDAEVNLKYLKNTFNLPQIENANDELEQFVKAFQGAMDDDFNTANGITVIFEMAKWINSGHYTSRVKETFAE
LLEIFGIVFQEEVLDADIESLIEQRQEARIANRDFATADRIRDELAKQGIKLLDFTKDGVRWTRD

SEQ ID 547

ATGATTAAAAATTTATGATACCATGACCCGTTGCTCCGCAAGTTGTACCTTGTACTGAAAATACGTCATATACGTTGTGGACCGACGGTC
TATAATTATTCATATTGAAATGCTAGATCAGCGGTGCTTTGACACCATTGCGACGTTATTGAGTATACTGCTATCAGGTCATTACATT
TCCAATTTCACCGATGTCGATGATAAAATATCAAGGCTGCTACTCAAGCAGGTTCTCTCTAAAGAATTGTCAGATCGCTTATTGAGCTTT
ATAGAAGATAACCAAGGCACTGGTGTAAAGGCCACACAAAATCCTCGTTATGGATTATAGCAGAAATCATTCTATTGAAAGTCTC
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GAGGTTCCTGGGAGATCCCCCTGGGGTTTGTGTCGCCAGCTGGCACATTGAACTGTTCTGTCAGGCTACTGAAATTCTGGTGTACATTGAT
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ATGTTAGCTGTTTGGCATTATCTTGTGAGAAGAGGTGCTTGTGACATTGCAAGGCCTGATTTGCAAGCGACAAGAAGCAGCCGAATCGT
GATTTGCGACAGCTGATGCCATTGAGATCAGTTAGCAGTTCAAGGCATCAAGCTGCTAGATACCAAAAGATGGTGTGAGGTGGCTCGTGT

SEQ ID 548

MIKIYDTMRSLRKFVPLTENTVNIVYVCGPTVNYIHNARSVAFFDTIRRYFEYCGYQVNYISNFTDVDDKIIKGAAEAGMDTKFSFDKFISAF
IEDTKALGVKPATQNPRVMDYIAEIIISFVESLIEKDFAVEADGVYFRVKEFAYEANGDVYFRVSKSHYAKLANKTLSELEVAGSRTDAETALKENPLDFALWKSASKG
EVSWSPWGKRGPGWHIECSVATEILGDTIDHGGGADLEFPHHTNEIAQSEAKTGKTFFANWVHNGFVNVDNEKMSKSLGNFVTVDMLQTVGD
QVIRFFLATQQYRKPVNFTEKAVHDAEVNLKYLKNTFNLPQIENANDELEQFVKAFQGAMDDDFNTANGITVIFEMAKWINSGHYTSRVKETFAE
LLEIFGIVFQEEVLDADIESLIEQRQEARIANRDFATADRIRDELAKQGIKLLDFTKDGVRWTRD

SEQ ID 549

GTTGATTGATGTTGCGTTGATTAATGGTATTGCTTAGCTTGAAGGGAGATGCAGTTATCTTGTATACCGACGCCATTAAATTATGCGAGGGTT
TTTACCAAACTTAATCAGTTACATCGAAAGCAACCCAAATATGTTCTGCTAATGCCAAGCATTGTTAAATAATGCCATGTTAGAAGAAAATATT
TTAACCTGATGAAAGAGCAGTTAATTATAAACGAGGACGTAATGCGAATAGTCATAACAAAGCTAAAATGCTGATATTATTACCTATCGTATGCTC
ACAGGTTTGAGGCTTATGGGTACTGGATATGACTGGTCAGATAAAGCGCTTGGAAACTCTAATACAGTGGTGTATTGAAACCATTGAAAAAA
SEQ ID 550

SEQ ID 350

MIDVRLINGIADAFEGDAVSYLIRRHLIMQGFTKPNQLHRKATQVSANAQALLINAMLEENILTDEBOLIYKRGRNANSHTAKNAIDIITYRMS
TGFEALMGYLDMTGQIKRLETLIQWCIETIK
SEQ ID: 551

SEQ D 551

GTGACTAATCCAGTTGATGTGAATTGGATTAAATGCCATTGCCCTTGTAGGGATCGGTTTATTCCTACTATGTTGTCGTATCTCATT
TTCAAGGTAACGAAACCTAGCCAGCTACACCGTTAGCAACGAGATATGTTCTGCTAAGGCACAAGCCAACCTGATTAGGCTATGTTAGAA
GCGCAGCTATTGACCGAAAAAGAAGAACATCTATAAGCGTGGTCGAATACCAATAGCCATACTAAAGCTAAGAATGCCGATATTATTACCTAT
CGTATGTCGACAGGTTTGAGCATTATGGGTTATCTTGATATGATGGGCCAAAAGAGCGGTTAGAAGAATTGATCAGATGGTGTATTGAGTAT
GTAGAAAAGCAACAATTGATATCCTCA

SEQ ID 552

VTPNPDVNLLINGIALAFEGDAVSYVRRHLIFQGKTKPSQLHRLATRYVSAKAQANLIQAMLEAQLTEKEEDIYKGRNTNSHTAKNADIITY
RMSTGFEEAIMGYLDMMGOKERLEELIRWCIEYVEKOOLISS

SEQ ID 553

ATGACTATGAAAGATAAACAAATTAAAGAAGAATCAAGTGACCTTGCTATGGCTTACATGCTGTGACAGAGAGTTAAGAGCTAATACTGGTAAT
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AAAACCTTATCAGACATGACAAATGGTGGAGTTCCAAGGATTGTTCTAAAGTTTGGAAATTGCTATGGGATTATTCAAGAGATAATGACA
AAGGCAGAGAATGAAGAAAATCCTCTCATTTAATCCTTGATGGTCTGACCAGACCCCTCACAACTAGGTTCTATTCTACGCACAGCTGATGCAACC
AATGTAACAGGTATTATCATCCCCAAACATCGTTGTTGGAGTGACCCAGTGGTTCAAAGACATCAGGAGCTGTTGAACATGTTCTATT
GCAAGGGTAACATAATCTCAGTCAAACCTTGGATACTTTAAAAGATAAGGAGTTCTGGATATTGGCACTGATATGAATGGACACCATCGCATAAG
TGGAAATACCAAGGTAATTAGCCCTAGTTATTGGTAATGAAGGAAAGGTATTTCTCATATAATCAAAAGCAAGTAGATGAAATGATTACAATT
CCCCATGAATGGTCATGTTCAAGGTTAACATGCCAGTGTGCGAGCCGCTATTTGATGATGAAAGTATTTAGAAACCGCTTA

SEQ ID 554

MTMKDKQFKEESSDLVYGLHAVTESLRANTGNKLYQDDLRGKNDVKVAKALATEKKVSISWTPKKTLSMDTNGGVHQGFVLKVSEFAYADLSEIMTKAENEENPLILIDGLTDPHNLGSILRTADATNVTGIIIPKHRSGVTPVVSKTSTGAVEHVPARIARVTNLSQLDTLKDKEFWIFGTDNMNGTPSHKWNTKGKLALVIGNEGKGJISHNIKKQVDEMITIPMNGHVQSLNASVAAILMYEVFRNRL

SEQ ID 555

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SEO ID 556

LKH SWYNKL MEDK DTI ETND I VYGV HAVTESL QANTGNKLYI QEDLRGKKV DNI KSL ATQKKVA ISWTPKKTL S QMTDGA VH QGF VL RVSA FAY TD
VDE ILEIAEQ BANPL LILIDGLTD PHNL GSI LRTADATNV CGVII P KHR SVG VTPV VS KTS TGA VE HIPIAR VTNLS QTL DKL KARG FWIF GTDMN
GTPS DCWNTNGKL ALVIGNEKG KISTNIKKO DEMITIP MN GHVOSL NASVAA ILLM YEV FVN RR

SEARCHED
SERIALIZED

ATGAAAAAAACATTCTATCTTACTCGTGATGGCTACAATATGATTGCTTTGGAAAGATACTCGACAGCTTTAAAAGCAATCGTTAGAAGAG
GCAAGGGAAAGTATTACTTAGAAAGCTAACATTACGCACATTGCAACACATTGATATTATTGTGTATTGATGACAGTATGTTCTGGTGTAA
CGTCAACGTTATGACCAATACAAAATATCCGTTATCTTACTGAGGAGGACGAAACTGCGGATAGCTATATTGAACGAGCAGCGGCAGAACTTAAT
CAATCTGTGTTAAATTAGTCCTCTGCTACCAGTGATTAAATGAAACATGGACTATATTTCAGGGTCTTACGTGTCAGGCTAGAGAAA
TTGGAACAGCGTCTAGCGACAGTAAAATCAGATTGGATAAGATGTCCAGTCAGTAAATCGATTGAGTACGCCAAAGTTAAGGCGTGGAAATGATGAA
CAACTAGGAAAACCTCAAGGATTTAGATGGTATG

SEQ ID 558

MKKHISLLVGDYGNMIAFWKDTRQLFKSNRLEEARVELLRKLHNHYAHFEHIDIICVFDAQYVPGVRQRYDQKISVIFTEEDETADSYIERAAAELN
OSVNLIVSVATSDI^NEOWTIESOGLRVSARELFORVATVKSNDIJKMSSOIDLSTRKLPRWVNDFOGLKLDELDGM

QSVNLEVS
SEQ ID 559

ATGAAAAAAACGGATATTAGTAGATGGGTATAATGATTGCCCTTGGCAATCAACCGTCAGTTGTTAACGACAATCAGCTTGATCAGGCACGTAACACACTTTAACAAAACCTTAACTCATTATGCCCATTTGAGAATATTAAATATTATTTGTGTTTGATGCCCAATATGTACCGGGGTTAACGCAACGATATGACCAGTATTATCTCAGTGGTATTACAGAGGAAGACGAAACAGCAGATAGCTACATTGAGCGCATGGCAGCAGAGTTAACACGCTATACATATGCTAGAAGTAGCTACGAGTGTATTAAATGAACAATGGACGATTTTCTCAAGGAGCTTCGTGTACTGCAAGAGAATTAGAGCAAAGAGTTCAACTGTCAAAGCTGATTTAGATAAAATGTCTAGAGATATTGATCTCAAAACGCCCTAAACTGCGGCCTTGACCAAGGACAGCTTATTCAATTGAGGATTATGTCAGTTAGATCGA

SEQ ID 560

MKKRILVGDGYNMAFWQSTRQLFKTNQLDQARNTLLTKLNHYAHFENINIICVFDAQYVPGLRQRYDQYYISVVFTEDEDTADSYIERMAAELNT
AIHMVEAVATSDLNEOWTIFSOGALRVTALEORVHTVKADLDKMSRDIDLKTPKLRRPFDQGOLIOLKDFFMSOLDR

SEARCHED
SERIALIZED
INDEXED
FILED

SEQ ID 562

MTFKILTDSTSDLDEKWAQEHNVDIIGLTIELDGKTYETVGDEKITSDFLLERMQEGAKPTTSQINVQFEEVFSTYAEENDHALLYLALSSHLSGT
YOSATIAREMVLKYPDAQEIEIVDVTMAASCGEVLAAMLATKERQEGSKSLEEVVKQKIESLLPKLNNTYFLVDDLNHLMRSGRSLSKGAAIIGSVAKIKP
LLKLDSSEGKLVFAKTRGRKKGIKEIVTQATKTLSYSTLIIAYSGEKDQAQMVEQLLADERIEEVIIRPLGPVISAHVSGALALFSLGEENR
SEQ ID 563

ATGACCTTACAATAATGACAGATTCAACCGCTGATTGAATCAAACCTGGGAGAAGATCATGATATTGTCCTTATAGGATTAACGATTGTGCG
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ATTAATGCGGAGAGTTGAGAAGGTTCTGTAACATGCTAGAACAAACAGACTGCTTATCTGCTTTCTCGGTTTATCGGGTAC
TATCAAAGCGCTTAATGCCACCGATCTGTTGAGAAGATTATCCCGATGCCGTTGATTGAAATTGTTGATACCTTGCTGCTGCAGGAGAGAA
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ACCTATTTCTTAGTAGATGATCTTCTGATGCGTGGCTGCTGCTAAAGGTTAGCAGTTAGGCACTGAGTCAAACCT
CTTTGTGGATTGAGAAGGAAATTGTTGCCCATTGCAAAATTGCGGAGCCAAAAGCCATCAAAGAAATGGTGGCTCAAGTGGAAAAAA
GATATTGCGGATTGAGCAGTTATGCTCTTATACAAAGCGATCAGGGTAGTGGCGAAAAGTTACGAGAAGAGCTGCTGGCGCATGAAAATATTAGC
GATGTTCTTAGTGCCTAGGACCACTAGGACCACTTACGCTCACGTTGGCTAACACCCCTGGCAGTTTGTTGATTGGGCAAAATTCCCGT

SEQ ID 564

MTFTIMTDSTADLNQNTWAEDHDIVLIGLTLCDGEVYETVGPNRISSDYLLKKMKAGSHPQTTSQINVGEFEKVFREHARNNKALLYLAFSSVLSGT
YQSALMARLDLVREDYPDAVIEIVDTLAAAGGEGYLITLAAEARDGKNLLETKDIVEAVIPRLRTYFLVDDLFHLMRGGRSLSKGSAFLGLSLASIKP
LLWIDEEGKLVPIAKIRGRQKAIKEMVAQVEKDIADSTVIVSYTSDQGSAEKLREELLAHENISDVLMMPGPVISAHPNLAFFVIGQNSR
SEQ ID 565

TTGTTGATGAAAGTTTGGAAAATGTTTGTGCTGGCGCATTGCCCTCATAGGAATAACTATTTATTGATGCTTTACTAGGAAGGTTGAT
ATTGCTACTATTTCAAGGGGAGATGATGCAATTAGCAGTTATAGGAATATCATTGATAGCTATGGAAATTCACTGTTAGTGTACTACATAAGTAT
AAGGACAGA

SEQ ID 566

MLMKVFGKCFCCWRICPHRNNYFIDAFTRKVDIATYFSRGDDAILAVIGISLIAMGISVYYHKYKDR

SEQ ID 567

TTGTTACCCATTGTAAGGCCCCGGAACCTTCAAATACTCTCGTGGACCGGAACATCCACACCTGTAACAAAAAGAATTGCTATAGGAGAA
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GCAGTAGTGTCTAGCGTACTCGCGGAAAAAAACAAACCAACTTCACACCACACTGATAACGGTACTTGTGATTGTTATCAATGCTGAAAAAA
GTTAAATTAACTGGTAAAAGCGTCAGATAAAACTACTACACTCAATGTATCCAGGTGTTGAAACAAATCTCAGCAGGTGAACTTCG
TCTAAAATGCTGTTGATTGAAAATCAGTTAAAGGCATGCTTCCACATAACACTCTTGACGTGACAAGGTATGAAATTGAAAGTATT
GTTGGCGGTGAGCATAACATGTCGACAACACCAGAGACTTGTATCTCAGGACTTATC

SEQ ID 568

MFTPFPVRPNLSNTLVDRNIHTCKQKRIRIGEIMNKTTFMAKPGQVERKWYVVAADVPLGRILSAVVASVLRGKNKPTFTPHTDTGDFVIVINA
VKLTGKKASDKIYTHSMYPGLKQISAGELRSKNAVRLIEKSVKGMLPHNTLGRAQGMKLKVFGGEHTHAQQPEVLDISGLI

SEQ ID 569

TTGTTACCCATTGAAAGGCCCCGGAACCTTCAAATACCTCGATGGGACCGGAACACCCATCACCTTGTAACAAATATTACGAATTGCTATA
GGAGAAATCATGAACAAAACAACCTTCATGGCTAAACCCAGGCCAAGTTGAACGCCAAATGGTACGTTGACGCAGATGTGCTACTTGGACGT
CTTTCTGCTAGTTGCTAGCGTACTCGCGGAAAAAAACAAACCAACTTCACACCACACTGATAACGGTACTTGTGATTGTTATCAACGCT
GAAAAAGTTAAATTACTGGTAAAAGCAACTGATAAAAGTTACTACACTCACTCAATGTACCCAGGTGTTGAAATCAATCAGTCTGTTGAA
CTTCGCTCTAAAACGCACTTCGCTTGATTGAAAATCAGTTAAAGGCATGCTTCCACATAACACTCTTGACGTGACAAGGTATGAAATTGAAA
GTTCTCGTGGCGGTGAGCATACTCACGCGCACAAACACCAGAGACTTGTACATCTCAGGACTTATC

SEQ ID 570

LFTPFPVRPNLPNTFDGTEHPSPCKQILRIRIGEIMNKTTFMAKPGQVERKWYVVAADVPLGRILSAVVASVLRGKNKPTFTPHTDTGDFVIVINA
EKVKLTGKKATDKVYYTHSMYPGLKSIAGELRSKNAVRLIEKSVKGMLPHNTLGRAQGMKLKVFGGEHTHAQQPEVLDISGLI

SEQ ID 571

ATGGCACAAGCACAATATGCAAGGTACTGGCGCGTAAAAACGCTGTTGCACCGCTCGTTGGTCCAGGTACTGGTAAAATTACAATCAATAAA
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GTTAACGTTGAGGTGGGGATATGCAAGGTCAATCAGGTGCGATCCGTATGGTATCTCAGTCGACTTTAGAAGTTGACCCAGATTCCGCGAT
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AAGCGT

SEQ ID 572

MAQAQYAGTGRRKNAVARVRLVPGTKITINKDVEEYIPHADLRLVINQPFAVTSTQGSYDVFVNNGGGYAGQSGAIRHGISRALLEVDPDFRD
SLKRAGLTLRDARMVERKKPGLKKARKASQFSKR

SEQ ID 573

ATGGCACAAGCACAATATGCAAGGTACTGGCGCGTAAAAACGCTGTTGCACCGCTCGTTGGTCCAGGTACTGGTAAAATTACAATCAATAAA
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GTTAACGTTGAGGTGGGGTACGGTGGACAATCAGGTGCGATCCGTATGGTATCTCAGTCGCTCTTCAAGTAGACCCAGACTCCGCGAT
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AAGCGT

SEQ ID 574

MAQAQYAGTGRRKNAVARVRLVPGTKITVNKKDVEEYIPHADLRLIINQPFAVTSTEGSYDVFVNNGGGYAGQSGAIRHGIARALLQVDPDFRD
SLKRAGLTLRDARMVERKKPGLKKARKASQFSKR

SEQ ID 575

ATGTCATTACACAAATACCAAGCAAAAAGCCAAAAATGGCTATTGTTGATTTGTCAAAATCTATATGGTCAAAGACGTCAACGTCAGACCAT
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CCAACCTATAACGAGATATTGAGAAGGTTATCAACGCTTACAGGCTTCAAGGAAAGTGGAAAGGTTCAAGGAAACAACTGCTTACGTTACTCTGATATG
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SEQ ID 576

MSIHKYPSSKAKGNGYLYFVKIYMKDSQRADHIKRGFRTRKEAKDYEARLIYLKASGKLEEFIKPHTKTYNEIFEKWYQAYQDMVEPTTASRTLDM
FRLHILPVMGLPIKSPLDQNFITDKAKTFKNIKQIKSYTGKVFDFAIKMKLKHNPMAEIIIMPKRKTRIENYWTVQELQFFLAIVLQEEPY
KHYALFRLAYSLRKGELEYALKWADIDFQETTLSVDKSLGRLDGQAEIEKGTKNDFSVRKIKLDSSETISILQEWKSISQKEKAOLAVAPLSIEQDF
LFTYCTRSGSIEPLHADYINNVLSRIIRKHLKKISPHGFRHTHATLMIEIGVDPVNTAKRLLGHASSQMTLDTYSHSTTGEDRSVKQFADYLKAK
SEQ ID 577

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GCAGGGATTGAACGCTTACCTTACGCTTACGCTAGTTATTGCTGAACGCTGGTATTAGTTAACAGGAACTTACGTTACGCT
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ATAAATTTA

SEQ ID 578

MERMFIMKITEHKKNGTIVYRASIYLGIDQMTGKRVKTSITGRTRKEVNQKAKHAQDFLNSGSTIKRKKVVIKTFKELSHLWLETYKLTVKPQTY
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HLETSQHKRYNLYFDALVYQLLSTGLRIGECALEWDIDLENGTIAINKTNKLNFKLSTAKTQSGNRVISVDKTLRSLKLYQMQRQLFNEV
GARVSEVVFPTRKYFNASVRQSAUDTRCKEAGIERFTFHAFRHTHASLLLNAQISYKELOQRLGHANISMELDTYGHLSKGKEKEAVLYYEKAM
NNL

SEQ ID 579

ATGTACAATAGACTAAAAGAACCTACGAAAGACAAGGGTTAACCTCAGGCTGATCTAGCTAAAGTCATCAATACTAATCAATCTCAATATGGAAA
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AATTCAAAATAGCAACAACTCAAAGATACTAAAGGTTATTAAGTTTTGAAACAGTCAAAGGATATGGGTCAAGATTATTTCTACT
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CAGAAAATTGATGAACTTGAACGAGGGCTAAAATCTTCGAAAAGCTTGTGATAAAAGAGTAAAAGAGAGATTAGAACTTTAAAAAA

SEQ ID 580

MYNRLKELRKDKGLTQADLAKVINTNQSQYKGYENGKTSIENSKILADFFGVSIPYLLGLDNNSKIANSTIKDTNLLSFFEQQVKKDMQDYFST
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SEQ ID 581

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TATCCGTATCGTTCTATAATAAA

SEQ ID 582

MYPRIRNLREDNDFTQKFVANLLSFHANYAKIERGEVALMADVLVQFYKLYNVSIDYLLGQTDYPYRFHNK

SEQ ID 583

ATGGCTTACACACTAGAACGAGAACGATTGTCGTTATGATACTGGATAACTGTTGGTATTTGAGAGTAATGTTAGGAAACACATTACT
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GATTATGTTCTCCATTGTCGAAAACGAGTTAACAGTAAAGACTGAAGAACACAGGAGAGAACAGAAAATGGCAAGATTAC
TCTAAGTCGAAATA

SEQ ID 584

MAYTLEERETIVRYDEMNCWYFESNVRKHITKIMKTIDSCQILGQEKEDDRIIWIHAKLTNLDYMVSPFVRKRVKREMTEEQREARKRMARLH
SKSEI

SEQ ID 585

ATGACAGAAGGATTACCACTCAGCTCCCCAAAGTAACGAAAGTTACTGGCTCGCTATGACACTATGGTTCAAAAGCAATAGAAAAGC
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GCAGGCATGCCACATAGGTTATTGACGGAGTGACTCTGTACGATAAGCGCAAGGTCGCTCAATGGCTACAACAAATTGAAAGA

SEQ ID 586

MTEGFTIQLPKVTEKLLARYDTMVQKAIKEKALEDKELEYKPMVRMAGLCRFLDVSTTIVKWQKAGMPHMVIDGVTLYDKRKVAQWLQQFER

SEQ ID 587

TTGAAAGATAGGAAATTGGCATGGATAAAAATAATTAGAACGTTGACAGGAAAAAGATACTTAGAAATGGTTGGTGTCTCGTTGGAA
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TTAACCTTGTGTCATGTTCCCTGCTTACTTGGGATATGGTGTGGAGAGAGA

SEQ ID 588

MKDRKFGMDKNNLEDLTGKKILRNFGGLRLEYGTIFLDVGLFTYIVLILSIFFLVERWFLGALTFLVHVPLLLLGIWCGER

SEQ ID 589

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GACGATTAGGAGAAATCAGGAGGTTCTTACTACAGGAAAGAACAGGTTCCGCTGATGACATTATCGAAAAAAATCCTC
AAGATATTGGTGTGACCGAGAGACTTTCAAAAGCTAACAGGTTCCGCTGATGACATTATCGAAAAAAATCCTC

SEQ ID 590

MIKIYFGKDITLNQAIQSRLSDSYQIDYQAFSSKDIDAKTLMEMWLFSTDIFELLSTKMLKYLNQITLSQFVRKILKDVNSTLKLPIVVTDEVY
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KIFLVDRDEFFKKSVDL

SEQ ID 591

ATGTCGACATCTGAAGTGCATTACTACACCCGTTTTGGCAAGTTGGCTGGAGCAAATGAAAATGGTCCGACTCCGAAGGGGTCGGCTGGTGG
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TTTGT

SEQ ID 592

MCTSEVHLHPPFGKFGWSKMKMVRLLRRGRLGATPRMSFYVGLCADKKIGAVRRPPKRKEVCLKLKVSLDNITMTAYIKSKYLMQIETHLA
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SEQ ID 593

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CAATATCGAGATAGATAGACTAGCTGATAAGTTAACCTTTACTTGAGGATAACCAAACCTGGTACAAAAAAATTATGAGTTACTCAACTATGTT
CGGAGCTTGGAAACGACAGAAGCTATTGCTGATTATTGCTTACGGTCAATCTTATTAGTGGCAATATGGCTTACCTGAGGTTACCTTGAT
SEQ ID 594

MLKIQYYGVTRSKMIRKYDADSLGVSSQSIIYKRIKSPKYKERLKGHLYRDNQKVENLDLIGIKILEDYHFENDVIELEKTLGDIQEFEQEKKG
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SEQ ID 595

ATGAGTTATGTTGTTGCTAGAATGGCTAAGTACAAGTCAGGTCAAGTGCACGGCTATTATAATCATAATGAACGGATTTTAAAATCACTCAAAT
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AATAGT

SEQ ID 596

MSYVVARMAKYKSGQLTAIYHNHERIFKNHSNKEIDVEKSHLNYYELTNRDQAQNYHKQIKEHENENRLSTRGVRKDAILCNEWIITSKTFDSL
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GKLKMDKETYNRLFQTASKHASSNAELKRDVLKAQSQNNHLSRELLNHRKTAEKNIKLQSENRLKDKVKMLDEQVKILNKSLSVWKEAKEFMPK
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SEQ ID 597

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SEQ ID 598

MFLKHQDVQKQNWRMRKVKKVFVSSCMLLTVGLGVAVPTGFSQSNGVMVVKAEEVPATDLSRQASDSERVDDESSLQKENLSVDSFKLENLNGWEA
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 VESNNKLKGELVIRVDNKNVSTKHDWLPDISDGTHTVDFGLDKLKSVAFRFSRQTSNVYEFNSININIKNISPASVPAIPSKVLEGSVLSGTAI
 SSGDTLEKRKSFDGDILRVYKDSKIIARTVIKGNKWDVLSKPLIAGEKLDPEILHPRSQNVSKISKQVEAKPFDPSYKEKVIAKLKPVYEATS
 EKITNDALDENAKDLQKQKLEEYQISGKVAISEAGTKQEADAYNKYSSQTDPSLPSQYQGNKENEQKGRQDLIQTRDLTLKAIQEDKWL
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 RLDEGLKALKAAADSLETLKVTTEEAVFDEKEKNPDSIPNQHKGATADQARKQALDSLDKEVQEKELESIDNDNTLTTDEKAACKKVNDAYDVAKQTAM
 EANSYEDLTTIKDEFLSNLPHKQGTPPLKDQSDAIAELEKKQOEIEKAIEGDKTLPRDEKEKQIADSKERLKSDTQVKDAKNADAIIKKAFEEGKV
 NIPQAHIPGDLNKKDEKLLAELKQKADDTEKAIDVDTKLTDEDEKKEQKVTKAELAKTDVKNTQTREELDKKPELKKAIEDTHVKGNLEGVK
 KAIEDLKKAHETEVAKINGDDTLDKATKEAQVKEADKALAAGKDAITKADDADKVSTAVTETHPKIAAHKTGDLKKAQVDANTALDKAAEKERGE
 INKDATLTTEDKAKQLEKEVETALTAKDNDVKAAKTADAINDARDKGVATIDAVHKAGQDLGARKSGQVAKLEERAAKATKDKKISADPTLTSKEKEEQ
 SKAVDAELKKAIEAVNAADTADKVDALGEVTDIKNQHKGSDSIDARREAHGKELDRVAQETKGAEKDPTLTTEEKAKQVKDVAAKERGMAKL
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 GVTSIKNQHKGSDGPDVARRGLHNKSDIVEQAQTKDAITADTTLTBEAKETQRGNDKBEATKAKEELAKADADALDKAYGD
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 AAIAAVDKATTAEINGQELGKGITAINKAYRPGEVGKARKEAAKADLREAAKVREATANDPTLTKADAKQTEAVAK
 NQELGKGITAINKAYRPGEVGKARKEAAKANLEKVAKETKALISGDRYLSETEKAVQKQAVEQALAKGQVEAAKTVEA
 VAGLAKDTQATAALNEAKQAAIEALKQAAAETLAKITTDALKTEAQKAEQSENVLALKTATIAVRSQA
 AKSSSANHLPSGDANSIVLVGLGVMSLLGMVLYSKKKESKD

SEQ ID 599

ATGACAGATAAAAAATTGTTTATTACTTGTGACCATGACTTATCAAAAAAGATATGGGAGGAGTAGGACCTACACCGTAAAAATCTTTA
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 AATGGTCTAGAGCTTATCAAAAGACTAGCTAAATTACAATATCAGATTTGGATATGAGGTTAATCCAAAAGATAGTACAAAGATGCTG
 ATAGGTATTGCTAACGACTGATGAAGAACATTGTTAAGGATATGAGAATTTTATTGCTGATATTTCACACAGCTTACGCAATCTAT
 CATGCACTAATTAAACCATGGACACAACTGCTACCGATTGAAACAAATTATGTTTATAAAGCCTTGTGAAAAGGTAAATAAAAAG

SEQ ID 600

MTDKKIVYYFDHDLSSKDMGGVGPTYTGKNLLFLWWWTYSVVAEDNLIDITSLFEVPEFNFYNNGLELYRIKNELANYNIRGYEVNPDKSTKML
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SEQ ID 601

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 AAAATCAGTAAGTACACAGCACTAGAGGTTACCTTAAGTAAAGATTATATTGCTCTATACCATATCGAGGAGGAAGAGAATAGGTCGTTATT
 GATTACTCTCCTACTCGAAGCGACTATATGAAATTGTTTAA

SEQ ID 602

MDYKKYQIIYAPDVLEKLKEIRDYISQNYSSSTSGQHKMEQIIISDIEKLEVFPFEGFDADEKYGSKISKYHSTRGYTLSKDYIVLYHIEEEENRVVI
 DYLPLTRSDYMKLFK

SEQ ID 603

TTGGACTATAAGAAATATCAGATTATCTATGCTCTGATGTTAGAGAAGCTAAAAGAAATTCTGATTATATTCTCAAAACTATTCTCAACA
TCAGGTCAAGCTAAAATGGCAAATCATTAGCGACATAGAAAACCTCGAGGTTTCCAGAAGTTGTTGATGCCGATAAAAATATGGTTCA
AAAATCATCATTACAGCACTAAAGTTACCTTAAGTAAAGATTATTCCTATACCATATCGAGGGGAAGAAAATAGGATCGTTATT
GATTACTTGCCTACTCAAAGCGACTATATAAAGTTATTCAA

SEQ ID 604

LDYKKYQIYAPDVLEKLKEIRDYISQNYSSSTSGQRKMEQIISDIEKLEVPEVGFDADEKYGSKIIHYHSTKGYTLSKYIVLYHIEGENRIVI
DYLLPTSDYIKLKF

SEQ ID 605

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AAGCAATTCAAGCTGAAATCAACAAAATATTGAAGATGTCGTCAGGGAAATTTCACCTCTGAAGAAGTGAGGCTGAACCTGGACTA

SEQ ID 606

MVTAEKNRRAVTFOANKELVSEAMTVLNKNLTLSALRLFLQNVVVTNEVDLLTEEELEKEKLFQFQAEINKNIEDVRQKFYTSEEVSELGL
SEQ ID 607

ATGACTACAGTAAAAAAACAGAGCGGTTACCTTCAAGCTAACAAAGAATTGGTAAGCGAAGCAATGACAGTATTAAACAAGAAAAATTAAACC
TTATCATCTGTTAAGATTTCCTCAAATGTCGTTGTCACAAACAGGGTTGACTTATTGACCGAAGAGGGCTAGAGAAAGAAAACCTTT
AAGCAATTCAAGCTGAAATCAACAAAATATTGAGGATGTCGTCAGGGAAATTTCACCTCTGAAGAAGTGAGGCTGAACCTGGACTA

SEQ ID 608

MTTVKKNRRAVTFOANKELVSEAMTVLNKNLTLSALRLFLQNVVVTNEVDLLTEEELEKEKLFQFQAEINKNIEDVRQKFYTSEEVRAELGL
SEQ ID 609

ATGATGTCACAAATTAAACTAACACCTGAAGAACCTCGTATTTCAGCACAAAATACAAACAGGATCACATCAATTACAGATGTTAACAGTT
TTGACTCAAGAACAAAGCTGTTATTGATGAAAATTGGGATGGTACAGCATTGATAGCTTGAAGCCAATTCAATGAATTATCTCCAAAATCACA
CAATTGACAATTATTAGAAGATATAAACAAATTATTGAAAGTTGCGGATGTCGAACAAACAGACTCAGATATTGCTCACAAATTAA
AAA

SEQ ID 610

MMSQIKLTPPEELRISAQYTTGSQSITDVLTVLTQEQAVIDENWDGTAFDSFEAQFNELSPKITQFAQLLEDINQQLKVADVVEQTDSIASQIN
K

SEQ ID 611

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GATATGTCGCTATCAGGGTATGGCAGTGGCACCAATTATCAAGGGTAAAGTAGATTATAACAGTGTGTCAGTTATATCCGCCAACGGATTCA
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CAGTCACATGACAAATGGACTGACTCAGCTTCAGGCTATTCTCAATCTGCTATATGTTAAATTAGGTGCTCAATATCATATCCGACTACA
GTATTAAATGGATGGTTAGTATAGCAGCTTAAATGAAGATGAAAAAAATTATGGCTAACGATCTGATATTGCTAACAGTGTGTCATCTGATATTG

SEQ ID 612

MVFTYTEREKFREFNIGDNVYSVNPDYAEKNHSTVITDLPQKDNETNIITTEDRKKFKVLKTSPPDDMSGYQGMAMAPIIKGKVDYNSVAVISAATDS
SNYKDLIGAVSSAQPHQSSTQLKSADKFLKDVSQSHDKWTVTQLSGYSQSAYMLKLGQYHPTTVNGWFRYSTLNEDEKNSWLSILNL
SEQ ID 613

ATGGCTAACGATCTGAATTTGTAATTTCGACATAAAGAGGATAATGTAACCTGGTGGAACGATTAAATAAACTAGATGATAAAGATTAT
GGTACCGTGAATGGGAAATGGGAAATGGGATAAAAGCTAAATAGAGAGCTGGAAATTACTGATGATGTTAACGTTAAAGATGAAAAGGTAACATCGTA
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AATGCTGAATTAGTAAAGAAAAGCATCAGAACTATTGCAAAACTAAAGTGTGCTCTGGTAAACAGATTAAAGTCCGGAAATTAGCT
GATACATATAGTGAGGGCGGAGTTAGAGAGGACACCAGTAGTAACACCAATTGAAACCTTCTTGTGATAAAAGTTACTAATGCACAAGAGATTACA
ACTTCATATATTAAATCTCAAAACAAATTGAATCTGGTGTCAAAATTGCTAGAAGAGGACTCCAAATTAGCAGGAGAATTAAAGGAATGGTCA
CAGTAC

SEQ ID 614

MAKHPRFVNFRHKEDNVITWWNDFNKLDKDYGTVKVNNGKSHKIESWKFTDGKLKDEKGNIVNPKSPAVQSVLYBEVFQKAKAKLKKSGGKLS
HSEKVKYLDESEQAIFIANGLTTASQTAASDDIKKNAELVKEKASELFAKTKVMPGIFTDSLPEELADTYSEGGVREDTIVTPIETFFDEKVTNAQEIT
TSYINLQKQIESGVQKLLLEEDSKLAGEFKEWSQY

SEQ ID 615

ATGGTCACAGTACTAGATCAAATGAAAACAAATTAAATAGTCTAAAATAACCTAGGGAAATTGGAAGATAATTATCATCGCAGAAAAATGGAG
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AATGATTCACTGGTTGACTTTATGAGTTAAATCGAATAATTGAAAGTTCAATGGAATTATGATGAATATGAAAACATAAACAGACT
ATCATTGTCAGAGGAAAATAGTCGACACAGTTCTAAAGACGGAGTAAATTAGAAATGACATTCTAGTTAGAAGGAAGAAAATAC

SEQ ID 616

MVTVLQDNKINSLKINLKGLEDNYHRENMEIEDKLYSLEDKKNELETYLQEVYBETSHLLRQNDSDGSTFMSLNRIIESYQMLEIDEYENYKQT
IIVQEENSRTQFLKDRVKLENDISSLEGRKY,

SEQ ID 617

ATGAGTTAAATAGGCGCTGTATTGAAAGGAACAAAGAACGAAAGAACGAAATTCAAAAGCAGTTAGTAAAGGATTGTCTATGCCCT
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AATCAAATAGATTCAAGGACTGTAGGACAATTGGGAAAAGTAAAGGCACAGGTAGATTAAATAAGGTAGTTATGATGATTAA

SEQ ID 618

MSLIGAVLKGTKEFQQJQRALVRIVYAPEIVEEADSIKMYSIDKIDNVSETAKSSIKTIANQIDSGLVGQFGEKVKAQVDLNKGSYDDL
SEQ ID 619

ATGAAGGATAACAAAGTTATTATTCACATTGGTAAAGCAATAGATAAAATGAAAGCTAAAATGATAAGTATCTCAATCAAATTAAATAAT

SEQ ID 620

MKDNKVVYIHFKAIDKNEAKNDKYLQIINN

SEQ ID 621

ATGATGGAGGAATTGGTATGGTAAGTACTCAATATGAAAGTAACCTTACGGAGAAAATTCCAGATAATTAAACATATGTTGATTAGAAGAA
CTTGTGATA

SEQ ID 622

MMEFCMVSTQYMVKTLREKFPDKLTYVDLEELVI

SEQ ID 623

GTAATGTGACTCCTAAGAAAAATGTCGGAAGAACCTTGCCTTTGTCGGATTACCTCTTCAAAAGGATAGTTGGGAAATTAGTGACTATA
TTTT

SEQ ID 624

MNVTPQEKKCRKKTEAECRITSEKRIVGKLVYIE

SEARCHED

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SEQ ID 626

MFKYVPIFREFRFLNRQFSLKQVASNELSVSQLSRFERGESDLSLTKFLGALEAIDLSSIEFMDRVNKYQKSDQISLMSQMAQYHYQRDVAGLEKMSVEEGKLKKDSSDIRCLNIVLFRGMICEDCDSRKMSSEIDLCFLSLDYLFKQDSWEISDYILIGNLYRYYNTRHICQLVKEVINQKEYYRDIYTNRNVVEATLNNVVTETLIERRALEEATFFLEKVEALLNNERNAYHRIILLYEKGLAYAKGDSRGIQSMKQAIFCFOQAIGSKHHVENFQEHNFRVTRL

SEQ ID 627

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GACGAATTGTTCGGCTCATCCTCAAGCAGCATACGCATTTCACGCTTAAAGTCAGGCCGAGAAAATGTTATGCTGAGAAAACCTGGTTAAA
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TCTGAGGGAGATTAA

SEO ID 628

VVKVGKMEKELGKTLRRLRKKGQVSISFLADEYLSQLSKSQISRFERGESEITCSRLLNLDKLNTIDEFVSAHSKTHTHFFTLLSQARKCYAEKNVVK
LTKLLKDYAHKDVERTMIKAILFSIDSSIAPSQEELTRLTDYLFKVEQWGYYEIILLGNCRSFRMNYNTLFLLTKEVASFAYSEQNKTNKMLVTQL
SINCLIIISDHSCFEHSRYLINKIDLLLRLDELFNFYEKTVFLYVHGYYYKLQEEMSGEEDMRQALQIFKYLGEDLSLYSYKEHYRQIVLGGKGDEDW
SEAD.

SEADE
SEQ ID 629

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AATATTCTATTCTCAGTCAGGTACAAATCAGGGCTGTGATGTCGACTATATTACTATTGCTATTATGTTATG
CCTATAGGAACACTATTATGACTATCTTTCTATTGCTTATCAAATGTTAGCTTATTGTTATAGGATGTCGCCATTGCTATATTGGGAGGATTA
GGATTAGCTATAGTAAAAACAAATT

SEQ ID 630

MNINGIKLLSSRAVSKLGDVFYDYGNSTWIASMGLGQKILGTQIVELLVSIVLNPFGGALADRQRRKILLITDAICAIMCFLLSFIGDDKVMV
YGLIVANAILAVSNAFFSPAYKSYIPEIVDKADITYNANLETIVQIISVSSPVLGFLIFNNFGIRITLIVDAITFLISFLFLYAIKVERVQLSKQ
EKVAIKNITADIADGFTYIKKEKEIMFFLIIAALLNTFLAMFNYLLPFTNSLLKTSGAYATLISAIGSIIGALIARKIKSSINSMLSMLVFSSL
GVIVMGPSLFELPIWIPIYSGSFLFNSLLTMFNIHFFSQVQIRVDEAYMGRVMSTIFTIAIMFMPIGTLMFTIFSALSNVSVIIGCAIAILGGL
GFSYSKKQF

SEQ ID 631

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SEQ ID 632

MNNRKKNIQYLVYSKVIYRIGDVMFDFANNTFLAGLNPAASLSLVAVYQSLESVIGVLFNLFGGVIADSFKRKKIIITTNILCGTACLVLFLTKEQWLVYAIYLTNVILAFMSAFSSPSYKAFTKEIVKDKSISQLNSLLETTSTVIKVTPVMIAIFLYKLLGIHGVLLDGLSFLIAALLISFILPVNDEVVIKEKVTFIREIFNDLKIGFKVYVSHKSIFIITVLSALVNFFLAAYNLLLPYSNQMFGEISTGLYGTFLTAEAGGFIGAILSGFVNKELSMRILFLSLSGLMLMPLAPPFYIMFHNAIILALSPALFSLFLSIFNIQFFSLVQKDVDNDFLGRVEGIFTITILFMPIGTGFVSVLPNNNSFLNFIIGSCITTLSSLVERFLKKYNR

SEO ID 633

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GGTATTACAGCCATTGGCTTCTCGCAGGGGAGGGGACTTGGAGATATCATCATAAGAGAACTAATGCAACAAATGGTGGTCTATTATCTTA
GCAGGATCTTCAACAGCCCTATGGCAATTCTGATTAACTCTAGGGCGTATCCAACGCATGCTGAACCAAGAAAA

SEQ ID 634

MGIANVIQTIPSLAMISIIMI.GLGLGIKTVVATVFLYSLPIITNTYTGIRNVDSLLDAAKGMGMTKRQRLFMVELPLSISVIMAGLRNALVVAI
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SEQ ID 635

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SEQ ID 636

MLLWSIYLEVMSMPSLFVTFQNRFNEWLAALGEHLQISLLSLMIALLIGVPLAALLSRSKRWDIMLQVTGVFQTLPSLALLGLFIPLMGIGTLPA
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LIGAISALLAIIFNSNLQYLEKASLRRIMISFGITLLALLASYTPMALSQFSKGKDVTIVIAGLGAEPDILINLYKELIEDQSDISVELKSNFK
TSFLYBALKSGDIDMYPEFTGTTITSSLRDKPPLSNDPKVYEDAKGIAKQDKLTLKPFAYQNTYAVAMPKELAKEYQIETISDLKAHADTLKA
GFTLEFKDRADGYKGMQSQYGLQLSVATMEPALRYQAIQSGDIQVTDAYSTDAEITKYHLKVLKDDQQLFPPYQGAPLMTSLLTKHPELKGILNQ
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SEQ ID 637

ATGCTTTAAAATCGACTTTTACAGATATTACACTTCTAGCCCTCTAACGATTCTGTTGTCATTAAACGATACTAAAAGTCTGGT
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GATCCTAAACAAAAAAATTACTCCATGACTCGTGGTAAATCAATTAAAGCAGTGCACAAACCTTAAATTATGTTGAGATGATAAAACTTTA
GAACCTTCAGTTGCAACAAATTAGGAAACCTTATGRRGARRWWAAWAWKRAAMMAWKAAWWMYTCCMAMMATTWTWY
YWMYWNYTYCMAMMWWAWKGKWRK

SEQ ID 638

MLKKSHFLQIFTLCALLTISGCOLTDKKSHTTIKVAAQSSTESSIMANIITELIHHGYNTTLISNLGSSTVTHQALLRGDADIAATTRYTGT
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FSHIYPMQIGLVYDAVESNMKMQSVLGYSTDRGRISYDLEIIRDDKKFFPPYEASMVNNNSIKKDPKLKLLHRLDGKINLKTQMNLNYMVDDKLL
EPSVVAKQFLEKNHYFRXXXXXXXXXXFXXXXXXXX

SEQ ID 639

ATGGCTAATTCTTATCACAGTATGGCATGCAAATATTAGAAAAACATGGGAAACAGTCTATCTCATTCTTGTATAGCACTTGGGATTGCA
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GCCTTATTAGCTTAAATGATTCCATTGGAAATTGGAAAATCCCAGCTATGCTGTTCTTATTATTCCTGCTTCTATACTAAGGAAT
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CCTTGTACTCCATTATTAGGCTGGTATTGCTGTTACTATTATGTTATTGCTGGGCTACATTGCTTCTTATATAGGTGCAAGGGGTT
CTTGGTATCTCATTAGGGTTAAATCTTCTAGGTTAAATTCTAGGGGACAATTCTGTTATTATCTGTCACATTATAGAT
TATCTTTAGGATTACTGGAAACAGCTAACGCCAGAACAAAGAAGGGGGCT

SEQ ID 640

MVNFLSQYGMQILVKTWEQYISFFAIALGIAIAVPLGVVLTRFPKVAKIIIAIASMLQTLPSLALLALMIPLFIGKIPAIVALFIYSLLPILRN
TYIGMNNVNPTLKDCAKGMGMKPIQSIFQVELPLATPIIMAGIRLSTIYVIAWATLASYIGAGGLGDLIFSGLNLFQSKLILGGTIPVIIILSIID
YLLGLLETALTPRTTRREA

SEQ ID 641

ATGGGCCAAGAACCTATCGAATATCAAAATATCAATAAGTGTATGGGAAAATGTTGGGTTGAAGACATTAAACCTTAAATTACCCCTGGT
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ATCATCTTAGTTACTCATGATATGGATGAAGCCCTCAAGTTAGCAACAAAATTATTGTTATGACAATGGTAAAGGTTCAAGGCTCAGGACACCC
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AATACTTAAAGGGCATTGTTACTCGTGCATCCCTAGTTGATATGTTACGATATTGTTGGGCGATACTGAAACGGAGGATCAA

SEQ ID 642

MGQEPIIEYQNIKVKVYGENVAVEDINLK1YPGDFVCFIGTSGSGKTTLMRMVNHMLKPTNGTLLFKGKDISTINPIELRRIGYVIQNLGLMPHMTIYENIVLVPKLLKWSREAKRAKARELIKVLPEEYLDRYPTSELSGGQQQRIGVIRALAADQDIILMDEPGALDPITREGIQDLVKSQEEGMKTIIILVTHDMDAEALKLATK1IVMDNGKVMQEGTPNDLHHPATSFVEQMIERGEERLLHAQADITPVKQIMLNNPVSITAETLTERAITLMRQKRVDSLLVTDNGKLJGFIDLESLSKYKKDRLVSDILKHDTFYVMEDDLRLNTAERILKGLKYAPVVDHENNLKGIVTRASLVDMLYDIIWGDTETEDQ

SEQ ID 643

ATGATACAGCTTTAAATAATGTTCTAAAACCTTTGGTCAGACAAGGCTTTGCAAGAGCAGACCCATTCAAATTAATGATCGTGAATTTCGGCTGGTGGCCCCAGGGATCGGCAAGACACACTTTAAAATGATTAATTGCCTTATTGAACCAAGCTGGAGATATTACTAAATAACGCTCCACAGACAGAGTTAGATTAACGTGAGATGAGGCTATCTATTGGATACTGAGCAAATTGCTCTGCTTCCCACACTCACAGTAGCTGAAAATATTGCGATTATCCCTGAGATGAGCAATGGTCAGCTGAAGAAATTAGACAAAAACTGAAGAATTATTGATAAGGTGGCCACCTGCTAAAGATTATCTATTGATGGATGAACCATTTTCAGCCTTAQATCCTATTTCACGTAACAAACAATTGCAAGAGTTAATGTTGAGTCCTCACAAGGAATTGACATGACGATTGATTGATGGACACATGATTGATGAGGCCATTAAATTAGGAGACCAGCGCTACCTATTAAATGAGGGAGAAATTGTCACACTGGATGCCAGAAATGATTAAGACCCACCCCTGCTAATGCTTTGTGGTCAATTATTGAGGTGATGAGCATGCC

SEQ ID 644

MIRFNNSKTFQGQTKVLQEQTQFQINDREFFVLVPGSGSGKTTLLKMINCLIEPSSGDILLNNVPQTELDIREMRLSISGVVLQQIALFPNLTVAEANI AIIPEMKWQSAEEIROKTEELLDKVGLPAKDYLDRYPTSDLSGBECORIGIVRAIISHPKILLMDEPFSALDPISRKQLQELMLS LHKEFDMTIVFV THDIDEAIKLGDRVAILNEGEIVQQLRPEMICKTHPANAFVNVNLFGGDEHA

SEQ ID 645

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SEQ ID 646

MMGTSGLEPPTSRLSGVRSNHLSYAPKLLLGFYFLIK

SEQ ID 647

TTGATATATAAAATTTATCTAAGAAAAGAGAACATGATGAGAAAATATAAAATGGTTAATTCCCATATCAATTGGGATGATACTTGGAGCTGCTAAATGAACAAAAAA GAACAATTAGCCTATCTCAAAGAGCATGAGCAAGAAATCATGATTATGTAATTACATAACAACCAATTGAGTCCTGCTCAATTGAGTGGTCA AGTGTAAAAGTAGAACAAAGCGGGATGGAACCTCCACAAGGGGTGATTATACTTTCACTGAGAGGAAAGTTAATCATCTACAAAATTCAAA TTAATAGTTGATTTTATTTAGCTCATAAAATGATATCCCAATATCAAATCAATGGGAATGCTAATAAGCCGTATACATAAAAATGGTATTGGCACATTATGAA

SEQ ID 648

MIYKIYILRKENMMRKYIWKLIPIISIFGMILGGCQMNSEHKIQSNEVKNSKQSEVKDKKKMKEQLAYLKEHEQEIIDYVKLHNNQIESVQFDWS SVKVEQSGNGTPQGGDYNLSLRGKFNHLQNSKLIVDFYLAHKNDIPNIKSMGMLNKPYIHNGIWHIYE

SEQ ID 649

TTGAGTAATTGGAACCTAGATAATTGATAACTTACATAGCTTTAGCAGAAAAGTCATATAATAGTCACCTAATTCTATTCTGAATTATTGAGACTGACTCAGTAACAGAAAGTAAAATTCTCAACCCCTCAGAAGATAACAAAGGTCAAATCACACAGGGTGGCACTAACCTCCCAATGATGGT ATTGTCTACCTGCAACACAGATAAGTCCTAAAATCTATTGATGAAAATGTAAGGCTCTATTCCAGATGTCAATGGAGGCTATCACACTGAGCAT TATGTTACTCTATTCTATCAAAGGTGTGCTACTGACGATAAGGCAGGTTTAATGCTTACTACCTGTCAGATACTGAAAGTAAAGATAGACT ACAAAAGCACACTTACTAGCCTATTGTTAGTGGATTGCTAGATAACACTAAACGATTGGGTTAGTAACATGCAATGTTCTGCTCT AACAAGTATTCTCACAAGCGAAATTGGCTAATAAGGCTATGAAAGAAAAATTGCGCAGCTAAAGGAAAAGCCCTGGAGCTATTATAGATGTT ACTGGTCACTACTCGGTACGATTGTATCTCTCAAGCAGGTTTAATCTAGCTATGCAAGAATTGGAGAATGTTGTCAGTAGTCCTTCTGAT GGCCTGATGTATCAAGAACCTGGAAAAATGGAAGGCATTCTGCTAAAAAAATCCAAGAAGCTGGGAAGCATGTTACCTACTATGTCATCC TTTGATATAGTTAGTATGCTTAATGTTGAAAGCCA

SEQ ID 650

MSNWNLDFNLHSSLAESAYNSRPNSPPELFETDSVTEVKFSQPSEDNKQQTQGGTNLPNDGIVYLQPDKSLKSIDENVKVLIPDVNGGYHTEH YVTHSYQKVLDDKAGFNAYLSDTEKIDSTTKHTYLAIRGSDIGLDTLNDWVSNAMFAVSNKYIPOAKLANKAMKEKIAELKGKAPGAIIDV TGHSLGTIVSSQAVVNLSYAELENVGQVVLFDGPVRSLEKMEGISAKKIQEAGKHVTYYVNPFDIVSMLNRKPE

SEQ ID 651

ATGCTCTATATGGCAACCAATTAGCAGAACATGATGTTTCAAGAAAAGTCCTGCAACAAAAACATATTAGTGAAGCTAAGGATACGATTGTA GAAAATATGACATCCACTATTCTCATGCTGAAATAATGGCTATGCACCTTGACCAATCAGAAGTTGATGCTCTGGTTCAAGATATAAAAATGTCA ACAGTTGGATGATGGCTAGAGACTCTGATTATGAAAGCACTTGATCACTATAAAACAAAATGACCACTTTACGACCAATTGGTAACAGTT GCACAAAATTAAACAGCTCAAGATGAGCAACTAGCTGGTGTATTGTCACGAACTTAC

SEQ ID 652

MLYMATQLAESDVSEKVSATKKHISEAKDTIVEIISTSTISSAEIMAHLDQSEVDALVSDIKMSTVWNDGVETS DYEALDHYKTMFTFTNLVTV AQNLTAQDBQLAGDIVTNLS

SEQ ID 653

ATGTCACAGAAATTGAAATTGCCCCCTGAATGAAATGTTGAAAGAACAGAAAGAACATAGCTATTAAAGCAATTAGCTTACAGCAAAAGCACTATTACGGATACTGGAAACAATTAAAGCAACTTGTAGAGTCAGATGCCAAGACCTAAAAACTATGCACTCCACCTATAACGCCAATATCACGGATGGT CTTGAAGGGCAGTCAGCTCAAGCAGCATCTGATTCTGACACAACCTCCAAAACAGAGTTAGATAATCCAGTCAT

SEQ ID 654

MSKELKLPLNEMLKEQERIAIKAIVATAKSTTIDTGTNLKATLSEDAQDLKNYASTYNANITDGLEQOSQAASDFTLQPLPKPELDNPVN

SEQ ID 655

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SEQ ID 656

MIDTKKLQELDQEYDQNLRNIYRNREQLEDDFHLMARTDSLKESVYQATLGQGWELPQEAHAHLYNMDDNKDTFISEFNEYMEKLEEKEIDLRRV YNDRVDELYQAKQNEAKKG

SEQ ID 657

ATGAAAATTATGAAAGAATTAGACAATATAGGAATTACCGTAAGAACATCTTTCGGGATCATGATAATATAGCAAAATATCTAATTGAAAAGTA

SEQ ID 658

MKIMKELDNIGINRKNLFRDHNDIAKYLIEKV

SEQ ID 659

TTGGGAGTTTATGAACAATAAAACAAATGGACTATAATTACTTATTTACTATCATCGTAATTGATGTTAGCTACTATTTGGCGGGAAATCGTTAACGTTACCAATCAAATTATTAATTAGTAAACCAGTATAGCAGAATTGTCGATTTTATATGATAAAAGTTCCGACTCCTCAA
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TACCTTAATATATGGAACGTTAGAGTTAAACAGGCTACCTTATATTAGTAGGTTATTACTAATGTTGCTTACATATTACTTT
CTTGAGGGACGGAGA

SEQ ID 660

MGDFMNNKNKWTIILLIFTIIVIDVSSLFGGNRLSLPIKLLLILVTSIAEFCSIFIMIKVPTPKYKKEPFGLKAKFYSIVLFLSTILYTIGIWNVTPASPYNVKESILVGVLIQVFFIYFLKKINESPDERFYSNLALSASLMFLISIMLLILIAIYLNIYGTLEKSGYLYIMVGLLMMFAVTYYFLEGRR

SEQ ID 661

ATGGGAAAGAAAACAAAATTATCAGTTCTTAAACAGGTTAGAGAAGATATCGGAATGACTCAACAAGAGTTAGCTATTGGATAGGTGTTAGGAGAGAACAACTGGTCATTAGAAAACAGGTATAATCCTCTAGAGATGGCATTAAATTGTTAGATTCGACATGAAGATAGAAGAT
ATTITTCATTAAGGAAAGAGGAT

SEQ ID 662

MGKETKIISSLKQVRDIGHMTQQELAIRIGVRRETIGHLENNRNPSEMALKIVKIFDMKIEDIFQLRKED

SEQ ID 663

TTGAATAAATTTTTAGAATCAGAGAGACTTATTATAAGGCCACTAGAAGAAAGTGATTATGATAGTTGATACTAGTTTATGAATCGTGGACCATCTTAACTCCATTGATGATGGACTCTGATATGCTATGTCGACATTAAATTGGTTAAAATTAGTAAATTACAAAGGAAAGAATGCAA
GAAAGTGACATAGTATATATTTGGTTCTAAAAGCGGTGAGCCTAGGAATGTTAAATTTGGTACCCCTTGCAAGAGCAGATATGCAA
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AAAGATTTCATTTGAGAATGGAAAATGGACAGATAAACTGATTATAGTATAATTACATAATAATTAGAA

SEQ ID 664

MNKFFLESERLIIRPLEESDYDSWYTSFMNRGPSPDGFDDGILDMSMCINWFKNLVNLRKEWESDIVYIFGVFLKSGEHVGMLNIVTLARADMQWGELGYVFHNQFWNSNGYAFESILALLNSTYKLGFFHIEAQITPGNERSEKLVRRLGLTYETTRKDFSFENGKWTDLIYSINLHNNNLE

SEQ ID 665

ATGAATAATTGGATAACACTATATTGTAATTAGCAATGTGCAACACAGTACTAACGGAAAGATTACGACTCCAGCCTGTTGAATTAACTAATGTA
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AATGTTGTATGAAATCACCATTAGGAATTATGCAATGTTGAAAAGAATCACAGAAGATAGTATTGTAATTAGAAATCAGAGATGAA
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CTTCGTATCTGCAAAATCCAAAGGTGAGTGAAAACAAGAGCGTATTATTCTATTAAAGAAGAATATTTAATAAAAGTTAATCTAA

SEQ ID 666

MNNLDLTLCKLAMCNVLTTERLRLQPELTVNVNDFLEFSSDSETVFYMQRKYKANTVEEAQVVLANVMKSPPLGIYAMIEKESQKMIGIELEIRDE
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SEQ ID 667

ATGGGATTTGGACAAAGCTTGAGTGTGCTTTTTGAGACTCCGAAAGTAAATTACGGCCTTTTGCTATGAAGATCATGGGATTTTAC
AGCATGGTTAACGACACTAAAAACCTTATTATGTTTCCAGAACAAAAAAACTAAGGCAAGCAGTACTATCTTGTACATAGTTTATAAAG
TTTCCTTAAAGTCAGTGGCAATAGAAGATAAGCAACCCCACCAAGTAATAGGTTCTATTAGAATTGAGCATTATGCTAAACCGCTTGTGCT
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CTCAAAACGTTGTATTATAACTCATTTAGAAAATAAGGCCAGCAGAAAGTAGCTAAAAACGAGGTTTCAACTAAAACCTGTTAAAGGA
AGTGATGTAATACTCATAAAATCTGATTAAATGTAACAACTAATGATAGG

SEQ ID 668

MDIWTKLAVFAFFETPKVILRPFRYEDHDFYSMVNDTKNLYVFPEQKTKAASDYLHVHSIFKPLQWAIEDKATHQVIGSIRIEHYDAKTRCA
DIGYFLNYAFWQGQIMTEVVIVKLVYLSFHEGLKTLRIITHLENKASQVKAGFQLKTCFKGSDRNTHKICIFYKMYQLTNDR

SEQ ID 669

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CTTGGTTTACTTTGAGAAGACTTTAGACAAGCTGTCGTTATAAGGGCTAACAGAGATAAAATTGGTATTCTATTAGATAAAAGAGTGG
CCAGAAAAAAACACGGTTGAAAATGGCTAGATGATTCAAACCTTGCTGTTAAATGGGTTACAAATCAGATCACTACAGCATTGAGCAGAAG
ACAAAA

SEQ ID 670

MGDVVENFTEGKNPKIDTNGKTVRIEKINPDHFEDLFQVYGELSTEDSLTYISFSKFNKNEFDVFFQTLKSESDPYYLAIVDNNNTGKVLGTFSL
MRIDTKNRVVMGWVWVYSSKLKQTRIATEAQYLVMKYFEELCYRYEWKCDLSNAPSNNSAKRLGFTFEGTFRQAVVYKGRNRDTNWYSILDKEW
PEKKTRFEKWLDLDSNFVAVNGYQIRSLSSIEQKTK

SEQ ID 671

ATGATAAAAACAAAGTTAGTGTACTGGAACTTACGGAAAAAGGAAAAGGAAACATTATTCAAGACCGTAGTATTGGCATTAATAACT
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AAATATGTAATAATTGAAATAATGATCTTATTGAAATTGCAATAACTTGTATAAGTCTTACAAAGAAATAAAACAAATGATACCAAAAT
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SEQ ID 672

MIKTKFSDPLEQLAKKRKRKTLFPTVVLALITVLLVVGIAFKGFTYLTSKNGQKTYHNFELLSEIAYPNISYDSLYYQPSGQFTGKVHADRFKDID
GVQIPYSSFEENYSISGTFGTNADEKSEKNGLYDRGTRQKVPQFFNKNVKYKKGEAKTPTNDLKVNKNNDLIEIAITFDKSYKBEIKTMIPN

NIKQNWLGITSTELDTSYWPWKYQPGTDPELNTPQIFIDKIKENLKGN SKVYFNNINIYSDLEKYAKKYDKVNNSDKLKFGSIILTGKAENFKQLKEKEWVHASSIGANIEKYKPYYKLDE

SEQ ID 673

ATGATGAAAAAATATAAAATGGTTAATTCCCATATCTATTATTGGATGTTACTAGTAGGCTGTCAAATGAATAGGGACCTAAAAGTCAGTC
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SEQ ID 674

MMKKYIKWLIPISIIGMLLVGCQMNRGPKSQSNEVKNSKQSEVKKGKNMICKNS

SEQ ID 675

ATGAAAAATAATATTCTATTGAACAGTATTAATGCCAAGAGATGCCAAAGAAAACAAAAGTTATTCGCTATAGAGCTC
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SEO ID 676

MKNNIIFSIEQYINDQEMPKGKQKVILSAIELFASQGFHGTTAQLAKNAEVSQATIYKFETKDKLLVFILELIVQTIGRPFTELSTFSTKEELIHFFVQDRFKFIEKNNDLIKILMQELLINSETSTIFTKLINSTDPNITKIFNCLSEGNSLNKMEILRAVIGQFITFFIQLYILNIKPENLEEEELKQIEKOILKLSS

SEQ ID 677

ATGCGGTATGATAACATATATCCAAATAACAATATCACTACGTTAACAGGAGTTGCAAGGAGTCGATCAAGTGTACCGAGTACGCCTCTTTAAT
AAAGCCATTCCAGAAATTAAAAAAACAAAGAAGAACCATAAATCCCATTAGTATTGGTATCATTGGCAAAAAGCCTGTATTTTATTCG

SEO ID 678

MPYDNIYPNTISLRLTGVARSSVPEVRSFNKAIP EIKKTKKTTINPISIGIIFAKKPVFLLP

SEO ID 679

ATGAGAATTATTGCAATAACTGAAAAGTTATAAAAGAACACTGTTCGTATAAAAGAACACTGCTATGATGTTTAGCACCTATTTAATTATGTTTTGATGAATGTTATGTTCTCGGAATAGTAATAACAAAAGTTAAGGACTTAACTGTTAACAGGAAGGTCGTTCAAATTAGATAATTAAAGCATATTCAAGGAGATCATTAACTCATCTGCTAAAAAGCACTCAATAACAGACTTAAATGAGCTTATTTCGGAGGACAATAAATCTTAACTGTCTTATGCGATAACAGATTCTCAAGAGCAGTTAAACAGAACAGCTTAAACAGCGCTTTAATACAATGAAACAGTAAGGAACGTATTGCGAAGTTAAAATTAGCTATAAGAACCTGACACATCCTTACAAACTCGCTCCAAATATACTAAAGAAAATATAATTACGGAAATAAAATACAGGCTTTTGCAAAATGATACCAAACTAATGGGATTTATGGCTTCTCTTGTGTTTTAATTCTGGAATGGCTTATTAAGAGCGTACTTCTGGTACACTGACTCCTGCAACTCCTGTTAACGTAGTGTATTTGGATATATGTTATCATAACGGCATTCTGAAATTATCACAACGATAGTTATCGTTTATCAACTATTGGCTACTAGATATTCAAGGTGAGGTGATTCTTGTCTCATGTGCAATTTTATTGGCTCTGGCTTACATTAGGAATCTTAAATGTCACTCTAGCAAAATCAGAATTTCAAATGATGCAATTATTCCCTTAATIATAATGCTCTTAAATTATCTTTCAGGAATAATCCTCTAGAAAATATGCCAGTTGGGCTCAGACAGTCGGTAAATTCTACCGCTCTCCACTCTGGTGTGCAACTACAAAAAATTATGTAACGGCTAACGGATTACCTAACGTTCTCAAATCTCTGGTACTTCTTATTTTAATTATTTAACCGCAAAATATCTTGACTAAACGATAACGTTAAAGTA

SEQ ID 680

MRIIAITEVIKELFRDKRTLAMMF LAPILIMFLMVFSANSNTKVKGITINVNTKVVSNLNDNIKHIQVRSFKFNSAKALKSNKIDALISEDN
KSYTIVFYANTDSSKTTLTRQFKTAVTNTMNSKELISQVKILANKNPKLAQSOLQTRSKEYKEKYNGNKNTGFFAKMIPILMGFMVFFFVFLISGMAL
LLKERTSGTLDRLLATPVKRSDIVFGYMLSYGILAIQTIVLSTIWLLDIQQVVGSIFSVIVNFIILVALSLSGLIMSTLAKSEFQMMQFPIPL
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SEQ ID 68

ATGATTTGGTTTATAAAAACCTCTATTGTTAAGATAAAGCGAAAAAAACAAGTTATGTGACATTCTTTAATGCCTATTTAACGACACTTTGGCTTTATCTTGAGTTTCAAAATAATCAAGCTAAAATTGGGATATTAGATAAAGATAATAGTCAGATATCTAAACAAATTATTGCTCAACTAAAGCAAAACAAAAGTAGCAGCATTTTACCAAAATCAAACAAAGAGCATATTGATCACTACTCTCAAGATAATCTCTAGAAGCGGTATTGACTATTGACAAAGGGTCTCAGATAAAGTAGTGTGCAAGGGAAATTCCTAAACTCAATACGTTCGATTGCTAATAGCAGAAATTACAGATGGTAAGGCCAGACCAATTATCTATTGGAAAATTATAATTATAGGGGATGTGGCTCTAGGTAACGAAGACTTTAATAGAATTCTCCAAAAAAACCAACAGCTTAAATTATGATGTTAAGCAAGTAACCTTGACAGACCGATCACGTAGCAAAGCAGTATCTCCACAAACGACAGGATTGGCTTATCTAATGTTAGGTAGTACAGCGTGTATTACAGTGGTATTGGCAGATAAATCTAGTCAGTTACCATCAGTTATGTTATCGAACTTATCGTTTCGCTATATGTTGAGTTACGTCTGTAGGATTGTTGCTTTACGATTCAAATTGTCATTATGCTGAGTTGTTAAAAGTATTAAATTAGTTTTTGTGTCCTGACATCCTTCTTGTGATTATTTCTTCTTGTAGTTATAGCGATAGGGCTTGGCCTGCTGATTGGAGCTATCACACAAAATCCTAACACAGTAGGCCAGTTAGCTAATCTTATTGTAATGCCGACTTCAGTGGCTGTATTGGCCATTGCTATTAGCCCTCTTATATGCAAGCAATTGGTAAGTTATCACCACAAAATGGGTTTATCAGGCGATAGCTTCAAGTTGAGGGACCTTATCAGGCTTGGCCATACTTGTAGCTAATGGGAAACAGCACTAGCTTGTAGTTCAAGTTTATTATAAAACCTACCAAACTA

SEO ID 68

MICFIKTLFVKIKRKKTSYVTFFLMPILTTLLAISLSFSNNNQAKIGILDKDNQISKQFIAQLKQNKKYDIFTKIKKEHIDHYLQDKSLEAVLTIDKGFSKDVQLOGKSQKLNIRSIANSEITEWVKAQTYNLLENYJ1JGDVALGNEDFTFNRLQCNQNLNYDFTVQKVTLTDRRSRKAWSSTTGFLLILMLGSTSVIYSGILADKSSQYLHRLMLSNSLRFYRMLSYVCVGFVAFTIQIVIMSLLKVNFSNFFVPTSSLI1IFFLFSLAIGFGGLIGAITQNSQQSSOLANLIVMTSMAGLCLWPMSITPSYMQAIGKLLPQNWWLSSAIAIFQSGGTLSQAWPYLLALMGTALALISFSSLLLKPTKL

SEQ ID 68

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TCTTTAACGGCTAGAAAATTATTATTCTTGGAAAAATGAAGGTATTCAAAAAACTGTAATTAAACAGCAGATACTCATATTCTAAAGT
GTAGATCTAGAAAACCAACTGTATAATTGGTCAGGTTACTCAGGGGTATGAAAAGACGGCTTCTAGGCATGCCCTACTTGGAAACCCC
ACAGTTTAATCTAGATGAACCTACGGTGGATTGATCCATCTTGGAGAAAATCTGGCAAGACTAATTAAATTAGGATGAAGGACAT
TCTATCTTATTACAACCCACGGTTGGATGAACAGAATTAAAGTAAAGGTGCACTACTATTACGGTGGAAACATTATTGCCCTTGATACTCCA
TTACATTAAAACAAATTAAATGTGAGTACTATTGGAGAAGTTCTTAAAGCTGAAGGGAGAA

SEQ ID 68

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VDLNEQLDKFVSGYSGGMKRRRLSLATALLGNPTVLILDEPTVGIDPSLRRKIWQELINIKDEGHSIFITTHVMDEALTSKVALLRGNIIAFDTE
LHLKKOENVSTIEEVFLKAEGE

SEQ ID 68

ATGAGTTTGTACAATTAAACAAATGGTCAAGTCTACAAAAACGGCAAGGAAGCTGTCAATGATGTTCTCTGTCATTGAAGCGAGTAATATT
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AACCATTGAAATTAGAAGAAATTCTTACACTTAACAGGTAAGAAGTTACGAGAT

SEQ ID 686

MSFVQLTVVKSYKNGKAVNDVSLSIAGNIYGLLGPNAGKSTLNLILGLIPLSSGKITVLGQSQKTRKISSQIGYVPQDIAYPDLTAYEN
VELFGSLYGLKGQLKKOVLKSLEFVGLHSQAKQFPSQFSQGMKRLNIACLVHSPKLIIIFDEPTVGIDPQSRNHILESIRLLNKEGATVIYTH
YMEEVEALCDYIIFIMDHGQVIEEGPKFELEKRYVANLANQIIVTLDSDRHELADKPDSLIEDGEKLMKIDNSDMTSVHVHQLTQANITFSEIRH
NHNLLEEFLHHTGKKLRD

SEQ ID 687

GTTGAGTAAACACTCACTCACTGAGAGAGGAGCAAAAGTTATCATGAAAAAGTCATCGATTAAAAACTACAAAAGCATATGCCTCAGAAC
CGTTTTAA

SEQ ID 688

MSKHSLTERGAKSYHEKSHRFKKTTKSICLNRFK

SEQ ID 689

ATGAAGGCTCAGGCAGTTGTCACAAGCCAAGGGAGAATTGTTCTTGGATATTGCACTGAATATTGCCACGATATGAAGTTGTTAAAATGAGT
CGCAGAACATCGGACAAGCTGCTAAATCTTGGCAGACAGTGGTTATCAAGGGATCATGAAGATGTATTCAACAGCGCAAACCTCCGAGGAAATCA
AGCAAACTTAAGCCACTAATCTGAAAGATAAAACTATAACCATACGCTATCCAAGAGAGAAATCAAGGGTGAGAATATTGTTGCAAGTAAA
ACGTTTAAATATTTCACAACCTATCGAAATCGCAGCAGAACGGTTGGATTACGAATGAATTGATTGCTGGAATGATCAACCGTGAACCTAGGA
TTT

SEQ ID 690

MKAQAIIVSQGRIVSLSIDIAVNCHDMKLFKMSRRNIGQAALKILADSGYQGIMKMSQAQTPRKSSKLKPLTLEDKTYNHTLSKERIKVENIFAKVK
TFKIFSTTYRNRRKRFGLRMNLIAQMINRELGF

SEQ ID 691

ATGAATTATGAAGCAAGCAAACAATTAACTGATGTACGATTTAACGCCTTGGTGTTCAGCGACTACTTTGAAGAGATGTTAGCTGTGTTA
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TACCGCCTTATGAACAAATTGCGGCTGATTGGCATTACGAAAGCAACTTAATCCGTCAGTCAATGGTTGAATCAACTCTTATTCAAAGT
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SEQ ID 692

MNYEASKQLTDVRFKRLVGVRRTTPEEMIALVLTAYQRKHAKGGRTPKLSLEDDLMATLQYMRERYTVEQIAADFGIHESNLIRRSQWVESTLIQS
GFTISKTHLSAEDTVIVDATEVKINRPKKIN

SEQ ID 693

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GATTAGGCCATTCTACTAATCTACAAATGATATTCTTTAGGAGGATATCTCATTACTGAAAGCACTTCAGTACAGTCACTTAACTC
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SEQ ID 694

MDKLKKLQKENTLLEGGRIDNSNNQTYTDMIVYLRGASISPYHQELIRNDIVNMLLEAQRQASLVSVFGE DRHDFINQVIKSTPKISKKEETLQRW
DLAILLTLIQMIIFLGGYLITEALQOSVDPDLIPITLVDLFAIFISIIAVKIADTIIYATYNFDKSKEKKYFFRYIFLILSIIAYLIGKYYHLP
FINIPLWIYLIILGGSFSLHIIVKYLNHY

SEQ ID 695

GTGAGTATGAAAATAGATAAAAAGACTTTGCACTTATTGCTAGTATTATTTATTAAATTGTTCTGTTACGTTTTCTTATTAAAGAT
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GAAAATGTTAAAGCTGAAGCAGCAGTCATAAGTTAAGTCTAAAGAAGTCTAAAGAAGCTTACAAAACGTTAGTATACTGTTAGACACAA
TATGGTTTATTGGGAATCAAACCTCCCTAGTTGAGCTAGTGAAGTACAGAACAAAGGGACAGCTAATCTGCTAGTCAGGATACTCTAGTTAC
GTTAACATCAGAACATGTTAGCACCAACTTATGACCAACCGCAAGCGAAATAACACCAGTTACTCCAGGGTTAACAAATCTGTTAGAC
GGTACTGTACTGCTACTATGGGACAGGTGTTGCTCAG

SEQ ID 696

MSMKDKKELLALIASIILLIFASVTFFLFKDHGTTQMDTVESSVNVHSDSLSQLTEAQMDLKFEEKPSEKLLKDVELALNKLNSSSKEALQKRFK
KAKDKYLKDEADKKATKDATLVEILEQAPSEENVLKAEAVNLTVKESKEALQKRIDTVKTQYGLIGNQTPSSVAETTEQGTANPASQDTSSY
VNQNQVAPTYEQPQANNTPVTPGVNNTPVTPGTGTVPATNGTGVQA

SEQ ID 697

ATGGCTACGATGAAACAAATCATAAGGAGATTCCATGACTAAATCACAAAAAGAGGCCTTATTGGATGTTGAGTGTCTAACTACTC
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GTTAACAGCTTAATGACGCTGATCGTTAGGCCACTGAGCTCAGTCAATGCTGTTAGGATAATCTCTAGTTAGGAGACTCTCAAT
AAAACGCTAACAGAACAGCTAACAGTCCAGGAAAGCAAGAGCAAGAGCTACTCAAGCTAACAGTCTGCTAGGAGACTCTCAAT
AAAATCTTAAGATATCGCCAAAAGCAGTTAACGACTTAAGTAACAAAGGTTAACATCTCGTTAGACGCTTACCTTAC
GCGAAACCCATTATTGATGAATTCCAAGACAAAGTGGAGAAATAACAGATAACTCTTACTGGACACCTTCCAGGGTTAACAA
GATAATTCCCACTGTCACCTACTTAGACCCAAGCTCAGAATCTCAGCTTACGTTACACCACAACTAGTCATCCTGATCCAATT
ACCTCTTCAGAACCTTCCGACTCAGGAGACAAGCAATCATCAAAGAG

SEQ ID 698

MTMKQYHKDSMTKSOKEALYWMVLTTTLLIGGSCLIFGSHPQTQDKVAKHSKSAASLLKKAVKAVNDADRLATAAAIQEAKAVD
KTLQEQLNVAKAKQEQEDAATQAVKAAEETLNQNLDIAQKAVNDLSNKGKKAALQSRLDAILPAKPIIDEFPQRSGEITD
DNSQSPTLDPSESSASDVTQPSPSHDPIPQPSSEPSDGDQKSSKE

SEQ ID 699

TTGCCCGCTACTGCCGCAACTGATTAGACGCCCTTCTAGTCGCTTGATCTGAAGTTAGGGTTGTCCGCAAGAAAGATGTGACTCCAGTAGAT
AGTAAGCCAGCACTATCGAAAATTCTCTGAATCACAAATCCATAACATCAGCGCCAGCAAACCA

SEQ ID 700

MPATAATLDASSSRVSEVRVVGKKDVTVPDSKPALIRKIPSESQSITSAPAKE

SEQ ID 701

ATGAGAGTGAATGGGGGAAGAAGATGACGAAGTACATCAAGGCTGACCGATTCTTTATGCTGATCATGTAAGGAAACGGTTATTTAGAAA
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CAAGGGTGTACGGTAGCTTGGTCAATTCTAACATGGGACATATAAGAAGCTAAAGGAGCTGAAGGGCGGTCTCAGTTGGTACATGCGTAT
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CACGGTGTACCTGTTGCTGTGACATTAAATGACACAAAAAGGCCATAATCATGCGCATTAAATAACAGATTGTATGGCAGCTGGAGGTGCCCT
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SEQ ID 702

MRVNGGKMTKYIKADRFYADHVKEGYLEIKDNHFGKWIEINISQEEILDYSGYQIAPGLVDTHIHGFAGADVMDCDSEGIILRMSAGLLSTGVTSFLPTTLTSDEKRLREEASKSVAAVAGKBEQGAKIQGIYFEGPYFTEEYKGQAQNPIYMRNPNLIEEFAQWQKAALKLITKIALAPEREGVEEFVSAITKQGVTFVALGHNSNGTYKEAKKAVKAGASVVVHAYNGMRLTHREPGMVGAVNLPNTYAEELICDGHVHDVPAIDLMTQKGHNHALITDCMAAGGAPDGDXMLGELPVVVNSGTRALXXLIN

SEQ ID 703

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GCTGATGTCATGGATAATTCTGCCAAGGGATTCAATCAAATGAGTGAAGGACTATTAGCACAGGAGTAACGTCTTTTACCGACGACCTTAAC
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SEQ ID 704

MTCYLKADCFYYPTEVRPAGYLSLHDGVFGEWTEIVPADAQIIDYTGYQIAFGLVDTHIHYAGADMDSAQHQIMQSEGLLATGVTSFLPTTLTSTFEQLEKVGSTIASVADQVKGAKIQYIYFEGPYFTEEVKGANQPSMVKTRPLEEFDAWQKAQKLGIKKLAPERDVGKFESTVAVTQGVFTVALGHNSNTYQEAKAVEQAGASVWNVHAYNGMRGLTHREPMGVGAJVNLPNTYAELICDGHVHSPIACIDLMQQKGHDHVAMITDCRMGRAGSPGDYLLGFESVVVANGTARLKESGMNLAGSILSKLKDGLRNVVAWGIATPEAEIHMATXVEAVSVGIDDVCGQIKAGHAADFIVLDKDTLVATYLNQKAFDA

SEO ID 705

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AAT

SEO ID 706

MNREVTMSIESDFRKKRFIGSSLEEEFGFIKSDQEYIYCQTFMDNDFKAITISLDGKIAGKVIDSLEEYPLRLAANYNGSFVGEVRSAVMAIL
GDISDSCCKDPLLTKDQSNSRLAEKIAKTFEDSVDPFAKHPOYASYRVSGKWYALLFPLKMKGKLENVPQLSEDEVEVLNIKVNPQDM
EILLQKEGIYPSYHMSKKTWVSIVLDNTLSDIEIFKLVSDSRKLVSHNKKNSNEPEFWII PANPKFYDXXLIN

SEQ ID 707

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GAGTATTTAAAGAGAACAAAC'

SEQ ID 708

MSLATDYSRQTPIVEKLMAYGFKEKRDNGFYNERFMEGEFEAQLRIDEAGNIWDRVIDCCLDEEDYLPLQQAAWQGTYTGQVRRAAYLELLERLSVACFEATPFQSMQANRLAKHITKEWSDPMDYPFEKHPDLATYRVGGKWKYAMIFSSLADKLDQIPIERLVGQTCVEMTVKVNPKAFPQLLQQEGIYPAYHMSKKNWISIILDDKVTDKLWLTVTQSRLQVLNPNGLSNPNGPDYWVIPANLKYYDIDAFAANDVILWTQKAGIAVGDYVLIYITAPVKSIRYVCQVLETIDIPNEGYZRKNPNDKLMRLRKCOQYKDGLLSFDLMMKHGVAAVRGPRRLSPQLIAFLKEKEYFKENN

SEQ ID 709

SEQ ID 703
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CGTCAAACAAAAAGAAAGTCGTTTCCCATTAGAAGAATCCCTAGAACGCTATCTCGTACACTATTAGTGAATCAACTCAAGCAAGGACAA
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SEQ ID 710

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ALGVTSGHKAILGYDIAPNENNNAWSDLERFKQGVQQVSLVVSDFGNGLDQLIQQQAFPMAKQQRCLVHIGRNIAVKRADRALILEQFKTIY
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SEQ ID 711

ATGACTCAGTTACCAGAATTACTTAACCTCTAGCACAAAAACAAGATATTGATGAATTCTTCGCTCCCTTTAGAAAATAGCTATGAATGAC
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CAGTTGAAACAAAGTATGGCTTAGTCATTTAATCCTCCAAAGAGATCGAAACGGCGAGTTTACCGAGTTTATTACCATCTTATGCTAGACGA
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SEQ ID 712

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SEQ ID 713

ATGTTTCGAGCGATTGGATTGAGATAATTATGTTGACGACCTATCCTGCAAGAGGAGAGATTTTACCTTCAGAATTGCTGGCTTATGCA
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CGTCATGCGCAGAGTGTACCTAGCTCTATTTGGAAAGAGATGGCTGGTATTAGCTAATCATAAAATTTAACCTTGTAAGGAAA
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SEQ ID 714

MFSSDFGEIINVDDLSLQEERFLPSELLAYARDENESSFVRDIEGHLALVYQLLDTQGHVDDVRHVPRVIPVTLFLKEDGLFVLANKNINLVKK
ALNRVEKVDSPKHLLSLVTAFSKQYFDVLDTISEERDKLINDLRKPNKSNLARLANLQSGTVHLMGKTQNFEMLTDLQNIEQDKENTRNEKMQ
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SEQ ID 715

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SEQ ID 716

MKQMFLSSAIEFKEIETFEPGAWIKLNVNPSEESMKIADQFNIDISDLRAPLVEETSRIAIVEDDYTLIIVDVPIYERNNKSYYITMLGIIVTE
NAVITCLHDMLTFDHFNRRVKNFTFMKTRFVQIYLRYNAELFLTALRTIDRQSERLEAQLEAATRNELIDMMLEKSIVYLKASLKFNERIV
KKLSSSTSSLKKYIEDEDLLEDLTIETQQAIEAGTYENVLNAMTTTASIINNNQNTIMKTLALMTMALIPTVIFSAYGMFQNNWLPNGLEH
AFWYITLIAMLLSSFVVYIFIRKKWF

SEQ ID 717

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SEQ ID 718

MSKVRYGVUSTAKVAPRFIEGVRLAGNGEVVAVSSRTLESAQAFANKYHLPKAYDKLEDMLADESIDVIVVATINQDHYKVAKAALLAGKHVLVEK
PFTLTYDQANELFALAESCNLFLMEAQKSVFIPMTQVICKLLASGEIGEVISISSSTAYPNIDHVTWFRELELGGGTUVHMAPYALSYQYLFDAT
I THASGTATFPKGQSDSQSKLQLQSLNGVLDFLTTRNLPHEMIIYGTGEGRLIIPHFWKTTAHLKVRNNTSARTIQVDMVSDFEKEAYHSQMI
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SEQ ID 719

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SEQ ID 720

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SEQ ID 721

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SEQ ID 722

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SEQ ID 723

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SEQ ID 724

MTELSPKYNPAEVEAGRQYQWLDAVFKPKSGDQAKPYSIVIPPPNVTGKLHLGHADWTLQDIIIRQKRMQGFDTLWLPMDHAGIATQAKVEER
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VLLYTLKDLKRLLHPIMPFTVTEEYIQAQGSIVTVDPVVRPAFENEAAHKGVESLKDLRFLRAVRNARAEVNVAWSKPTILVKTADSELEDFFNS
NINYIKCFTNPEKLEISSAIAAPELAMTSIITGAETYLPLADILNVEEELARLDKELAKWQKELDMVGKLGNERFVANAKPEVVQKEKDQKADYQ
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SEQ ID 725

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SEQ ID 726

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SEQ ID 727

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SEQ ID 728

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EN

SEQ ID 729

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AGAAGA

SEQ ID 730

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RR

SEQ ID 731

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SEQ ID 732

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SEQ ID 733

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SEQ ID 734

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SEQ ID 735

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TCTGTAAAGTT

SEQ ID 736

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SCKV

SEQ ID 737
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SEQ ID 738
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SEQ ID 739
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TTTAAAAAA

SEQ ID 740
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SEQ ID 741
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SEQ ID 742
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SEQ ID 743
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TATAAAATGGTAAAGCCTTACGATATTCCAGATGAGTTATTGGAGCAAGGCATTAT

SEQ ID 744
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SEQ ID 745
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SEQ ID 746
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SEQ ID 747
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CAAGTGTCTTGTAGAT

SEQ ID 748
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QVLLD

SEQ ID 749
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TTGCTTCTG

SEQ ID 750
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LLL

SEQ ID 751
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SEQ ID 752
MKKKLLGMLIAISTVFLVACSTNSLNVKYYKVDGEKMLVLEINDESGIYHNEGNFVVTNIDTKSKSFVLKGGSAKYTVLYDVKS DGKLNVDLGN
FYNNASGKETYYKEGSKALEKALRDKE

SEQ ID 753
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ATGTTTTGATTCAATCTGTTAAACTCAAAGTATTCTTTGAAATAAAAATAATCATCTGTTCTGATGAAGAATTCAAATTTGGTAGAA
ACAAAATTAAAGGAAATACGAGTTAAGGCTAGTGATCCAGAAAGTGTAAATGCTTTGGAGATGAAGATTTCAGAATATGAGGAATTAAA
AAA

SEQ ID 754
MSTVAVRVDDQLKDDATELFQSLGLDMSTAVKMFLIQSVKTQSIPFEIKNKSSVSDEEFQNLVETKLKGIRVKASDPESVNAFFGDEDSEYEYF
K

SEQ ID 755
ATGTCGTTACAAAAGGAGGATAACCATGGCTAAAAGGAACTTGTGAAATTACGAGTTGATGTTGACTAAAGTGCAGTCAGATGATATTGTTG
AAACGCTTAGGTTATCTGTAAGTGTCAACTGCGATTGATGTTGAAATCAGATTATTTGACTGGGGTATCCCATTGATGTTCTACCTGAA
GCGCCTCAACGAGTTAATGTTGATTACATGAGTCAGGAGAAGTTTATGATAAGCTTACCAAGCTTGAAGATGCGAAAATTGCAACCCAG
GATGTCGGGAAATTCTATTCCAA

SEQ ID 756

MSLQKRRITMAKTGTLNLRVDDSVKAADDILKRLGIPMSTAIDMFNLQIILTGGIPFDVSLPEAPQRVNVDYMSQEKFYDKLITSFEDAKTCNPQ
DVGKFYFQ

SEQ ID 757

GTGACTTACCCAGATGGTCAAAAGATACTGTAGATGTGACTGTTAAGGGTCGATCCACGTACAGATGCCGATAAGAATGATCCACGCCAGGTAAA
GATCAGCAAGTCAATGTAGGTGAGCACCGGAAGGAGAAAGATTCTATTGGTAACCTTACCGATCTTCCGAAAGGTACAAACAGTAGCCTTGAAGACT
CCAGTTGATACGGCAACACCGGGAGACAAACCAGCAAAAGTTGTTGACTTACCCAGATGGTTCAAAAGATACTGTAGATGTGACTGTTAAGGGTT
GTCGATCCACGTACAGATGCCGATAAGAATGATCCACGTAAAGATCAGCAAGTCAATGTAGGTGAGAACACCGGAAGGCAGAAAGATTCTATTGGT
AACTTACCGATCTTCCGAAAGGTACAAACAGTAGCTTGAACACTTACCGATGGTTCAACAGTAGCCTTGAAGGTTCTATTGGTACT
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CAAGTCAATGTAGGTGAGCACCGGAAGGAGAAAGATTCTATTGGTAACCTTACCGATCTTCCGAAAGGTACAAACAGTAGCCTTGAACACTCCAGTT
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AACTGGTAAAGGAATAAACTACCCAGCAACAGGTGAGAATGCAACTCCATTCTTAATGTGAGCTTGCACAATTATGTATCAGTTGGTTTATTAA
TCTGTTCTAAGAAAAAGAGGAT

SEQ ID 758

SEO ID 759

ATCGCTAGAGCAGAAAATAACAAACAGCCGCTATTCCATTGCCAAACTGAGCGTTGGGTAACGAGTATAGCAATTGCGAGTCTCTTTAGGA
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GGCCTTATTCCTTAGGTATAAGCTTAGAAGCTGCCAAAGAGGAATTAAAAAAAGAAGTAGAAGAATCACGTTATCTGAAGCACAAGAACG
TATAAACAAAAATTAAACTGCACCAAGACAAAGATAAGCTATTATTCACTAGTGAGTATATGACAGCCGTTAAGGATCTTCAGCGTCT
ACTGAGTCTACTACTCAGCCAGTTGAGGCACCCGTGCAGGAGACACAGGCATCAGCTTCAGATTGATGTTGACAGGTGATTCAACATCAGTTACG
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TCTTCAGTAGCAGCTACAGACAAGCCGCTCCATCACTCCAGCTGAATCTCAGAGACTCAGACGCCACCACTGTTACTAAAGACTCTGATAAGCCA
TCTTCAGCAGCTGAAAAACAGCAGCCCTTCACTTGTTCAGAACAAACCGTTCAACAACCAACTCAGAGAGATCTGATAAAAAAGAAGAG
CAAGAACAGTCTACTCTCCAAATCGCTCATTGTCAGACAGGGTTAGGGCCCATGAGTCAGGTAAGTACTTGCTTCACAGGTGAAAAGCACAG
CCACTCTTATAGCTACTATGACTTGTCTCTATTGGCAGCTTTAGTCACAAACGCCAAAAGAAACTAAAAAA

SEQ ID 760

MRRANNKHSRYSIRKLGVTSIAISLFLGKVAYAVDGIPISLTQTTATTSENWHHDKDGLIPLGISLEAAKEFKKEVEESRLSEAQKET
YKQKIKTAPDKDLLFTYHSEYMTAVKDLPPASTESTTQPVEAPVQETQASASDSMVTGDESTVTTDSPEETPSSESVPAPALSEAPAQPAESEEPS
VAASSEETPSPSTPAAPETPEEPAAAPSPSPSEEEPSVAAPSEETPSPETPEEPAAAPSQPAESEESSVAATTPSPSTPAESETQTTPAVTKDSDKP
SSAAEKPAASSLVSEQTVQQPTSKRSSDKKEEQEQSYPNRSLSRQRVRAHESGKYL PSTGEKAQPLFIATMTLMSLFGSLLVTKRQKETKK

SEQ ID 761

GTGACTGTAAAGTGTGCGATCCACGTACAGATGCCGATAAGAATGATAACAGCAGGTAAAGATCAGCAAGTCATGTAGGTGAGACACCGAAGGCA
GAAGATTCTATTTGTAATTACCGAGTCTTCCGAAAGGTACAACAGTAGCCTTGAAACTCCAGTTGATAACGGCACACCGGGAGACAAACCAGCA
AAAGTTGTGAACTTACCCANNNNN

SEO ID 762

MTVKVVDPRTDADKDNTAGKDQQVNGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVETYPXX

SEQ ID 763

ATGTATAGAGCTATACAGAATAAAAGTAAAGGAGAATTATGTGTTAGAGGCTAAAAATAACAGTTATGACTTACAGACGAAACACGGTTT
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TATGATGTGAAAATGGAAAATAGATCCTAACATTAAATTACGTTAACCTGATTAAAAGCTAGTATGTCATTAGGCAAGGCCAAT
TATTTCACACAAACCTTCTGAAATTGACTACTGTGTTGGCAGCTAGTATTAAATTACAGTATTGAAAGACAGTGGAAAGTCTCATACGAAGGCTGAT
GGACAAGTGGATATTGAAACAGTTTCAATTGACTATTCAACATTCTCGACTTGGAGAGATAAAATAGATGAGTTAAAAGAAGCGAAGACCC
AAATGGCAGGAGGAAAGTCGCGATAAAAGTTTGTAAAGTTAGATGATATTCAAACAGTATTGATAATACTCTAAGGCCAATCAGCATTGCC
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TCAAAAGATACTGTAGATGTGACTGTGAAAGGTGTGATCCAGTACAGATGCCGATAAGAATGATCCAGCAGGTAAAGATCAGCAAGTGT
GGTAGACACCGAAGGCAAGAAGATTCTATTGGTAACCTACAGATCTTCCGAAAGGTACAACAGTAGCCTTGAAGACTCCAGTGTGATACGGCAACA
CCGGGAGACAAACCGAGCAAAAGTGTGACTTACCCAGATGGTCAAAAGATCTG

SEO ID 764

SEQ ID NO: 704
MYRAIQNKVKENIMFRRSKNNSYDTLQTQKQRFSSIKKFKGAAASVLIGISFLGGFTQGQFNISTDTVFAAEVISGSAVTINTNMTKVNQNGRAYIDL
YDVKGKIDPLQLITLNSPDLKAQYVIRQGGNYFTQPSELTTVGAASINYTVLKTDGSPTHKDQGVDIVNVSLTIYNSSAI RDKIDEVKKKADEPD
KWDEGSRDKVLVISLDI KTDIDNNNPKTQSDIANKITEVTNLEKILVPRI PDAKDNDPAGKDQQVN VGETPKAEDSIGNLPDLPKGTTVAFETPVDT
ATPCDKPAKVVVTPDGSKD TDVTVKVVDPRTDADKNDPAGKDQQVN VGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTPDG
SKDTVDVTVKVVDPRTDADKNDPAGKDQQVN VGETPKAEDSIGNLPDLPKGTTVAFETPVDTATPGDKPAKVVVTPDGSKDL

SEO ID 765

GTGGTAACCTATGATTGATTTCTACTGTTGAATCATTACACAGTCTCTAGGTCTAACTATTACTGTTGTGATCAAATTTCTGTATC
AGAGAGTATAATCCGAGAAAACATTTCATTTTCAATCATTACCTTATTAAAGTAACTTAGTAAAACCTAACATGATTTTATTTCAT
TATGGCTCTTTAGGAGAACCTTTCTTGTCACCATATTCAACAAATTATATTATCATGGTCCCTGGCGTAGCAATGTTATTGACCCCTTACTT
CTTAAAGAAAAGCTGACTGAAACACAAATCAATGCTAGTGAACAAGACTACTTTATTGATAGACTATCCAAATTACCTTCTCACTTAGTCAA
ATCCGAGAATTACTAATAGTAACCAATTATGTCTACTGGGGTTGTGAAAGATAAATTATCAGAGGCCCTTACATTACTACAGGAAAGGGTGGAGC

AACTCCTTGATCTAGATAAAAATTAAGCAATTCTAAACAGAATATGAGTTCTAACAAATATCAGTATCATTGAAAATAATATTCTAAAAGCT
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GCTGCTAACAGCAATTACTAGATGAAAGAGTAAAGAGTTCAATTACTTGGATTCCACTCTCTCTAATTTTCAAGGACATTTAA
AAAATAGTGGAAATTAGCCCACTAGAATAAGCAAAGCCTAACAGACAATA

SEQ ID 766

MVTHMIDFLLKSLHSLGLTITVCDQNFSVIREYKSEKTISLFYNHYLILSNFSKTQHDFLFHYGSLGEFLFLVHHIQQYIIIGPWRNSVIDPLL
LKKKLTEQINASEQDYFIDRLSQLPFFSLSQIRELLIVMYCLGVVKDQLSEPLHYTKGSNSFDLDKIKQFSKQNMSSYKYQHFENNILKA
VKSGSEFLLKETVEQFSNIVPILISGDELSEKNYSIMIYDRLSQATIQAGLDIETAYRARDRIKENESTISLNEVLKLRDTAILFYTQQVHSLK
KHLETPHSQTIVAVIRYLENNLNRFIKTEIAKECHMSESKLRKLFQKQEKHITIQQYFLNLKIEAKQLLDENKKVEEVSNLLGFSTSSNFSRTFK
KIVGSPLEYKQPKT1

SEQ ID 767

GTGCTCTATATGGTAAAGATAGACAAATTCAAGAAAACAGTACGGTAAAGATCAACTTTTACTCTCACTATGAAAGCAAAGAGTGTACTCAAGGAGCTGT
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AGTATCGCTACGTTATTATCTGAGCTCCCTATTTCAGCTTAAAGCTTACAGTGTGAAATTAGAACACAGTGTACCCCTAGATTGCGTGGAG
TATATTACAAAGGTGGACATTCTGAAGATTTCTAAACAAATTCTTATTCAGCTTATCGAGACCTAAAGTGGTGGCTTCATCAAAGACAG
AAAATGACTGTTGAAGATTACTAAACATTATTAACTATGGTAGAGAGG

SEQ ID 768

MSYMKDRQIKKTKVIAINYAFISLLQENDYSKITVQDVIGLANVGRSTFYSHESKEVLLKELCEDLFHHFLKQGRDVTFEYLVHILKHFBQNQD
SIATLSSDSDPYFLLRFRSELEHDVYPRLREYITKVDIPEDFLKQFLLSSFIETLKWWLHQQRKMTVEDLLKYLTLMVER

SEQ ID 769

GTGTCGATATGACAAAAGACAGACAAATCAAAAAACAAAAACAGCTATCTATAGTCCTTATTGCTTATTACAAAAAAAGAATATTGAA
ATAACTGTTGAGATATGATTACACTTGCTAATGTAGGGAGATCAACCTTTATGCACATTGAAAGCAAAGAAATGTTACTAAAAGAAACTCTGT
GAAGAACCTTTTCATCATTGTTAGGCAAAAAGAAATGTGACTTTGAGGACTATTGTCATATTTAAAGCATTGAAACAAATAAAGAC
AGCATTGCGACGTTGTTACTCTAATGATCCCTATTTCAGTAAACATTGTTACCTAACAGTGTGTTACCTAACATTGCGTGTGAA
TATATGACAAAAGACTATTCCAGAAGTATTCTAAACAAATTGTTATCTAGTTTATAGAAACCTTAAAGTGGCTCCATCAAAGGCAA
AGGATGTCGCAAATGAACATTAAAGTATTAGAGCTCATAAAAA

SEQ ID 770

VSDMTKDRQIKKTKTIAISAFIALLQKEYSKITVRDMITLANVGRSTFYAHYESKEMLLKELCEELFHHLFRQKRNVTFEDYLVHILKHFEQNKD
SIATLSSDSDPYFLLRFRSELEHDVYPRLREYITKVDIPEDFLKQFLLSSFIETLKWWLHQQRKMTVEDLLKYLTLMVER

SEQ ID 771

ATGGAATCTGGAACACCATCTAAAAAAAGTTCAGGGTTGATAGTAATTAGGAAAGTGTCTTAGATAAGATGAAAGTAGATATGGCAACTGATAAT
AATGGATCAAGGATATAACACGGTTCCAATTAAAGATAAGAGATAAACTAACATAGCTAACACCCTAGAAATATCTTCAAAAAA

SEQ ID 772

MESGTPSKSFRVDSNLGSALDKMKVDMATDNNGSRIYNGFQFKIRDITIIANHPRISSKK

SEQ ID 773

ATGACATCAACAAAAAGTGGCTATCGTTTATTAATATCAGCTTTCCGTCCTGAAATTCACTTTGAAAGTCATTCTCTCAGGAGCT
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TTTCATTAGGTATAAACGTTTACGGCTTTAGGAGCTCTTACAAAGTCTAATTCTTATAAGTGGATCTCTAGTCATGATAGAAAATATC
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AAACCTTCTAGATGGTCCAGATTGAGCTTACGGTGCATTACATGTAAGTGGACTTGCAGAAGTAAGATCTATCAATCAACTC
AAATATCTGGTCAATGGATGTATTGATAATCGAGCAATTCTACTGTTCTTAAATCAATTGATCTGAAAGATTGTAAGAGCTATTGCA
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SEQ ID 774

MTSNKKVAIAFLNISFSVLEFIGSLFFSGAILADAVHDFGDATAIGISATLEKKSKKDEDTIFSLGYKRSLLGALTSLILISGSILVMIEI
PKLWHPTPVYHGMFILAVIAIIINGLASFILHSGQSKHEEILSLHFLEDILGWLAIIIVISLILNWKPILYILDPLLSVAISTFILSKALPKLLSTL
KLFLDGVPDSIDYALHDELKGLSQVR SINQNLNWSMDGIDNR AIIHCCLNQLISEKDCRAIRTI CQHYKINDVTEIDSYSLREHQNHCPLKN

SEQ ID 775

ATGCCAGCAAGTAAAAAGTCACCATATTAAATCTAGTTTCCCTCATTGAAATTCTAGGAAAGTCTATTCTTGGGACATTATTCTTCCGGGTGCT
ATTAGTGGAGATGCTGTCACGATTGCTATGGTATCTAGCTATCTAGCTATTAGGAAAGGCTGTTAAAAGAGAGTCCAAAT
TTTCACTAGGCTATAACGATTGCTTACGGCTTACGGCTAAACGAAATCTAATACCTATTAGCCTGTTAGCTATTAGTAAATGTTAGCTCATCATT
CACTCTAACAGACAAAAAATGAAGAAATTAAAGCCTTCACTTTAGAGATATCCTGGGTGGTAGCCATTATCATACTGTCATGATCTTAA
AAATGAAACCTTGGTACATTCTGATCTTATTATCAATTGCAATTGCTTCTTTATATTCTAAAGCTTCTCAAAGTGTAGCTAGCAACTGCT
AACATTTTAGTGGTCTGTTCTGATTAGACTATTGCACTTTGCACTGGTACACTGCAACTTCTCATATAGTGTCTTAAATCAGCTT
AATGTTGGTCGATGGATGGTATTGATCATAGAGCAACTATACATTGCTGCTTGGAGAGAATCTACCAACTGAAACATTGCAAAAAACTATTAGA
CTGATTGTCAAAGGTACAATATAAAACTCAGTCAGTGGAAATCGATACTTCTTAAACGAACACCAACTGTTCTCTTCTAGTATT
GAAGTCAC

SEQ ID 776

MPASKVTTIIFILNLSFSLIEFIGTLFFSGAILADAVHDFGDATAIGISAILERKAVKKSPEPNFSLGYKRSLLGALTNLILISGSILVMIEI
PKLWHPTIVYDGMFVLAIFI IINGFASIIHNSQTKNEEILSLHFLEDILGWLAIIILSLILKWKPWILYILDPLLSIAIASFILSKALPKLVATA
NI FLDGVPD SIDYCTLHHELSQLPHIVSVNQLNWSMDGIDHRATIHCCCLRESTTEKHCKKSIRLICQRYNINSVTVEIDTSNLEHQNHCSSLSSI
EVN

SEQ ID 777

ATGACAGATACAATGATATTAAATGACAATCATAAAATACCAACTTTAGGTTAGGTACGGTGGATGATAGATAATGATAGGGTAGCTCAAGITGTT
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ACAGCTGAATCTTATTGCTTACGACTAAAATTGCGCTGAAACATAAAAGATTGAAAGTGTCTACAAATCAATTGATCAATCACTAGAAGCTTAA
GGGCTGATTATATTGATTAAATGATCATAGTCCACAGCCTTGGAGGAATGGCGTGAACAGATAAACTTTGACCAAGGAAATTGAA
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ATGGTCATGTTAACCTGCTGCAATCAAATCTTAGCTCACATCGGAAATACACCTTCGACTTGAATTGATTACTGTCAAAGTAAAGGTATTCAA
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AGTGACGAAGATATGTCGATATTAAACACTTATGTTGACGATTATGGGAATTCTAATTCCCTGTTAGTGGAAAA

SEQ ID 778

MTDMLNDNHKIPTLGLGTVMDNDRVAQVVKDAIELGYRHIDTAQAYNNEKGVGVIKESGIRTESLFVTTKIAAEHKDYESATKSIDQSLEAL
GLDYIDLMIHSPQPWEREWTDKHFQGNLEAWRALEDAQKSGKMSIGVSNFLEKDLENILKNGHVKPANQIILAIGHNTPDFLDIDYCQSKGQ
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SEQ ID 779

GTTGATGGTAACACAGTAAAAATGACAAGTGGCTATGAGATTCCGTTTAGGATTGGAACTTACCAAGCAGCCGATGGTGGAGAAGCTTACCAA
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GGGGTCTACAGAGAACATTATTATACAACAACTCTGGATGACGCCATTAGTTGAAGGGGCAAAGACGCTTACCTGGAAAGAGGCCAATGCCAAGCATGG
CGTCTTGGCTGGATTATGTTCTATCTTATCCATTGGCCAAACCCAAAGCTCTGGTAACACTGGAAAGAGGCCAATGCCAAGCATGG
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GCTTGGTCTGGCAGAAGGTTTATCCCTGCCAAATCGGTGATGAGCAGTCAAGGAAATATGGCTATTGATGTGAGCCTGACA
CAAGAAGATAAAAACAATTGCTATCTCAGGAATGTCAGCAGATTCTAACAGT

SEQ ID 780

VMVTVKMITSGYEIPVLGFETYQAADGEEAYQSTLAAIKAGYRHIDTAIAIKNEESVGRAIKDSVLREDFIFTKLWINDAHSYEGAKDALAASLD
RLGLDYDLYLIHWPNPKALRNTWKEANAQAWQYMEAVEAGLISIGVSNFMVHLEALQETAKITPAINQIRLAPCYQKEVVVDYCKANEILLE
AWSPLGQGEIFDNEMTQQQLANKYDKTVQVALAWSLAEGFIPLPKSVHDERIENMAIFDVSLTQEDKKTIRYLSGMSAIPNPDTTSF

SEQ ID 781

GTTGATTTGTTATTGTTCCCTTACACATGGCTGGCCAATGTCGCTTGTAAAGGCTGGATTGATGAAATTGTACAAATCATCAAGCTGCAA
AAAATG

SEQ ID 782

MLLFLPHMAVANVRLVRLDLMEIVQIILQKM

SEQ ID 783

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GCTGGATTGATGGAAATTGATCAAATCATCAAGCTGCAAAGGTGATAATGAGACTCTTAACTCTGTCACCTTACAGATGTAATGCAACTGGCATTG
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SEQ ID 784

MKVATFIEPGKVMITDTPKPVIEQETDAVIKIVRACVCGSDLWWYRGISKRESGSFAGHEAIGIVEEVGKVTDVDSKGDFVIVPFTHGCGQCPSCK
AGFDGNCTNHQAACKNVGYQGQYLRYTNANWALVKIPGQPSDYNDTNSLTLSDVMATGYHAAATAEVKEGDTVVVMGDGAVGLCGVIAAKMLGA
NRRIAMSRHKDRQELALTGATDIVEERGDEAVKRVLDLTLNQAGADAVLECVGTEQSVDTATQIARPGAVIRGVGIPQNPDMMTNNLFWKNIGLRG
GIASVTTFDKSVLLDAVILTHKINPGLVFTKSFVLDIQQKAYEAMDKRDAIKSLVIVD

SEQ ID 785

ATGAATTGGTGTATTACCTCTAACCTTATAAGAAGTTAAATATGAAAGCAGCAACTTACCTTCAACCGGAAATCTACAGCTCATAGACAAACCA
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GCCTGAAAGTTATTGATAATGATATTAGC

SEQ ID 786

MNWLTISPYKKLNMKAAATYLSTGNLQLIDKPKPVIIKPTDAIVQLVKTTCGTDLHILGGDVPACKEGTILGHEGIGIVKEVGDAVTNFKIGDKV
IISCVTSCHTCYYCKRGLSSHQCDGGWILGHILINGTQAEYVHIPHADGSLYHAPDTIDEALVMSLDILPTSYEIGVLPVSHVPGDNVCIVGAGPV
GLAALLTVQFFSPANIMVDSLQRLEAAKTFGATHHTICSGSSEEVKAIIDDITNGRVDISMECVGYPATFDICQKIIISVGHHIANGVHGKPV
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SEQ ID 787

ATGCAAGAAACAACAACTAAGTCTATCTTCTAACGGTGAAAAAAATCCATATGGTAAATTCTTATTGGGCAATCCTATCTCGCAGCATTAGCAAAA
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TGGCATGGCTAAAAAGATTCTGAAATTGCACTATTGCGATTACAGCTGGTAAGAGTGTGAGTTATGAAGCTGTTAGTGTGAGAAGAATATTCA
AGACTAGGT

SEQ ID 788

MQETTKSIFPKGEKNPYGEFFIGQSYLAALAKSPDGNVSVGNVTFEAGCRNNWHVHLDGYQILLVTEGSGWYQEEGKEAVSLKPGDVIVTDKGVRH
WHGAKKDSEFAHTAITAGKSEFYEAWSDEEYSLRG

SEQ ID 789

ATGAAAGAAAAACAAACAGCCGACGTCGTCATTAGAACATTGCAACCTGAATTGCCAGATATAATGATGATATTGTTGGTGGAGGTTGG
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CAATTTCGCAACAAACCGGAGTTACTAAAGAAGAAAATTGCTGACATTATCACTCACCTCGTTTTATGTTGGATGGCAAAGCTTGGTCAGCC

SEQ ID 790

MKEKQTAGRRQLEEFAPFARYNDDILFGEVWAKEDHLTDKTRSIITISALISGGNLEQLEHHLQFAKQNGVTKEEIAIDIITHLAFYVGWPKAWSA
ENKAKETWT

SEARCHED

ATGCTTAACTATTCAAGAAAATGAAAGATAACCTTGAAATTACAAGAAAATTAGAAGGTTAAATTATCCTTAAACAAGTTGCTAAAGACTG
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AAAAAAAGAGGGTAAAGAAGTTTATCCATTTCAGATTAGCATCTTCAGCAAATCGTTGGTACCCATTGAGACACCATGGCGTTAT

SEQ ID 792

MLTIQEMKDTTFELQENFRRLNYPIKQVAKDLQLNISEVESLSSLVDVTYPGDDVCMLRDYLEDMLKKEVYPFSRASHSANRWYPYETPWRY

SEQ ID 793

ATGCTATCATTCAAATTGTTGAAAGCCAGCAATGATACTTGTGGAGTAACTTAGAAAATGTAAGTCAAATCAAGAAGGTATCCAGCAAGCC
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CTTGCTATCGAGATATTACTAAATCTGAAAACAACTTAATC

SEO ID 794

MLSFQIVEKPAMILAGVTLEENVKSQEGIQQAIGICKTQPDRFDYSATYQVETSVQAPKGLEIIIRPSATYAVISVKGPMPSLQETWRKIIQGF
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SEO ID 795

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GCCCTTGTGATCGTGAACGCTTTAGGTTACAGGTTGTGGAACTGCTGAAATTCAAACAGAAGGTACTTATTACAAAGCAGCGAAAAATGG
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ACT

SEQ ID 796

MITQEMKEIINSQLAMVATVDAKGQPNIKGPKRSMLWDDKTFIYNENTDGQTRINIEDNGKIEIAFVDRERLLGYRFVGTAEIQTEGTYYEAKKW
AEGRMGVPKAVGIIHVERIFNLSQGANAGKEIT

SEO ID 797

ATGATAACACAAGAAATGAAAGATCTTATTAAACCAATTAGCAATGGTTGGCAGCGGTGATGCCAAGGTCAACCCATATTGGTCCAAAACGT
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GCCCTTGTGATCGTGAAGCGCTTTAGGTTACAGGTTGAGGAAGTGTCAAACAGAAGGTGCTTATTACGAAGCAGCAGGAAAAATGG
GCACAAAGGAGCATGGGGTACCAAAAGCAGTTGGTATTATTGTGAGCGTATTAAATTACAACTCTGGTCTAATGCAGGTAAGAAATA
AACAGTGAAGTCAAC

SEQ ID 798

MITQEMKLINNQLAMVATVDAKGQPINGPKRSMLWDDKTFIYNENTDGQTRINIEDNGKIEIAFVDRERLLGYRFVGTAEIQTEGAYYEAAKKW
AQGRMRGVPKAVGIHVERIFNLOSGANAGKEINSESN

SEO ID 799

ATGACAAAAAAACATCTTAAACCGCTGCCACTTACTACAGTATCAGTAGTGCACATACAGCCAGGAGGTATATGGATTAGAAAGAGGGAA
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SEQ ID 800

MTKKHLKTLALALTTSVSVTYSQEYGLEREEVKQEQTOSASSEDDWFEDNERKTNVSKENSTVDETVSDLFDSDGNSNNSSSKTESVSVSDPKQVPM
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AEYTSRLGENGKPSRLIDIDQKEIIDEGEIFNAYQLTKLTPNGYKSIGQDAFDNKNIAEVNLPESELETISDYAFAHMSLKQVLPDNLKVIGELA
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TENTYVNPLSLLWRATPDMDYTWKBLLEEDFTYQKNSVTGFSNQKLGVRRNKNLEIPKQHNGITTEIYGDNARFNRVDFOSKTLRKYLDLEEIKLPSTI
RKIGAFAFQSNNLKSFEASDELEEEIFKEGAFMUNNKRIGTLDDKLKLIKGDAAFHINHIYAIVLPESVQEIGRSAFRQNGALHLMFIGNKVKTIGEMA
FLSNKLESVNLSEBQKQLKTIEVQAFSDNALSEEVVLPPLNLTQTIREFAKRNLHEKEVKGSSTLSQITFNAFDQNDGKRFQGKKVVVRTHNNSHMLADG
ERFIIDPDPLSSTMVDLEKVLKIIEGLDYSTLRQTTQFREMTTAGKALLSKSNLRQGEKQKFQLEAQOFFLGRVLDLKAIAKAEKALVTKKATKN
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AYGNPILNVDEDNEGHTLAVATLADYEGLYIKDILNSSLDKIKAIRQIPLAKYHRLGJFQATRNAAAEEADRLLPKTPKGYLNVEVPMYRKQVEKN
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SEQ ID 801

SEQ ID 802

MKKHLKTVLTLTTVSVVTHNQEVFLSLVKEPILKQTOQASSISIGADYAESSGSKSLKINETSGPVDDTVTDLFSDKRTTPKEKIDNLNAKGPREQL
KAVTENTSESEKQITSGSQLEQSKESSLNKTVPSTSWEICDFITKGNTLVGLSKSGVEKLSQTDHVLVLPQAADGTQLIQVASFAFTPDKKTAIA
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FDNQITGKLSPRLMRLAERAFKSNSHIKTIEFRGNLSLKVICEASFDQNDLSQLMLPDGLEKIESEAFTGNPGDDHYNNRRVVLWTKSGKNPSGLAT
ENTYVNPDKSLWQESPEIDYTKLEEDFTYQKNSVTFGSNKGQLQKVCRNKNLIEIPKQHNGVTITEIGDNAFRNVDFFQNKTTLRKYDLEEVKLPSTIR
KIGAFAFQSNNLKSFEEASDLEEIKEGAFMNNRRIETLELKDKLVTGDAAFHINHIYAIVLPESVQEIGRSASFQRONGANNLIFMGSKVKTGLGEMAF
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SEQ ID 803

ATGACACAATCAGATGCATATCTCTCGTTGAACCGAAGACACGCTTAGAGATCGCACAGGTAAATTATCATTTACTTCGGATAAAAGAGGCTGTT
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AAACGAGGGTGTGGGTAGCACTTCTTAAACCACTTACGGGAATTGGTGTCTCAAATAAAAGGTATTAAAAAACTCAAGCTACTGTTATGACCT
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SEQ ID 804

MHQSDAYLSNLNAKTRFRDRTGNYHFTSDKEAVEQYMIIEHVPEVNTMVFITSIELKLDYLVSNNYYESDLKKQYNLEFICQIFEHAYAKKFALNFMGA
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KRGGVALCLTNLREFGAPIKGIKNQATGIVPVMKLLEDGSFSYANQLQRQGAGAVYLHAAHPEVLTFLDTKRENADEKIRIKSLSLGLVIPDITF
ELAKANKDMALFSPYDIERVYKGPMDSISITEEYETLLANADIRKTFSIARKLFQTIACHELFHESGYPYIILFEDTVNAKNPHKKEGRIVMSNLCEI
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SQEAIDFTDCFFYAMAYYAFKASNHLAKEKTFEGFSESSYADGSYFYQYTEQNFEPKTQRVNLLAEYGLTPSQEDWRKLVLQSIEIGLANAHL
LAVAPTSISYLSCTPSLQPVVSPVEVRKEGALGRVVPAYKIDADNVVYKKGAYEVGSEAIINIAAAQKHIDQAISLTLFMTDQATTRDLNK
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SEQ ID 805

ATGTCACAAACCAATGCCTCATACCTCTCATTAATGCACTGACCCGTTTAAAAACCAGACGGCAGCTACCATTTGATAGCATAAAGAACGTT
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SEQ ID 806

MSQTNASYLSLNTRFKKPDSYHFDSDEKEAVRYLEEHVSPNQMAFNLEDKLAYLINEGGYEQQAIFDAYPNLIDEKAFFHYAYQQGYRFLNLMG
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FQIAKENKDMALFSPYDICKRAYGKMDSDISITEEYKLLANPAIKKTYISARKFFQIATELHFESGYPYIILFDDTVNKRPHAKKGRIVMSNLCE
IAQVSTPFDLFFHAMAYYAFKASCQLAKEGAFAGTYSYDGTYFAKYLOQEDAKPQTAKVATLLQDYGFTLPTVADWQALVADIQKQFLANAH
LLAVAPTSISYLSCTPSLQPVVAPVEVRKEGSLGRIVPAYQIDQANYAYVERGAYEVGPKAIIDVVAQQKHDQAIISLTLFMTDQATTRDLN
RSYIQAQFKQNCASIYVVRQDVLAGSEQYDEDSLVTAPGASDETTTCQCSCMI

SEQ ID 807

ATGGATAGTACAGTGAAGGTGGCTATTTTACATCGAAATCTAACAAATACCCATCGTTGTTCAAAAGTTGGCTTCTAACCAGCGTATTCCA
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CAAGTTGCTACAGTTTAAATGTTGCAACAAATCGGAACATTGCCAAGGGTTATTTCTCTGAAATACCAATTGTTGACACTTATGCCATT
GCTGGACCTATTATGCTGCAAAATTAAATGTCCTTGCTTACATCAATTGAACTATTAGGCACTGCTACAGATGTCAAAAGGTACAGCGATT
CTTGCCCAATTCACTAGAAAGGATAAA

SEQ ID 808

MDSTVKVVFSSKSNNTHRNVQKLCACSNQRIPSDGSSILVTEYILIVPTYAGGGDDTKGAVPKQVVQFLNVRQNREHCQGVISSGNTFGDTYAI
AGPIIARKLNVPPLLHQFELLGTQEDVTRVKELLQCPFRKDK

SEQ ID 809

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GCCCTATCTTCAAAATTGCCAGTCCCTTATTACACCAATTGAACTATTAGGCACTGCTACAGATGTCAAAAGGTACAGCGATT
GCCCTTAAAGCATCACACACAGACAAGAAAACAAACACCTGATTACAGAAAGGACACACCCATGTCACAAACCAATGCTCATACC
TCTCAT

SEQ ID 810

MAELIIVYFSSKSNNTHRNVQKLGPAQRIPVDNRPLEVSTHYLLIVPTYAGGSDAKGAVSKQVIRFLNNPNNRKHKCKVVISSGNTFGDTFALA
GPIISQKLQVPLLHQFELLGTATDVVKVQAIARLKHHHDQKQTNNLITERTHPCCHKPMRHTSH

SEQ ID 811

ATGCAATCATACTATGATCGTTCTCAATCGCCACTTGAATGCTTCTATGCGTTCTGTTAATTGAAATAAGCTAAAC
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TTGGATGCTGATTGGCAGCAATTAACTCGGACTTTACTGCTTAACCTTATGATCTGCTGAGCTTCTGTTAATTGAACTTCTGCTCAGATT
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SEQ ID 812

MQSYYDRSOSPLDYALSEKAFPMRSVWNWLNLNDKDLEVWNRVTQNFWLPEKIPVSNDLNSWRQLITRTFTGLTLLDSVQATVGDIAQI
KHSQTDHEQVIYANFAFMVAIHARSYGTIFSTLCISQQIEEAHVVVDTESLQARSRLIPFYTGDDPLSKVAAAMMPGFLLYGGFYLPSR
GKLPNTSDIIRLILRDVKIHNYSGYKQQKVALSVEKQAEAKTFVFDFLLYQLIDLEKAYLYELYDGFDLAEDAIRFSIYNAGKFQNLGYDSPF
TEETEIRISPEVFAQLSARADENHDFSGNGSSYIMGITEETLDEDWEF

SEQ ID 813

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ACCCCTTGAGCAGCAGCAAATCGAAGAACAGCATGAATGGGTTCTCAACACAGAGCTGCAAGACGGTGGCGTCTTACGGGACGATTTTCG
ACGGGTGATGACCCCTTGAAATCAAGTAGCAGCAGCTATGAGCCAGGATTGGCTGATGGCGCTTACCTTCTTACCTATCAGCA
CGTGGTAAATGCAACACATCTGATCATCGCGTGAATTTCAGCAGAACAGTATTCAACAAATTACAGCGGTACAAATACCAACAAAAA
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SEQ ID 814

MTQHYYERSQSPIEYALSETQKQLRSINWNLNDDKLEVWNRVTQNFWLPEKPVPSNDLNSWRSLGEDWQQLITRTYTGLTLLDTVQATVGDVAQ
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RGKMPNTSDIIRLILRDVKIHNYSGYKQQKVALSPEKQAEKAFVFDFLLYELIDEKAYLRELYAGFDLAEDAIRFSIYNAGKFQNLGYESP
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SEQ ID 815

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SEQ ID 816

MIAMTKTIDWQINICLATYNGQKYLRLQQLDSIIQOQYTDWICLIRDGSTDVTAAIKEYVNRSRFIFIFINSNDDRKLGSRSFYELVNYKKADFY
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AVGNVAYISDSTVWLWRRQVGAESLNYYGRQYGVATFWQMINTSFDRASLIFAQVSDKMSLERKLFFSRFIELKNANLMRRIYLLSKLKLRRSKLKE
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SEQ ID 817

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CCAAATGACCATGAATTGGTAAACGGCTATGTTCTTATTGGATATGCCCTTACCCGCTTACCTGAAAGGTTACGGTTAGAAAA
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SEQ ID 818

MNINILLSTYNGERFLAEQIQS1QROQTVNDWTLIRDDGSTDGTQDIIRTFVKEKDRIQWINEQQTENLGVIKNFYTLKHQKADVYFFSDQDDIW
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SEQ ID 819

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-81-

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SEQ ID 820

MEEIGKVDKHSKKAILKLTLITTSIILMHNSQNVNAEEQELKNQEQLSPVIANVAQQPSPTTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
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EGAAPNAQVLMMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGKTADSLIINDLKVKLALKLASEKGFDVAVVAAAGNEGAFCMDYSKPLSTNP
DGYTVNSPAITLETSVASYESLTISIESEVETTIEGKLVKLPIVTSKPDKGKAYDVVANYGAKKDFEGDKFGKJIALIERRGGGLDFKJTHAT
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GLDKDGGKVVADGFYTYRLRYTPVAGANSQESDFKVQVSTKSPNPLSRAQFDETNRTLSLAMPKESSYVPTYRLQVLVHVKDDEYGYDETSYHYF
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SEQ ID 821

SEO ID 822

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IVTSAGNDNSFFGGKTRPLADHDYPGVGVTAAADSTLTAVASYSPKDQLTETATVKTADQDKEMPVLSTRFEPNKDAYAYANRGMKEDDFKD
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OQVKVNNDLASTLGSTRFEKTRWDGKDQDGKVANGTYTYRVRYTPISSEGAKEQHTDFDVIVDNTTPEVATSATFSTEDRRLTLASPKTSQPVY
RERIAYTYMDEDLPTTEYIPEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVTKLLEGHNSNKPEQDGSDQAPDKPETKPEQDG
SGQAPDKKPKETKPEQDGSGQTPDCKPKETKPEKDSSGQTPGKTPQKGPSRTLEKRSSKRALATKASTKDQLPTNDKDT
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SEQ ID 823

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TATCTAGAAGATAATTCCCATCTTGATATGGTTTATA

SEQ ID 824

MWNVKTFDNLTTTHELFQIYKLRVSVFVVEQDCPYQEVDDELDLICLHGMNWVDGQLAAYYRLIPEDDKVHLGRVIVNPDRKKGLGNOLVEYAIKFS
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SEQ ID 825

ATGGATGTCCTCAATTGACGAATCAAGGACGCCACATGTTCAAAAACAATTAAACTTCCATTCAAATACTATAATATCTCCAAGATTGCT
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SEQ ID 826

MDVSSIDESRTPHPKTIKLSIPNTIISSSKIATQAEAPT

SEQ ID 827

ATGAATGTTTAAACAGCGAATTCTTTAAAAATTAAAGCAATGGAATTAAATGGTAAGGAATAGGTTTTATAAAAAACACTAATCTT
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CGTAAGGAA

SEQ ID 828

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IAGIRTVMIRRAQASGEVQLIFITSKRLFDVVIELVRFEPKLTVAVNINASKTSIDYQGITEVINGQESINBEVLDYGFSLSPRIFYQLNPQK
TQILYSEAKVLDVKEDDDLIDAYCGVTLGAFAGKVKSVRGMIDIPEAIDAKENALYMGFTNTHYEAGKAEDIIPRWTSEGRANALIVDPR
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SEQ ID 829

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AAACGTTGA

SEQ ID 830

MVVVKVQKIPLKIKRGMINGEGIGFYQKTLVVFPGALKGEDIFCQITAVKRNFNAEAKLLTVNKASKNRVKACSVYETCGGCQIMHLAYPKQLDFK
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IAGIRTVMIRKAQASDQVQIIVVSSKEVRLANFIGELTKAFPVQVTKVALNSRNSKSSEIYGDETEIILWQGEAIHEEVLDYGFALSPrIFYQLNPQK
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SEQ ID 831

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TATTTA
SEQ ID 832
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SEQ ID 833
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SEQ ID 834
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SEQ ID 835
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SEQ ID 836
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SEQ ID 837
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SEQ ID 838
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SEQ ID 839
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SEQ ID 840
MKKNKEELNVLREKQVRKESRKTVMVLFTGATVBEAIKGLQELNISRLRAHIVVSREKKGFLFGKPKA KVEIEGITDEVTDINESVALKNIKNVP
SSV DVVEEYIEEVDETLEKEDVSQPELPKIDDKNVTTSEAIKIDLLPNIEAAQVTKYVENI IYEMDLDATIETTSKRQINLQIETPEAGRI
IGYHGKVLKSLQLLAQNYLHDRFSKSF SVSINVHDYVEHRTE TLDFSKKIARRVLETNEPYHMDPMNSERKTVHKTIA TIEGVESYSEGNDPNR
FVVVTKK
SEQ ID 841
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SEQ ID 842
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SEQ ID 843
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GAGGGAGTTAACCCATATGCAAGTGTATT
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GGGCTCTTTCCAAGCTTGTACTAGGG
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TGAGCTAGAATT
TCACAGCGGGACCCATT
ATATTTACCTGTC
ACTGGCGCCT
TATTACCTTT
TATCAACT
TTGTTAAC
AAAGCAGCT
GTTGAAAAAA
ATTGCTTAA
CTCTTATGACT
TTAATGCGTT
ATCATATT
GTAAACAAGCTTAA
ACTTGCT
ACTGGTGT
TTTATACT
GGACGGTGTCT
AATGCTTCAAGT
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ACAACCC
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AAAGGTT
CGAGAAGA
CAGTAAG
ACTGG
GCACATG
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CAAAGAGTT
AAACGT
CTAAGAG
AAAGCA
AGTAAG
AAAAAGAA
G

SEQ ID 844

MKKKLKTFSLILLTGSSLVACGRGEVSSHSATLWEQIVYAFAKSIQWLFSNHSIGLGIILFTLIIIRAIMMPLYNMQMKSQKMQEIQPRLKELOKK
YPGKDPMNRKLNDDEMQSAMYKAEGVNPyASVPLLIQLPVLWALFQALTRVSFLKVGTFLSLELSQPDPYIIPVLAALFTFLSTWLTKAAVEKN
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SEQ ID 845

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SEQ ID 846

LRKVLRVKNIKARIPLVLLVACGRGEVTAQSSSGWDQLVYLFARAIQWLSFDGSIGVGIIILFTLTIRLMLMPLFNMQIKSSQKMQDIQPELRE
ELQRKYAGKDTQTRMKLAEEQSALYKKYGVNPYASLLPLLIQMPVMIALFQALTRVSFLKTGTFLVLAQHDHLYLLPVLAAVFTFLSTWLTNLA
AKEKNVMMTVMIFYVPLMIFFMGMFNLASGVVLYWTVSNAFQVVQLLLNNPFKIIAERQRLANEKKERRRARKKAMKRK

SEQ ID 847

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ATC

SEQ ID

MSLLGYLW

YDFVVIARKGVEELDYQALEKNLHVLKIAGLI
SEQ-ID 849

TTGAAGAA

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CATGTTATCATGGCATTAGGGCATCAGCTGAAGTCAGAGGATTCGTTGGTATTGCCGTAAAGGGTGTCCACTCTTGAGTATCAAGAGCTTCAA
CAAAATTATCACATCATGTTAAAGTAGCACAATTGCTTGAGAAAGTTTGAGAGTGAAGAAAACAT

SEQ ID 850

LKKTYRVKREKDFQAFKDGSSTANRKFVIYHNRQDHFRVGISVGKKIGNAVTRNAVKRKIRHVIMALGHQLKSDEFVVIARKGVHSLEYQELQ
QNLHHVVLKLAQLLEKGFESEEKH

SEQ ID 851

MLALYALL

TKVTRLVAKQVANLLKHKVVLMHASKGLEPGTHERLSTILEEEEISQEYRSDDIVVVSGPSHAAEEAIVRDTITLITAASKDIEAAKYVQKLFSNHYFRL
YTNTDVVGVTAGALKNIIAVGAGALHGLGYGDNAAAIITRGLAEITRLGVQLGADPLTFSGLSGVGDLIVTGTSHSRSNRWAGDALGRGEKLED
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SEQ ID 853

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CTTGATTTAGGTCAAGCCCTATCAGATGTTGATGCCGCTTTTGTGCAACTAAAGTAACAGTATTGTGCTAGACAAAGTGGCCGCC
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SEQ ID 854

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LKNIIAVGAGALHGLGYGDNAAVITRGLAEITRLGVKLGADPLTYSGLSGVGLIVTGTSHSRNWRAGAALGRGEKLEDIERNMGMVIEGIAT
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SEQ ID 855

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SEQ ID 856

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EKPSPEEAPSNLAIIGRYLLTPEIFNILETQKPGAGNEIQLTDAIDTLNKTQRVFARKFTGDRYDVGDKFGFMKTSIDYALQHPQVKDDLKYIID
LGKSLEKTSKK

SEQ ID 857

ATGCCAAAGTCAGAAAAGCATTATTCCTGCTGCAGGTCTAGGAACACGTTTACCTGCTACCAAAGCTTGCACAGAGATGTTGCCATC
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SEQ ID 858

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VEKPQPEDAPSDLAIIGRYLLTPEIFGILERQTPGAGNEVQLTDAIDTLNKTQRVFAREFKGNRVDVGDKFGFMKTSIDYALEHPQVKEDLNKYYII
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SEQ ID 859

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SEQ ID 860

MIFLCYDRNLFLCDYNLLGSFSVNRIIIGLTLSSLVLTACGNRSDKSANKSDIKVAMVTNQGVDDKSFNFQSAWEGLQKGKKGTLKGNGF
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GVVVKRFEEAGFKAGVKSIDPAIKVAVSYAGSFTDAAGKTIATQYATGVDVIYQAAGGTGAGIFSEAKTENETRKESENKVVWIGVDRDQSQEGRN
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SEQ ID 861

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SEQ ID 862

MNKKFIGLGLASVAVLSLAACGNRGASKGGASGKTDLKVMVTDTGGVDDKSFNFQSAWEGLQSWGKEMGLQKGTFDYFQSTSESEYATNLDTAVS
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T1QVKVVDYAGSGFDAAKGKTIAAAQYAAAGADVYQAAGGTGAGVNEAKAINKRSEADKVVWIGVDRDQKDEGKTSKDGKEANFVLASSIKEVG
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SEQ ID 863

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GTA

SEQ ID 864

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KQNGSLLFKTWSILALMIFIIVSISLIGLSLV

SEQ ID 865

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SEQ ID 866

MILLFRRFILDDTVIKTISYYFPFVNRLNFYSNASGIWTFSNWCSYLSWRVWITSKSNARPVAIGDSDIYSYRLWSFFCQWINTIFCWSN
RRRLPLGPFLLYVLSGVMGNATFWLTPETVAAGASTSLFGLFAIVVLSFLGKNQALKDGLKSYQTLIVNLLMNLFLMPNVSMAGHIGGVGG
ALLSIVFPTKMRVITVKTKRMALVSYGIILVGVLVLGFL

SEQ ID 867

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CGTATAGGTTATGGTGCAGGTTATTTGATCGTATTGAGTGAAGGTGATACTATTAGTACTATTAGTACTATTAGTGTAGAGACAGGATTT
GTAGAAGAGAACGATGACGTTAGCAGTTAAGGAGGTATTATGTCTA

SEQ ID 868

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SEQ ID 869

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SEQ ID 870

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SEQ ID 871

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CTC

SEQ ID 872

MSHITFDYSKVLESFAGQHEIDFLQGQVTEADKLLREGTGPDSDFLGWLDPENYDKEFARILTAEKIKADSEVLVVGIGGSYLGAKAAIDFL
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AGESEGKDQKGIYPTSANFSTDHLHSLQFQIYEGYRNLFETVIRDVNPRKNVIPELAEDLDGLGYLQGKDVFVNKKATDGVLLAHTDGGVPNMFV
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SEQ ID 873

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SEQ ID 874
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 VIRYNGTRPAKTATWPKYNNYRADEKYQDIAKLLGLPAATPEEAVESYAKAVYDLGTRLGIKMNRDQGIDEKEWKEKSRELAFLAYEDQCSPANP
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SEQ ID 875

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SEQ ID 876

MTEGHNTVETTSVSVTIDALVQKGLAALEMRKLDEQEVQDYIVAKASVAALDAHGEALKHAYEETGRGVFEDKATKHLFACEHHVVNNMRHQKTVG
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SEQ ID 877
GTGCATTATAGTGATAGCGATACTACAGGGCTGATTATATGTTAGTAACGTCAAAAAAGCTATTCAAAAATCAGCTAACGAGCTGCAAAA
SEQ ID 878
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SEQ ID 879
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SEQ ID 880
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SEQ ID 881
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SEQ ID 882
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SEQ ID 883
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SEQ ID 884
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SEQ ID 885
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SEQ ID 886
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SEQ ID 887
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SEQ ID 888

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IILNDLEPGDVLFIDEIHRMPMAVEEVLYSAMEDFYIDIMIGAGETSRSVHLDLPPFTLIGATTRAGMLSNPLRARFGITGHMEYYEENDLTEIIER
TADIFEMKITYEAASELARRSRGTPRIANRLLKVRVDYQIIMGDLIIDDNTDKALTMLDVDHEGLDYDQKILRTMIEMYNGGPVGLGTLCSVNIA
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SEQ ID 889

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SEQ ID 890

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RARFGITGHMEYYQEKLDEIERTATIFEIKIDHEAARKLACRSRGTPRIANRLLKVRVDYQIIGDGIIITAQITDRALTMULDVREGLDYDQK
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SEQ ID 891

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SEQ ID 892

MLKHFGSKVRNLRVTRNITREDFCGDETELSVRLARIESGQSIPNLTKAHYIAKQLNVKLDILTGGESLELPKRYKELKYLILRIPTYADAERLK
LRECQFDHIFEEFYDNLPEDECLAIDSLOAKFEVYQTDINFGEVLCECFDKVVKYKEKYTLNDLIIIDLFLTCAVVSFKNNRAFTKEVFQTIKLT
LISQNHKLTAEDLFWFNFNVLLNCVVFGLCLNSEECLAEMLEVSRQTMVSTHDHKMPFLYFMYQWKYFITIDNDIKSAENAYQOSIMFSKMIDDKL
IKKLELEWQEDITGH

SEQ ID 893

ATGTTAGAACATTGGGAGAAAGTAAAGACTGTTAAGACTGAAAAGAGGATTAGTCGCGAGGACTTGTGTTGGGATGAGTCGAACCTTCTGTT
CGTCATTAGCACGGATAGAACTAGGTCAATCCATACCAAGTTAAGTAAAGTTATTGCAAAAGCTTAAACGTTAGTGTGGTTACTTA
ACTGATGGTGTGACTACCTAACGGTAAAGAATTAAACCTTATCTAAAGGACACCAATTACATGGATGATGGAAAATTACAA
GTACGAGAAGAGCAGTTGATGAAATTGGGATTATTGATAAAATTACAGAGGAAGAGAAAATAATCATTGATTGTTACAGGCAACTTTA
GATACTTATTGAGTGAGAAACTAACTTGGCATTGACTTACTTCAGAATATTAACTAAATAAGACTAAGGTACGCTTGGCAAATGAT
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CTATCAGAACAAATTGAAATTAGATGAAATTGTTATAAGATTATCATTGATATTCTACACTAAGCTTAAAGAAATTACCGA
CTTGATAATTGAGAAAGCGATTGAAATGAGTCAAAATTATGGCAAAATTCAAGATGGAATAGAATGCTTATTAAACTAATAAGATGG
AAATATTTTTAATCAAAACAAAAGATAAAAGCAGAACAACTATTATGAAGGCATGTTGGTCCCAAATGACAGCTGATCAGTATTG
GAAACAAAGTTAATTCAAGAGTGGGAAAAGATGTTAAAGTAT

SEQ ID 894

MLEHFGGKVVKLRLKRISSREDLCGDESELSVRLARIELGQSIPSLSKVIFIAKALNVSVGYLTDGADLELPKRYKELKYLILRIPTYMDGKQL
VREEQFDEIIFEDYDQLPEEKIIIIDCLQATLDTLSENTNFGIDLLQEQYFNQIKTKVFRQNDLILLELYLAYLDIEGMQYSDKIFYDSLLDN
LSEQFQFELDELFLIVNKIIIDISLSSLKNRDNLEKAIEMSQKIMAKIQDWRMPILKLIIEWKYFLIKQDIIKAQSFMKACLFAQMADQYL
ENKLQEWQEDVKS

SEQ ID 895

ATGATCGAACGTTATTACGCCCTGAGATGGCGCAATTGGACAGAGGAAAATAACCGTCTGGGGATGAGCTGAACTTGGCTGACGAG
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GACACGGCTCACGATGTTGGCTTCTACTGTCGGTTCTGAGACGCTTGGTGGAGGAGCGCAAGTGGGTGACTACGGTTGACGTGACTGAC
GTGCTGGACACTGCCCTACGGTTACCTCTACAAGCAGGCTAACGATATTATCCGCTGTGACCTTGAGAATTTCACAATATTGTTGCTGATAAGGCT
AAGGAGCACAAAGTTCACCATCATGATGGTGTGACCCACGGTGTACGCTGAGCCAACGACTTCCGGCTTAAGTTGGGACCTGGTACAGCGAG
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TACACAAACGTTGATGATAATTGAAAGACTAGGATTAGAAAAA

SEQ ID 896

MIERYSRPEMAAIWTEENKYRAWLEVEILADEAWAELGEIPKEDVAKIREKADFDIRILEIEQDTRHDVVAFTRAVSETLGEERKWHYGLSTD
VVDTAYGILYKQANDIIRRDLLENFTNIVADKAKEHKTIMMGRTHGVHAEPPTFGLKLATWYSEMKRNIERFEHAAAGVEAGKISGAVGNFANIPP

FVEQYVCDKLGIRPQEISTQVLPRDLHAEYFAVLASIATSIERMATEIRGLQKSEQUEEFFAKGQKGSSAMPHKRNPIGSENMTGLARVIRGHM
VTAYENVALWHERDISHSSAERIITPDPTILIDYMLNRFGNIVKNLTVFPENMMRNMESTFGLIYSQRVMLKLEKGMTREEAYDLVQPKTAYSWD
NQVDFKPLLEEDTKVTSCLTQEEIDELFNPIYYTKRVDDIFERLGEK

SEQ ID 897

ATGCTAGAACGTTATTCAACGCCCTGAGATGGCGGCATTTGGACAGAGGAAAATAACCATGCTTGGGTGAGAGATTTGGCTGACAGG
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AATCAAGTGGATTCAACCAACTTTAGAAGAAGACACAAAGTTACCTCTGCTTACACAAGAAGAAATTGATGAACTATTAATCCGATT
TACACAAACGTTGATGATATTAAAGCTTGTAGGGT

SEQ ID 898

MЛЕРЫРРЕМАИВЕНКИYHAWЛЕVEИLADEAWEALGEIPKEDVAKIREKADFDIDRILEIBQDTRHDVVAFTRAVSETLGEERKWHYGLSTD
VVDTAYGYLYKQANDIIRRDLLENFTNIVADKAREHKMTIMMRTHGVHAEPPTFGLKLATWYSEMKRNIERFEHAAGVEAGKISGAVGNFANIPP
FVEEYVCDKLGIRPQEISTQVLPRDLHAEYFAVLASIATSIERMATEIRGLQKSEQUEEFFAKGQKGSSAMPHKRNPIGSENMTGLARVIRGHM
VTAYENVSLWHERDISHSSAERIITPDPTILIDYMLNRFGNIVKNLTVFPENMMRNMESTFGLIYSQRVMLKLEKGMTREEAYDLVQPKTAYSWD
NQVDFKPLLEEDTKVTSCLTQEEIDELFNPIYYTKRVDDIFERLGEK

SEQ ID 899

ATGAATAGAATAATAACAGGGATATTACCTAGAATTCTAAAGATTCTAAAGATAAAAGAGAAAGATTACTATCTATAGCTTATATTACT
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TATTATGGAAGCCTTCAATTGGGATGGACAGCTTAACTACACCTCCATACAGTTTGATTGGAGTTGGAGGCTATA
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TTCTAGTAGAGATAAAAGAATTAGTCTGAAAGATGAGTATTGAGGAACTTGAATTGTTAGGCAATGGTAAATTGTTGCTAG
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TTAGAATTGATAAAATTCCAACACTACACTGAAATTAACTAGAATCAATTGATCATATAAATCAAAGATAATTGTTACTAACT
TATGAGGAATACATATACATCTAATTCTTAGGAGAAGTTGAAAAGCTAAAGAAATTAAAAGAGTGTGGATTATTAACTGAAAGATCT
TTGAATTATTGAAAAGAATATGATAAGCTAAGGGTAGTAAT

SEQ ID 900

MNRIINRDILPRISKISKNNKEKDLSIAYITWLIFIIFALGVVTVNLDLKPMFNQLIVNLLNIVYYMEAFILGMDSYLQYNLPYSFDFWSIFVEAI
NLFKVKVFLIAFIPSVKVLKESFFNEVVIILGAVTIIIVSFHYLEILIVVGLILLIIFAVSIGKNRVNFVQNLNYFEEVINYFEENPVKIK
EKSLIKFLTISFVVFVUDFAMVRLLNPNIKFSTILACSAILLAWLYQNKSVTETPFLKKLVYFIFIATLIGNLNKELSILETPLLFI
SIFTMDRIILSKEMRDLIISKSILFYDHENIKPSILLSEIKEIKYLENVDIGELELVRQMVRLLRELEEEFLILSDIYMKNGYEKIYFVQGNVYFIN
LELDKIPNVTNLKLILESIFDHNNQKIFIPKLYEEYTYILISLGEVEKAKEILKEVSDYLTEESLNLYFEKEYDKAKGSN

SEQ ID 901

ATGTCACCACTTATAGGGAGCGACAGTCACGCCAGCCTTATTGCGAGAAAGTCTTTTCAAAGATACGGTTTGAGAAATGCGGAGCAGATCAG
TCCCCTCGGGTAGCTGACAGACACAGGACATCCAGACCTCGGATCGACATTCTCAAACACTCATAGGTCAAACATCGCAACCGCAGCAGCTA
ATGTTCCCAAAGCCTCAACATCATGTAAGGTGCCACATCACCTCG

SEQ ID 902

MSPPYRERQSROPYLPESLFQRYGFEKCGADQSPAVADQLTQRHPDHRHRHSQTHRSKRNAQLMFPKPQHHRKVPQSPR

SEQ ID 903

ATGAGGAACAAGGAAAATCGCAGAGGAGTCAGCAATGAACTCATTAAAGACCATGGGATTATTGGTGGTGGTCAGCTGGGCAGATGATGGC
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TCAGCTGGTCACTACCCAGGGACTGATGCTCCGCATTCTCAAACCGTATCTTGGAAAAGACTTCTGCAAATAAGCTGGCGTACT
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AAAACCATCTGCTCAGCTCAGACCAACTAGCTGACAAGGCTAAGGAAATGGTGTGCAAGGTTAGGCGCAAGAACCTCAGCTATCAGGAAAC
CTCTGTGTTGAAATTGTTGCGACCGCAGATGACATCTGCTTAAGGAAATTGCGGACCCGTTCCGCAATCAAACCTCATGCTCCAGCGTTATGTC
GACTTTACAGTTGACACCCACATCTGGGCGACTGGGCGACCCGTTCCGCAATCAAACCTCATGCTCCAGCGTTATGTC
GGACAAACATGTCAGCAGGCAATTGACCATGTTGCCAAAACCTAGGCCACCTCCACATGTATGGTAAACTAGAAGCAAACATAACCGCAA
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SEQ ID 904

MRNKEKSQRSQAMNSFKTIGIIGGGQLGQMMIAAAIYMGHKVITLDPASDCPASRVSEVIVAPYDVEALGTLAARCDVLTYEVENVDADGLDAVV
SAGQLPQGTDLLRISQNRIFEKDFFLANKAGVTAPYKVVTSSLDEGLDLTKTIVLKTATGGYDGHGQKVRSAEDLPEAQQLANSACQVLEEFVN
FDLEISVIVSGNGQDVTFVFPVQENIHRNNILSKTIVPARISDQLADKAKEMAVQIAKKLQLSGTLCEVMFATADDIIVNEIAPRPHNSGHYSIEAC
DFSQFDTHILGVLGAPLPPPIKHLAPAVMFNVLGQHVQQAIDHVAQNPSPAHLHMYGKLEAKHNRMKGHTVFSDPDEVEEFEERMDF

SEQ ID 905

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GACTTTCACAGTTGACACCCACATCTGGGTGTTGGGCACACTCTCAGATTAGCTCACGCCCCAGGGCTATGTCATGTCAGGCTTA
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ATGGGACATGTGACGGTGGTGCAGGATGAGGTGAAGGAGTT

SEQ ID 906

MRNKEKSQRSQVVSFKTIGIIGGGQLGQMMAIAIYMGHKVITLDPASDSPA
SACQLPQGTDLRISQNRIVEKDFLANKAGTVVAPYKV
FDLEISVIVSGNGKDVTFPVQENIHRNNILSKTIVPAR
DFSQFDTHILGVLGAPLPTQLHAPAVMLNVLGQHQ
VAPYDDVEALGOLAARCDVLT
IRSAEDLP
QVLEEFVN
CQLA
AQC
VLS
TAD
VNE
APRPHNSGRYSIEAC
GKLEAKHNRMKGHVTF
FAKDADEKEF

SEQ ID 907

GTGGGTACGTCTCGAAATCAAAGATTCCGACTTACCGCATATTTTCTACGAAAATTTGACAAGTCGAAACGTCCTTGTATCTTAATATT
ATGCAACCAATTATTTCTATTATCATGGGTTCCAATCCGACTGGACAACCAGCAGGGCTGAAGTCTAGATAACTTGGCATTGCTTAC
GAGAAGAAGTCGCTCTGCCCACCGTAGCCGACCTCATGTTCAAGCATGCTGAGGAGGCGCGTGTGGTATCAAGATTATCATCGTGGG
GCAGGTGGAGCAGGCCACTTGCGGGTATGGTAGCAGCTAAAACACCCCTGCTGTGTTATCGGTGTGCTGTCAAATCACGTGCCCTCTCAGGTTTG
GATTGCGCTACTCTATGTGCAGATGCCCTGGTGTGCCCTGTGGCGACCATGGCTATCGGAGAACCGAGGAGCGACTAACGCTGCCCTGACAGCC
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CTCATT

SEO ID 908

MGTSSKS KISDLPHIFLRKFSTS RNVPLYLNIMQPIISIIMGSKSDWTTMQKTAEVLDNFGIAYEKVVSAHRTPDLMFKHAEEARGRGIKIIIAG
AAyahLPGMVAAKTTLPVIGVPVKSRALSGLDSL SIVQMPGGVPATMAIGEAGATNAALTALRILSIEDQNLADALAHFHEEQGKIAEESSNE
LT

SE0 ID 900

SEQ ID 909
ATGCTAAAGCACCTAGTCGCCCTGACGTGGTTCGTCTCGAAATCAAAGATTCGGACTTACCTCATATTTCTACGGAAAGTTCGACAAGTC
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GTTCTAGACAACCTTGCCATTGCTTACGAGAAGAAAGTCGTCTGCCACCCTACGCCAGACCTCATGTTCAAGCATGCTGAGGAAGCAGCTGGT
CGTGGCATCAAATCATCGCAGGAGCAGGTGGGGCAGCTCACTGGCTGGTATGGTGCAGCTAAACAAACGCTGCCCTGTTATCGGTGCT
GTCAAATCACGTGCCCTTCAGGTTGGATTGCTATATTCCATTGTCAGATGCCCTGGCGGTGCGCTGGCAACCATGGCTATCGGAGAACGCG
GGAGCGACTAACGCTGCCCTGACAGCCCTCCGTATCCTCTATCGAGGACCAAAATCTGGCTATGCGCTAGCTCATTCATGAGGAACAAGGA
AAATCGCAGAGGAGTCAAGTGGTGAACCTCATT

SEQ ID 910

MLKHLVALTVRLRNQRFRTYLIFIFYGKFRQVETPLCILIMKTPPIISIIMGSKSDWATMQKTAEVLDNFGIAYEKVVSAHRTPDLMFKAEEARGRGKIIAGAGGAALHPGMVAKTTLPVIGPVVKRSALSGLDLSYSLIVQMPGGPVATMAIGEAGATNAALTALRILSIEDQNLAHALFHHEEQGKIAEESGELI

SEQ ID 911

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SEQ ID 912

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EFSLFCAFANGDKFYIMPATQDHDCKRAYGDGKGLNTGGMAYAPVPHLPQSVVDTAVETIVKPVLLEGMAIEGRPYLGVLYAGLIL
TADGPKVIEFNSRFGDPQTIIQLPLRTSDFAQNIDIMMGIEPYITWQDGTVLGVVVASEGYPLDYKEGVPLPEKTDGDIITYYAGAKFA
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SEO ID 913

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SEQ ID 914

LANRVFLISRIVVYYHIFTMFQLLITNTLCKKANVYDIISNYNTKEVDVLKLVVVGSGGREHAIAKKLLASKGVHQVFPVAPGNDGMTLGGLDLVNI
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KADGLALGKVVAETVEQAVERAAQEMLLDNKFGDGSARVIEFFLDGEESLFAFANGDKYIMPTAQDHKRAFDGDKGPNTGGMAYAPVPHLP
QSVDVDAVEMIVRPVLEGMAEGRPYLGVLYVGLIITADGPVIEFNSRGDPETQIILPRLTSDFAQNIDDMGGIEPYITWQKDGTGTVLGVVVAS
EGYPDYEKGVPPEKTDGIITYYAGVKFSENSELLLSNGGRVYMLVTTEDSVKAGQDKIYTQLAQQDTTGLFYRNDIGSKAIRE

SEQ ID 915

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GAATTGTTTGTAAATATTAAAAGCCATGAGACCATCAGTCACAATTACGGCTTCTCAAATGACAACACTAAAGAAGTATTGAAATT
CAAGAGATGATTCTAAATCTGCTGATTTAGCTGAAGAACAGCTTCAAGAAGTATCACATGATTGAGCAAGCTGATCGTGTATTGAAATT
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SEQ ID 916

MTIYDQIESALDLMDLEREIAKYFMQPIKSDALASTIVTKQLHISQAALTRFAKKCGFKGYREFVFEYLKSHETISQOLYGLQNDNTKKVFMNY
QEMISKSADIIDEELQLEVSHMIEQADRVYFYKGSSSLVAKERFKIRLMRLGVICEALDDTDSFSWTSNSIVNDCLVIAFSLSGNTNSIGALKIA
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SEQ ID 917

GTGTGCTTGTATGCCAAAAACCCGCTAATTACCAAATCGAACATATTGGAACATATGACCAAGTTAGAAAAAGGGATTGCTCATTT
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SEQ ID 918

VCFAMPKNHLITKIEASLEHMSTSLEKGIAHFFITDLPQELTASEIVKRLHISQAALTRFAKKCGFTGYRAFAFDYLHSLQESQETFQSIHLEL
TKRVLMDYDALINKTYELVNEEKLLNLAKLIDS SERVYFFGKGSGLVAREMKLRFMRGLICDAYSDTDGFTWANSVNENCLVFGFSLSGKTNS
VITALHQASQRGAKTVLTTDNQTEFDDSLDIIIPVSSTHQLHYGNRVPQFPLIMMDIIYAYVLAIDKPHKEIFKNTIIDKENNDL

SEQ ID 919

ATGATTGAAACAATGCTCTAGATGACATGAGAGAATACCTAGGTCAGACCAAATTCCGAGGATTTGATGACTCTGGAAAAAACAAACATG
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TCTATTGCTATGCCAAATTGTTTACCCCTAAACAAATAACCTATCCTGTTAGTTTCTGTTTCTGTTTATGTTTCTGTTTCTGTTTCTGACTGG
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AAAAAGCATTTTATTACAGATTGACATGATCCAATGACAGTGAAGTAAAAGACCATATTGATCACTGACAGGAAGTCAATTACA
AAGCAAAAATCGAG

SEQ ID 920

MIETMSLDDMREYLQDQIPEFDFFWKQTMKYQGNIEYRLDKDFNITFAQAYDLHFKGNSNSIVYAKCLFPKTNKPYPVVFHGYQNQSPDW
SDQLNVYAAGYGVVSMVDVRGQAGQSQDKGHFDGTVKGQIVRGMISGPNHLYKDIYLDVFQLIDIIATLESVDSNQLYSYGWSQGGALALIAAL
NPKIVKTVAVYVPLSDFRVLDLGGVSEPYDELFRYFKYSDFHKTEENNVLKTLAYIDVKNFAHRISCPVLLTALKDDICPPSTQFAIFNRLST
KKHLLLPDYGHDPMTVQVKDHIFDQLTGSQFTKQKIE

SEQ ID 921

ATGACAGAACAGTAGCAATTGATATTGGCGGTACAATGATGGCTTGTGAGGCAAGTGGCTTGGATAATTAGGTTGATTGAGGCAAGTGGCTTGGC
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GCGCTTGTCTACTATTGAAACAGGTATTGGTGGTGTCTGATTATTGATAAAAACAGTTTCTATGGCTTGTGAAATTCTGCTGTGAGGTTGGC
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SEQ ID 922

MTRTVAIDIGGTMKHGIVDNLGICIVEASELATEAYKGPGILQKVCQIIDNYLAEGSIDGIAISSAGMVDPEGCFYSGPQIPNYPAGTQFKKL
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WDGRRIFQEAKGNEKCIASIDRMINYLGQGIANMVYVNPKEVVLGGGIMAQKDYLQDKLSESLSKRNLTSLAETAIIVFAQHENQAGMLGAYHH
FKNRG

SEQ ID 923

ATGAAGCATTATTTAGCAATTGATATTGGGGTACTGCTATCAAGTATGGCTGATTCTGAAACAGGGAGACCTGTTGGAAAAAGAGGAAATGGCC
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SEQ ID 924

MKHLAIDIGGTAIKYGLISETDLLEKEEMATEAYKGPSILEVKVGLVKTYQDQMDLAGVAISSAGMVNPDEGEIFYAGPQIPNYAGTQFKKEI
EETFGLPCEVENDVNCAGLAEAAISGSAKDYPVALCLTIGGIGGCLLFNSQVFHGSSHSACEVGVLHLSDGQFDLASTTALVQEVVFLAYGDDISQ
WDGRRIPEQAKAGDAICIAISKQVDYLQGQIANICYVVNPVVVLGGGIMAQKDYLADKLKTALDSYLVSSLAKKTQLKFASHGNAGILGAYYH
FKQKNERSCSFITLEKIENNLLASS

SEQ ID 925

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TATGCTGTGATCAAAGCTGATTGGAAATCAATGAGCAACTAATAGGTTCCGTTACCTTACGATCTGTAACAGAAGATAAACCT
ATTATTAAGAGGCAGCAGAAATGATTAGACATGCTAAAAACAGTTTGT

SEQ ID 926

MKDLQKYQGIIPAFYACYDDKGDICPERVKALTNYFIDKGVQGLYVNGSSGEICIYOSVADRKLVLLENVMSVAKGKLTIVIAHVACNNNTKDSVELAMH
AEAIGVDAIAAIPIPYFRLPEYAIADYWNNTISQAAPQTDFFIYNIPLAGVALTSLYRKMLQNPQVIGVKNSSMPVQDIQNFVAIGENHIVFNG
PDEQFLGGLRMGAAAGIGGYGTVMPPELYTLNQLIVDKDLEKARELQFTINDIITKLCSGHGNMYAVIKAVLEINEQLTGSVRLPLASVTEEDKP
IIKEAAEMIRHAKKQFC

SEQ ID 927

ATGACAGATCTTACGAAATACCAAGGCATTATTCTGCCTTACGCTGTTACGATGACCAGGGGAATATCAGCCCTGAGCGTGTGCGCTGCCTTG
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TTAGAAAATGTCATGGCAGTCAGGCAAGCTGACGATTAAATCACGTTGCCTGCACAAACACTAAAGATAGTATTGAATTGGCAGCTCAT
TCGAAACGTTGGCGTGGATGCCATTGAGCTATCCGCTATTTCGGGTTACAGAATATGCGTTGCTGATTATTGGAATGCTATTTC
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CAACTTATTGCTGACAAGGATTAGAAAAGCCAAGGCCCTCAATATACTATTAAATGAGATTATGGTGTCTTGTGCTCACGGCAATTAGT
TATGGGTTATTAAGAAGTACTTCGTTAAATGAGGTCTGATATTGGTCTGCTGATCACCTTAGCTGAGTTGGTGTAGGAAGATAAGGTT
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SEQ ID 928

MTDLTKYQGIIPAFYACYDDQGNISPERVRALTQYYIDKGVQGLYINGSSGEICIYOSVFDQLVLLENVMAVAKGKLTIVAHVACNNNTKDSIELAAH
SERLGVDAIAAIPIPYFRLPEYAVADYWNNTISQAAPQTDFFIYNIPLAGVALTPSLYKTMANKRVLGVKNSSMPVQDIQTFCAIGGDDHIVFNG
PDEQFLGGLRMGAAAGIGGYGTVMPPELYTLNQLIVDKDLEKARELQFTINDIITKLCSGHGNMYAVIKAVLEINEQLTGSVRLPLASVTEEDKP
ICQRAAALINQAKETF

SEQ ID 929

GTGAAAAAAGCAAATCAATTAAATAGCAGCGATTGGTAAACAACCCCTTATGCAAGGGTCAATGTTGTTTGATCTGGCATTACTAAC
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GCTTACCGCTTGCCTACTTTAAATTATTTACAAAACAATTGCTTACAGCAACAAACAGGAGATTATCAA

SEQ ID 930

MKKANQLIAAIFDVNNPFMOCNCNVFDLALLNLLMFITCLPLVTIGAKISLYRTLWQKLEGDQTNLLILYIKHLKKEWFQGMLLGLVELSILVVI
IFDLTILHYQIGFIVSFLKITCYAFLLTVMTSIYLFPMARYEMSLLDTVKKSFIMACLNLKWTGVLMFLLIMTFIMVQSSLFMLTVSAIFIF
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SEQ ID 931

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GTTAGTCAGCTTGTACTACTTATAGCTCTCATTTAAATTACTTTAAAGTGGCTACGCCCTGGCTTATTGAGCTGGATAATGACTATT
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CTCTTTTGCTACGCTTACCTCAGGGCTCAAAAGAGACCTTCCATCTACGCTGTTAAGCGAAGCTTTTATTAGCAGGACTCTTTTCCA
TGGAGTTGCTTCTGGCTTTATTGCTCAGGATATTAGCCTACAATTGCTCTGTTAACGTTATTGGAGGGCTGTTGCTAGCTAC
ATCGGCATCAGTAGTCTAATTCTACTTGATTATCATGGAATCTCTTCTAGGCGATCCCACCTAATAATGACATTGAA

SEQ ID 932

LTSKKQHLHSLFKLDSKWMRASAALFDLLVFNLFLSCLPLLTIGVAKMALYASLLDWREGQVSQQLVITYSSHFKYFKSGRLGLIELGIMTI
CLLDLFLIRNQSGLVLQGFKVLCVAVLFLVVLFLYAYPOAVKRDLSLSTLFKRSFLLAGLFFPWFSFAFIACILTIFSQQLSLLTFLGGVSLLAI
IGISSLTLYLIIMESLIRRFPPLNNIE

SEQ ID 933

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CATAAAAAATACCTGATATACATTATGTCATTGAAGGACATGAAGGTTATCAAATTGGAAAAGGTGATAAGGAGAGGAGAAATACTTAGGC
GATATAGGATTATCAAGTGTCAAGAGAGACTCTTTGATTGAGAGATAATTATAGCCTTCTTCCAGAAGAAGCTCATGCCAAAT
GGTATGGGAAAGTCTAGGTAATTATGTCAAAAAGGGTATTGAAAGTGTAAAGGCG

SEQ ID 934

MIYDHLLNTHYKDINPNLDAIDYLLSHDLRNLDIGTYHISPEVILMVQSNQLSESFDHIFEYHKYLDIHVIEGHEVILKGDKVVEEYLG
DIGIFCKSEETSFLRDNYIAFFFPEEAHQPNMGSLGNVKKVGLVLM

SEQ ID 935

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AGAATTATCAATTATGGGGATACATGATACCTTATGGGCGGTTATTACCTCTTGTGTTGGCCTTTGGGGTCTCTTGATGAAAACAGTT
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SEQ ID 936

MKKKTF SAYNFLTALILCLLTVLFIFPFYWIMTGAFKSQPD TIIIPQWWPKAPTL ENFKALT VQNPA LRLWLN SVFISIMTMFLVCTSSMAGYV
LA KKR F YGQ KILF SFL FIAA M ALP KQV VL VPL VRII NFM G IHD TLW A VILPLVGWPFGVFLMK QFSE NI PTELLESAKIDGC GEIRTF INV AFPIVK
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SEQ ID 937

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CAAATCCAGCCTTAAATGGTTGTTGGAATAGTGTCTTATTCCGGTGGCGACCATGTTCTGGTTTGTGAAACCTCCCTGGCTGGCTATGCT
TTGGCAAAAGCGGGTTTATGGACAGCGCTTGGTTTGTGATTTTATTGCTGCTATGGCCTTGCCAAACAGGGTTCTAGTGCCTTGTG
CGGATTGTAATTATGGGAACTCATGACACTTGGCGCTGTATTGGCCTCTGGCTGGCATTGGTGTTCCTTATGAAACAGTTC
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SEQ ID 938

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SEQ ID 939

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SEQ ID 940

MRTNKLKMRETMIAAYAFLAPILLFFLIFVFAPMVGMFVTSFFNSMTQFTFIGLANYNRMFHDSIFMKSILINTVIIVIGSVPVVVFFSLFVAANTY
EKNVFSRSFYRCVFFLPVVTGSVAVTVVWKWIYDPMMSGILNYIJKSGHVGIEQNISWLGDKH WALLAIIIIILTTSGVQPIILYIAAMGNIDNSLCE
AARVDGANEQMVFQWQIKWPSLLPTTLYIAVITTINSFOCFA LIQLLTSGGPNYSTSTLMYYLYEKAFKLSEYGYANTMGVFLAVMIALISFAQFKI
LGNDVEY

SEQ ID 941

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AAAATTAGGTAATGATGTGGAAAT

SEQ ID 942

VFLTSGFFSMHMSNGHWKEAFLFRKVQEKKVEFQVNVLKLMRRTLISYAFLAPLVFFFVIFVLIPMIMGFTSFFNYSMTETFTVGFANYARMFQDPIMFKSLINTLIVIGSVPVVVFSSLFVAAKTYDKNVARSFYRAVFFLPVTGSAVTVVWKWIYDPMMSGILNYVLKYAHVIEQNISWLGDKHWWALLAIIVILLTTSVGQPITLYIAAMGNIDNSLVEAARVDGATEFQFWNIKWPSSLPTTLIYAVITTINSFQCFALIQLLTSGGPNSTSTLMYYLYEKAFKLSEGYANTMGVFLAVMIAISFAQFKILGNDVEY

SEQ ID 943

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SEO ID 944

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KTQAKLLESKVDYLEVPFPSEDGPKDLEYLVNGFAVFNNKDENKVKASKKFITFIADDKKWGPKDVRGAFPVRTSFGDLYKGDKRMMKISKWT
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SEQ ID 945

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SEQ ID 946

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SEQ ID 947

ATGCCACATCTAAGTAAAGAAGCTTTAAAAAGCAAATAAAAGCATTATTGTCATGTCAAGCTTGCCTGGGGAGCCTCTTAACTGAA
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AAATATCTGAACAGTTGTTAATGGTCAATGAGTACTTTGAAGAAGGAAAATGTTGAAGCAGGAGTTGATTGTTGGGTACAACCTCTA
TCTGGATACACAGATTACAGCCGCAAGAAGAAGGACGGATATAGAACCTCTTAAAGCTCTGTCAGCCTGGTATAAGATGTTGATTGCGGAAGGT
AAAATTCTACTCTAACGAGGCTAATGAAATTATCATATAGGTGTTGCAAGGAAATTGTTAGTTGTTGGCTATCACTAGACCAAAAGAAATAGCG
GAGCGTTTACATCAGGACTTAGT

SEQ ID 948

MPHLSKEAFKKQIKNGIIVSCQALPGEPLYTESGGVMPLLALAAQEAGAVGIRANSVRDIKEIQAETVNLPIIIGIIKREYPPQEPFITATMTEVDQL
ASLDIAVIALDCTLRERHDGLSVVEFIQKIKRKYEQPLLMADISTFEEGKNAFEAGVDFVGTLSGYTDYSRQEAGPDIELLNKLQAGIDVIAEG
KIHPKQANEINHIGVAGIVVGGAITRKPETIAERFISGLS

SEQ ID 949

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CAAGGCCAACACGACCTACCAATTATCGGATATCATCAGGTTAAACCGCCGCAAGAGCCTTATTACGGCAACAGATGACCGAAGTGGATCAATT
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GAAAAGTACCCCAATCAGCTTTGATGGCAGATATTGACCTTGTGAGTGAAGGACTAGTGGCCATCAGGCTGGCATTGATTTGTTGGAACACC
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GGAAAGATTCACTCCCCAGAAGAAGGCAAGAAAATTAGACTTAGGTGTTGGCAGGTATTGTTGTTGGAGGGCCATCACAAGGCTAAGGAATT
GCAGAGCGTTTATCGAAGCGCTAAATCC

SEQ ID 950

MDKPTKEKLMEQLKGGIIVSCQALPGEPLYSETGGIMPLMAKAAQEAGAVGIRANSVRDIKEIQAIDLPPIIIGIIKKDYPPQEPFITATMTEVDQ
LAALNIAVIAMDCTRDRHDGLDIASFIRQVKEKYPNQLLMADISTFDEGLVAHQAGIDFVGTLSGYTDYSRQEAGPDVALIEALCKAGIAVIAE
GKIHSPPEAKKINDLGVAGIVVGGAITRKPETIAERFIEALKS

SEQ ID 951

ATGAAAATGAAATAAAAGGTACTATTGACATCGACAATGGCAGCTTGCCTATTATCAGTCAGTCAAGCTTGCAGCACAAGAACAGATAACGACGTGG
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SEQ ID 952

MKMNKKVLTSTMAASLLSVASVQAQETDTWTARTVSEVKADLVQDNKSSYTVKYGDTLISVISEAMSIDMNVLAKINNIADINLIYPETTLTVT
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PVKSITSEVPAKEEVPKQTSTSVCQSTTVPSPASVAAETPAPVAKVAPVRTVAAPRVASVKKVTPKETGASPEHVSAPAVPVTTSPATDSKLQAT
EVKSPVVAQKAPTATPVAQPFASSTTNAVAAH PENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGTONQALGNKVAQYSTQNM
ANNISVVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHSFNK

SEQ ID 953

ATGATTATTACTAAAAGAGCTTATTGTGACAAGTGTGCTTAGTACCTTGCGACAGCGCAGGCACAAGAGTGGACACCACGATCG
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CCTGAAAATTCTGCTCTGGTACAGTGTCTAACATGCCATTGACCATATGGCAGAGCGTGGTATTTCATACGTTATTGAAACAGCAGT
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GTCTCTTTAATGCT

SEQ ID 954

MIITKKSLFVTSVALSILVPLATAQQAWEWTPRSVTEIKSELVLVDNVFTYTVKYGDTLSTIAEAMGIDVHVLGDINHIANIDLIFPDILTANYNQH
GQATNLTVQAPASSPASVSHPSSELPQASATSQPTVPMAPPATPSDVTTFASAKPDSSVTASSELSSTNDVSTELSSESQKQPEVPQEAVP
TPKAETTEVEPKTDISEAPTSANRPVNPESASEEVSSAAPAQAPAEKEETSAPAAQKAVADTTSVATNSGLSYAPNHNPMAGLQPQTAAFKE
EVASAFGITSFSGYRPGDPGDHGKGLAIDFMVPENSALGDQVAQYAIHDHMAERGISYVIWKQRFYAPFASIYGPAYTWNPMRDRGSITENHYDHVH
VSFNA

SEQ ID 955

TTGAATAAACTGGTTAGTTAAGGCAAGTCTTAGTTAGGTGGTATGGTTTATCTGGGGTTCCCGAGTTTACCGGATACTTATGTCGGT
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CGCGTTGACAACAGTCAAGAACTGCTTACAAA

SEQ ID 956

MNKWLVKASSLLVGGMVLSSGRVLADTYVRPIDNGRITTGFNGYPGHGVDYAVPTGIIIRAVADGTVKFAGAGANFSWMTDLAGNCVMIQHAD
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LKVVYRVDELQKVNGVWLKNNTLPTGFDWNDNGIPASEIDEVDANGNLTADQVLQKGGYFIFNPKTLKTVKPIQGTAGLTWAKTRFANGSSVWL
RVDNSQELK

SEQ ID 957

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CAGGCTAACGGACCACCTGACGGTGGCTAGCATCAGATGCCATTGCGGACAACATTGAGAAATCGCTGCCAGGGATCAA
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TTAGACAT

SEQ ID 958

MTKRALISVSDKSGIIDFAKELKNLGWDIISTGGTKVALDDAGVETIAIDDVTGFPEMDGRVKTLPNIHGGLLARRDADSHLQAACKDNIELID
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QVGEAKPEKLTITYDLKQAMRYGENPQQDADFYQKALPTDSIASAKQLNGKELSFFNNIRDADAAIRIIRDFKDSPTVVALKHMNPCTGIGQADDIE
TAWDYAYEADPVSIFGGIVVVLNRDVAATAEKMHPIFLEIIIAPSYSEEALAILTNKKNLRILELPFDAQQAASEVEAEYTGVVGGLLVQNQDVVA
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SEQ ID 959

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TTAGGCAT

SEQ ID 960
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SEQ ID 961
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SEQ ID 962
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SEQ ID 963
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CGCATCCAGAAACCGAATACCAACTCTACCCAGCTGTCTAGATAGCTGGGATAAAAGAGAAAA
SEQ ID 964
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SEQ ID 965
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SEQ ID 966
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SEQ ID 967
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SEQ ID 968
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SEQ ID 969
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SEQ ID 970
MSEKNAYAQSGVDVEAGYEVVERIKKHVARTERAGVMGALGGFMMFDLSQTGVKEPVLIISGTDGVTKLMLAIKYDKHDTIGQDCVAMCVNDIIA
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SEQ ID 971

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CAAAAGTGAAG

SEQ ID 972

MTYEVKSLNEECVFGIWGPQAAQVTYFGLHSLQHRGOEGAGIISNDNGKLYGYRNVGLLSEVFKNQSELDNLNTGNAIGHVRYATAGSADIRNI
QPFLYKFHDGQFALCHNGNLTNAISSRKELEKQGAIFNASSDTEILMHLIRRSHNPSFMGVKEALSTVKGFFAYLLMATEDKLIAALDPNAFRPLS
IQMQMONGAWVISSETCAFEEVGAKWVRDVEPGEVILIDDGQIQCDRYDDETQLAICSMEVYVFARPDSTIHGVNVHTARKNMGKRLAQEFKQDADI
VIGVPNSLSSAAMGFAEESGLPNEMGLVKNQYTQRTFIQPTQELREQVRMKLSAVSGVVKGKRVVMIDDSIVRGTSRIVGLLREAGATEVHVA
IASPELKYPFCYGIQDITRRELISANHSDEVCDIIGADSLTYLSIDGLIKSIGLETKAPNGGLCVAYFDGHYPTPLYDYEYRLSLEEKTSFYI
QKVK

SEQ ID 973

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TCAAATGACAATGGGAACTCTATGGTTATCGAAATGTTGGCTCTTCTGAAGTTAAAGATCAATCTGAATTAGATAATTAAACTGGGAAT
GCGGCTATTGGACATGTCGTACTGCAGGTTCTGCAGATATTGCAATTACGCTTTCTTATAAAATTCTGACGGCAATTGCT
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CTGGATGGGTGATTGAATCAATTGGACTCGAAACAAAGCACCAATGGTGGTTATGCTGAGCTTACTTGATGGCATTATCCAACACCGCTT
TATGATTATGAAAGAAGAATACCTCAGAAGTTAGAAGAGAAAAGTTTATATTCAAAAGTGAAG

SEQ ID 974

LCEKLSIFALLDSLIEVKSLNEECVFGIWGPQAAQVTYFGLHSLQHRGOEGAGIISNDNGKLYGYRNVGLLSEVFKNQSELDNLNTGNAIGHVRYATAGSADIRNI
QPFLYKFHDGQFALCHNGNLTNAISSRKELEKQGAIFNASSDTEILMHLIRRSHNPSFMGVKEALSTVKGFFAYLLMATEDKLIAALDPNAFRPLS
MTENKLIAALDPNAFRPLSIQMQMONGAWVISSETCAFEEVGAKWVRDVEPGEVILIDDGQIQCDRYDDETQLAICSMEVYVFARPDSTIHGVNVHT
ARKNMGKRLAQEFKQDADIVIGVPNSLSSAAMGFAEESGLPNEMGLVKNQYTQRTFIQPTQELREQVRMKLSAVSGVVKGKRVVMIDDSIVRGTT
SRIVGLLREAGASEVHVAIASPELKYPFCYGIQDITRRELISANHSDEVCDIIGADSLTYLSIDGLIKSIGLETKAPNGGLCVAYFDGHYPTPLYDYEYRLSLEEKTSFYI
QKVK

SEQ ID 975

GTGAAGGCCAGGTTAGATAGAAATTGCTATCTTGACAGAAGCGAGCTAACGTATCTTCCGCCGTATTGGTATTGGGAGTCATTGAGACT
AAGGTTCAATGGCTAGCT

SEQ ID 976

MKARLDRNSLSFERSELNRIFPPYWYLGVIETKVQWLA

SEQ ID 977

TTGCGGCTGTCGCTGTCACACCGAAAGCTACCAAGGTTGGTACTGTCATTCTCGAAAGTACCAAGACATAGAGTCCTTACGCCGATT
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SEQ ID 978

MRLSAVVTPKATVGGTVNSSKVPDIESLPPIDGKPN

SEQ ID 979

TTGGGCTTACTGAAATCTCAATTTCAGACGTCCTCTTCTGAGTCGCTCCCTGTGGACTTGGTATCTTATATGAATAACGTATTGGT
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CCAACAGAAATTGAGGCCATTGGTGGAGCGGACTTGTATGCTGCTGCACTTGTGACCCATTGTCAGGACGTTACGTTTATCAGGCTATG
CGTATTCTGGCGCAGGAGATATCAGCAGTCCGATTGCGAAACACGTGCTGGTAAATTGCCACACAGGTTATTCTAAGACTGCGGCCACGGC
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